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## OM protein - protein search, using sw model

Run on: July 26, 2005, 09:09:56 ; Search time 20.0758 Seconds  
(without alignments)  
394.147 Million cell updates/sec

Title: US-10-027-725A-12  
Perfect score: 549  
Sequence: 1 ELTQSPSSVSASVGDRTVITR.....QANSPFYFGQTKVEIKR 106

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTCUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518	94.4	233	US-08-812-586-45	Sequence 45, Appl
2	518	94.4	233	US-09-535-832A-42	Sequence 42, Appl
3	475	86.5	236	US-09-859-053-30	Sequence 30, Appl
4	466	84.9	109	US-07-934-373C-3	Sequence 3, Appl
5	466	84.9	109	US-08-437-642B-3	Sequence 3, Appl
6	466	84.9	109	US-08-146-206C-3	Sequence 3, Appl
7	466	84.9	109	US-09-705-686-3	Sequence 3, Appl
8	466	84.9	109	US-09-705-392A-3	Sequence 3, Appl
9	466	84.9	109	US-09-705-398-3	Sequence 3, Appl
10	466	84.9	109	PCT-US93-07832-3	Sequence 3, Appl
11	463	84.3	107	US-09-240-274-40	Sequence 40, Appl
12	460	83.8	107	US-08-276-852-104	Sequence 104, App
13	460	83.8	107	US-08-899-575-104	Sequence 104, App
14	460	83.8	107	US-08-899-575-104	Sequence 104, App
15	460	83.8	107	PCT-US95-08743-104	Sequence 104, App
16	460	83.8	108	US-08-974-899-3	Sequence 3, Appl
17	460	83.8	108	US-09-795-798-3	Sequence 3, Appl
18	459	83.6	128	US-08-259-372A-14	Sequence 14, Appl
19	459	83.6	128	US-08-468-671-14	Sequence 14, Appl
20	457	83.2	107	US-08-276-852-84	Sequence 84, Appl
21	457	83.2	107	US-08-899-575-84	Sequence 84, Appl
22	457	83.2	107	US-08-899-575-84	Sequence 84, Appl
23	457	83.2	107	US-09-240-274-175	Sequence 175, App
24	457	83.2	107	US-09-240-274-176	Sequence 176, App
25	457	83.2	107	PCT-US95-08743-84	Sequence 84, Appl
26	456	83.1	107	US-09-240-274-156	Sequence 156, Appl
27	456	83.1	109	US-09-157-370-3	Sequence 3, Appl

28	455	82.9	107	US-07-934-373C-18	Sequence 18, Appl
29	455	82.9	107	US-08-437-642B-18	Sequence 18, Appl
30	455	82.9	107	US-08-146-206C-18	Sequence 18, Appl
31	455	82.9	107	US-09-648-067A-14	Sequence 14, Appl
32	455	82.9	107	US-09-705-686-18	Sequence 18, Appl
33	455	82.9	107	US-09-705-392A-18	Sequence 18, Appl
34	455	82.9	107	US-09-705-398-18	Sequence 18, Appl
35	455	82.9	107	PCT-US93-07832-18	Sequence 18, Appl
36	454	82.7	109	US-09-025-7698-28	Sequence 28, Appl
37	454	82.7	109	US-09-025-7698-43	Sequence 43, Appl
38	454	82.7	109	US-09-490-070A-28	Sequence 28, Appl
39	454	82.7	109	US-09-490-070A-43	Sequence 43, Appl
40	454	82.7	109	US-09-490-153-28	Sequence 28, Appl
41	454	82.7	109	US-09-490-153-43	Sequence 43, Appl
42	454	82.7	109	US-09-490-324-28	Sequence 28, Appl
43	454	82.7	109	US-09-490-324-43	Sequence 43, Appl
44	453	82.5	108	US-08-652-816A-4	Sequence 4, Appl
45	452	82.3	107	US-08-276-852-105	Sequence 105, App

## ALIGNMENTS

RESULT 1  
US-08-812-586-45  
Sequence 45, Application US/08812586  
Patent No. 6048704  
GENERAL INFORMATION:  
APPLICANT: Martin David Tilson  
TITLE OF INVENTION: PRIORITD AND RECOMBINANT ANTIGENIC  
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)  
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/812,586  
FILING DATE: 07-MAR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/53862-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 233 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-812-586-45

Query Match 94.4%; Score 518; DB 3; Length 233;  
Best Local Similarity 96.2%; Pred. No. 4.1e-41;  
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITICRASQGISWTATYQHPGRAPKLLITYSASSLSGCVSRF 60  
DB 23 ELTQSPSSVSASVGDRTVITICRASQGISWTATYQHPGRAPKLLITYSASSLSGCVSRF 82

Oy 61 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTFGGTVEIKR 106  
Db 83 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTFGGTVEIKR 128

## RESULT 2

US-09-535-832A-42  
; Sequence 42, Application US/09535832A  
; Patent No. 6537769  
; GENERAL INFORMATION:  
; APPLICANT: Tilson, Martin David  
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated  
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and  
; TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof  
; FILE REFERENCE: 53862-AZ  
; CURRENT APPLICATION NUMBER: US/09/535, 832A  
; CURRENT FILING DATE: 2000-03-28  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 42  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-535-832A-42

Query Match 94.4%; Score 518, DB 4; Length 233;  
Best Local Similarity 96.2%; Pred. No. 4.1e-41;  
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ELTQSPSSVASVGDRTVITTCRASQGISLWAWOHQPKKLLIYASASSLQSGVPSRF 60  
Db 23 ELTQSPSSVASVGDRTVITTCRASQGISLWAWOHQPKKLLIYASASSLQSGVPSRF 82  
Oy 61 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTFGGTVEIKR 106  
Db 83 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTFGGTVEIKR 128

## RESULT 3

US-09-859-053-30  
; Sequence 30, Application US/09859053  
; Patent No. 6803039  
; GENERAL INFORMATION:  
; APPLICANT: Tsuji, Takashi  
; APPLICANT: Tezuka, Katsunari  
; APPLICANT: Horii, No. 6803039uaki  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIN AND  
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF  
; FILE REFERENCE: 06501-079001  
; CURRENT APPLICATION NUMBER: US/09/859, 053  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: JP 2001-99508  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-147116  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-859-053-30

Query Match 86.5%; Score 475; DB 4; Length 236;  
Best Local Similarity 88.7%; Pred. No. 4.4e-37;  
Matches 94; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Oy 1 ELTQSPSSVASVGDRTVITTCRASQGISLWAWOHQPKKLLIYASASSLQSGVPSRF 60  
Db 25 ELTQSPSSVASVGDRTVITTCRASQGISLWAWOHQPKKLLIYASASSLQSGVPSRF 84  
Oy 61 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTFGGTVEIKR 106

Db 85 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTFGGTVEIKR 130

## RESULT 4

US-07-934-373C-3  
; Sequence 3, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-07-934-373C-3

Query Match 84.9%; Score 466; DB 2; Length 109;  
Best Local Similarity 84.9%; Pred. No. 1.3e-36;  
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Oy 1 ELTQSPSSVASVGDRTVITTCRASQGISLWAWOHQPKKLLIYASASSLQSGVPSRF 60  
Db 3 ELTQSPSSVASVGDRTVITTCRASQGISLWAWOHQPKKLLIYASASSLQSGVPSRF 62  
Oy 61 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTFGGTVEIKR 106  
Db 63 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTFGGTVEIKR 108

## RESULT 5

US-08-437-642B-3  
; Sequence 3, Application US/08437642B  
; Patent No. 6034297  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.

Query Match 86.5%; Score 475; DB 4; Length 236;  
Best Local Similarity 88.7%; Pred. No. 4.4e-37;  
Matches 94; Conservative 5; Mismatches 7; Indels 0; Gaps 0;



STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437, 642B  
FILING DATE: 09-May-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-437-642B-3

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Query Match          84.9%; Score 466; DB 3; Length 109;
Best Local Similarity 84.9%; Pred. No. 1,3e-36;
Matches    90; Conservative   9; Mismatches   7; Indels    0; Gaps    0;

Qy      1 ELTSPSSVASVGDRTVTITCRASGGISLWAMYOHGPKAPKLLIYASSLSQGVPSRF 60
       ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      3 QMTSPSSLASVGDRTVTITCRASQDVSVSYLAWYQKGKAPKLLIYASSLSGVPSEF 62
       ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy      61 SGSGVGDFSLTIISSLOPEDSATYYCCOANSFPYFGGTVEIKR 106
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      63 SGSGSGTDFTLTIISSLOPEDPATYYCQYNLSPLYFGGTVEIKR 108
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 6
US-08-146-206C--3
Sequence 3, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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1      SOFTWARE: WinPatIn (Genentech)
2      CURRENT APPLICATION DATA:
3      APPLICATION NUMBER: US/08/146,206C
4      FILING DATE: 17-No. 6407213-1993
5      CLASSIFICATION: 530
6      PRIOR APPLICATION DATA:
7      APPLICATION NUMBER: 07/715272
8      FILING DATE: 14-JUN-1991
9      ATTORNEY/AGENT INFORMATION:
10     NAME: Lee, Wendy M.
11     REGISTRATION NUMBER: 40,378
12     REFERENCE/DOCKET NUMBER: P0709P1
13     TELECOMMUNICATION INFORMATION:
14     TELEPHONE: 650/225-1994
15     TELEFAX: 650/952-9881
16     INFORMATION FOR SEQ ID NO: 3:
17     SEQUENCE CHARACTERISTICS:
18     LENGTH: 109 amino acids
19     TYPE: Amino Acid
20     TOPOLOGY: Linear
21
22     US-08-146-206C-3

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Query Match	84.9%	Score 466	DB 4	Length 109
Best Local Similarity	84.9%	Pred. No. 1.3e-36		
Matches	90	Conservative	9	Mismatches 7
			Indels	0
			Gaps	0
Qy	1	ELTSPSSVSAVSDRVTTTCRAAQGISMWLAHYQHOGKAPKLLIYSASSLSQGSVSRF	60	
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Db	3	QMTSPSSLSASVSDRVTTTCRAQDVSSSIAMVQOKRGPAPKLLITLAASSLSBGVSRF	62	
Qy	61	SGSGCYGDFSLTTSLSLQFEDSATYYCOQANSFPYFGQGTVEIKR	106	
	:::     :	:::     :	:::     :	
Db	63	SGSGSGDFTLTISLQEPEDPATYYCOQNSLPFTFGQGTVEIKR	108	

RESULT 7  
 US-09-705-686-3  
 Sequence 3, Application US/09705686  
 Patent No. 6639055  
 GENERAL INFORMATION:  
 APPLICANT: Carter, Paul J.  
 Presta, Leonard G.  
 TITLE OF INVENTION: Method for Making Humanized Antibodies  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winpatin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/705,686  
 FILING DATE: 02-No. 6639055-2000  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/146206  
 FILING DATE: 17-NOV-1993  
 APPLICATION NUMBER: 07/715272  
 FILING DATE: 14-JUN-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee, Wendy M.  
 REGISTRATION NUMBER: 40,378  
 REFERENCE/DOCKET NUMBER: P0709P1D3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1994  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-705-686-3

Query Match 84.9%; Score 466; DB 4; Length 109;  
Best Local Similarity 84.9%; Pred. No. 1.3e-36;  
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTOSPSVASVGDRTYITTCRASQGISWLAWYOHOPGKAPKLLIYASASSLOGVPSRF 60  
Db 3 QMTQSPSSLSASVDRTYITTCRASQDVSSYLAWYQKRGKAPKLLIYAASSLSSGVPSRF 62

Qy 61 SSGSGYTDPSLTISLQFEDSATYTCQANSFPYTFGGTKVEIKR 106  
Db 63 SSGSGYTDFTLTISLQPEDPATYTCQVNSLPYTFGGTKVEIKR 108

RESULT 8  
US-09-705-392A-3  
; Sequence 3, Application US/09705392A  
; Patent No. 6719971  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; PRESTEA, Leonard G.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/705,392A  
; FILING DATE: 02-Nov. 6719971-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/146206  
; FILING DATE: 17-Nov-1993  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-705-392A-3

Query Match 84.9%; Score 466; DB 4; Length 109;  
Best Local Similarity 84.9%; Pred. No. 1.3e-36;  
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTOSPSVASVGDRTYITTCRASQGISWLAWYOHOPGKAPKLLIYASASSLOGVPSRF 60  
Db 3 QMTQSPSSLSASVDRTYITTCRASQDVSSYLAWYQKRGKAPKLLIYAASSLSSGVPSRF 62

Qy 61 SSGSGYTDPSLTISLQFEDSATYTCQANSFPYTFGGTKVEIKR 106  
Db 63 SSGSGYTDFTLTISLQPEDPATYTCQVNSLPYTFGGTKVEIKR 108

RESULT 9  
US-09-705-398-3  
; Sequence 3, Application US/09705398  
; Patent No. 6800738  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; PRESTEA, Leonard G.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/705,398  
; FILING DATE: 02-Nov. 6800738-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/146206  
; FILING DATE: 17-Nov-1993  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P1D2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-705-398-3

Query Match 84.9%; Score 466; DB 4; Length 109;  
Best Local Similarity 84.9%; Pred. No. 1.3e-36;  
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTOSPSVASVGDRTYITTCRASQGISWLAWYOHOPGKAPKLLIYASASSLOGVPSRF 60  
Db 3 QMTQSPSSLSASVDRTYITTCRASQDVSSYLAWYQKRGKAPKLLIYAASSLSSGVPSRF 62

Qy 61 SSGSGYTDPSLTISLQFEDSATYTCQANSFPYTFGGTKVEIKR 106  
Db 63 SSGSGYTDFTLTISLQPEDPATYTCQVNSLPYTFGGTKVEIKR 108

RESULT 10  
PCT-US93-07832-3  
; Sequence 3, Application PC/TUS9307832  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd

CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07832  
FILING DATE: 19930820  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 709P2PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE:  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-07832-3

Query Match 84.9%; Score 466; DB 5; Length 109;  
Best Local Similarity 84.9%; Pred. No. 1.3e-36;  
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAVSDRVITTCRASQGISWLMWYOHQPGKAPKLLIYASASSLQSGVPSRF 60  
Db 3 QMTQSPSSLSASVGDRTVITTCRASQDVSYLAWYQQRKPKLLIYAAASSLQSGVPSRF 62

QY 61 SSGSGYTDFTLTISLQPEDSATYTCQANSFYTTGGGTVKIKR 106  
Db 63 SSGSGYTDFTLTISLQPEDSATYTCQANSFYTTGGGTVKIKR 108

RESULT 11  
US-09-240-274-40  
Sequence 40, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 40  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain 109

US-09-240-274-40  
Query Match 84.3%; Score 463; DB 3; Length 107;  
Best Local Similarity 85.8%; Pred. No. 2.5e-36;  
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAVSDRVITTCRASQGISWLMWYOHQPGKAPKLLIYASASSLQSGVPSRF 60  
Db 2 ELTQSPSSLSASVGDRTVITTCRASQGISWLMWYQQRKPKLLIYAAASSLQSGVPSRF 61

QY 61 SSGSGYTDFTLTISLQPEDSATYTCQANSFYTTGGGTVKIKR 106  
Db 62 SSGSGYTDFTLTISLQPEDSATYTCQANSFYTTGGGTVKIKR 107

RESULT 12  
US-08-276-852-104  
Sequence 104, Application US/08276852  
Patent No. 5652138  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESS: Patent Counsel  
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,852  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCR1452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-852-104

Query Match 83.8%; Score 460; DB 1; Length 107;  
Best Local Similarity 85.8%; Pred. No. 4.8e-36;  
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAVSDRVITTCRASQGISWLMWYOHQPGKAPKLLIYASASSLQSGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITTCRASQGISWLMWYQQRKPKLLIYAAASSLQSGVPSRF 60

QY 61 SSGSGYGFSLTISLQPEDSATYTCOQANSFYTFGGTKEIKR 106  
Db 61 SSGSGYGFSLTISLQPEDPATYTCOQSYSTPYTFGGTKEIKR 106

## RESULT 13

US-08-899-575-104  
; Sequence 104, Application US/08899575  
; Patent No. 5770440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCRI452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

Query Match 83.8%; Score 460; DB 1; Length 107;  
Best Local Similarity 85.8%; Pred. No. 4.8e-36;  
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSNASVGDRTYITTCRASQGISISLWAMYOHQPGKAPKLLIYSASSLSQGVSRF 60  
Db 1 ELTQSPSSLSASVSDRTYITTCRASQGISISLWAMYQKPGKAPKLLIYVAASLSQGVSRF 60  
QY 61 SSGSGYGFSLTISLQPEDSATYTCOQANSFYTFGGTKEIKR 106  
Db 61 SSGSGYGFSLTISLQPEDPATYTCOQSYSTPYTFGGTKEIKR 106

## RESULT 14

US-08-899-575-104  
; Sequence 104, Application US/08899575

; Patent No. 5804440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCRI452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

Query Match 83.8%; Score 460; DB 1; Length 107;  
Best Local Similarity 85.8%; Pred. No. 4.8e-36;  
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSNASVGDRTYITTCRASQGISISLWAMYOHQPGKAPKLLIYSASSLSQGVSRF 60  
Db 1 ELTQSPSSLSASVGDRTYITTCRASQGISISLWAMYQKPGKAPKLLIYVAASLSQGVSRF 60  
QY 61 SSGSGYGFSLTISLQPEDSATYTCOQANSFYTFGGTKEIKR 106  
Db 61 SSGSGYGFSLTISLQPEDPATYTCOQSYSTPYTFGGTKEIKR 106

## RESULT 15

PCT-US95-08743-104  
; Sequence 104, Application PC/TUS9508743  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08743  
FILING DATE: 11-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULAR TYPE: protein  
PCT-US95-08743-104

Query Match 83.8%; Score 460; DB 5; Length 107;  
Best Local Similarity 85.8%; Pred. No. 4.8e-36;  
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy	1	ELTQSPSSVSAVGDRTVITCRASOGISWLAWYOHQKAPKLLIYSASSLSGVP	SRF	60
Db	1	ELTQSPSSLSASVGDRTVITCRASOSISYLNWYQKRGAPKLLIYAASSLSG	VPSRF	60
Qy	61	SGSGGTDFSLTISLQFEDSATYCCQANSFYTFGQGTKEIKR		106
Db	61	SGSGSGTDFLTITSLQPEDFATYCCQSYSTPYTFGQGTKEIKR		106

Search completed: July 26, 2005, 09:30:02  
Job time: 21.0758 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 09:07:26 ; Search time 13.6515 Seconds  
(without alignments)  
747.095 Million cell updates/sec

Title: US-10-027-725A-12

Sequence: 1 ELTQSPSSVSASVGDVRLTIR.....QQANSFYTFGGTKEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:.\*  
2: PIR1:.\*  
3: PIR2:.\*  
4: PIR3:.\*  
5: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	84.2	117	2	S46376 Ig kappa chain V-J
2	462	84.2	125	2	S40316 Ig kappa chain - h
3	459	83.6	125	2	S40333 Ig kappa chain V-J
4	455	82.9	125	2	S40336 Ig kappa chain V-J
5	454.5	82.8	124	2	S40336 Ig kappa chain V-J
6	454	82.7	130	2	S40368 Ig kappa chain - h
7	451	82.1	128	2	S46372 Ig kappa chain var
8	451	82.1	131	2	S40352 Ig kappa chain V-J
9	450	82.0	105	2	S36266 Ig kappa chain V
10	447	81.4	127	2	S40367 Ig kappa chain V-J
11	446	81.2	108	2	S19674 Ig kappa chain V r
12	445	81.2	132	2	S38646 Ig kappa chain V r
13	445	81.1	117	2	S46371 Ig kappa chain V-J
14	444	80.9	123	2	S40331 Ig kappa chain - h
15	444	80.9	132	2	S40334 Ig kappa chain - h
16	443	80.7	108	2	S49047 Ig kappa chain V r
17	441	80.3	108	2	S47182 Ig kappa chain - h
18	441	80.3	109	2	S31998 Ig kappa chain - h
19	441	80.3	124	2	S40318 Ig kappa chain V r
20	439.5	80.1	108	2	S30521 Ig kappa chain V r
21	439	80.0	129	2	S40369 Ig kappa chain V r
22	437	79.6	107	2	S36264 Ig kappa chain - h
23	435.5	79.3	108	2	S34007 Ig kappa chain V r
24	435	79.2	108	1	K1HUBN Ig kappa chain V-I
25	434.5	79.1	107	2	S36275 Ig kappa chain V
26	434	79.1	108	1	K1HUMS Ig kappa chain V-I
27	434	79.1	108	2	S44122 Ig kappa chain V r
28	433	78.9	117	2	S21527 Ig kappa chain pre
29	432	78.7	108	2	S36283 Ig lambda chain V

30	431.5	78.6	107	2	S47183 Ig kappa chain - h
31	431	78.5	107	2	S36262 Ig lambda chain V
32	428	78.0	107	2	S36269 Ig lambda chain V
33	427	77.8	109	2	S31981 Ig kappa chain - h
34	426.5	77.7	107	1	K1HUMR Ig kappa chain V-I
35	426	77.6	108	2	S36277 Ig lambda chain V
36	426	77.6	109	2	S31979 Ig kappa chain - h
37	426	77.6	110	2	PN0535 Ig kappa chain V r
38	426	77.6	122	2	S40370 Ig kappa chain - h
39	426	77.6	141	2	A49334 Ig kappa chain V-I
40	424	77.2	107	2	I69017 anti-HIV envelope
41	424	77.2	108	1	K1HUME Ig kappa chain V-I
42	424	77.2	129	1	K1HUMK Ig kappa chain pre
43	423	77.0	108	1	K1HUGL Ig kappa chain V-I
44	423	77.0	108	1	K1HURU Ig kappa chain V-I
45	423	77.0	126	2	S40335 Ig kappa chain V-J

## ALIGNMENTS

RESULT 1  
S46376  
Ig kappa chain V-J region (713-14) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000  
C:Accession: S46376, S38649  
R:Benjamin, C.; Chastagner, P.; Zouali, M.  
EMBO J. 13, 2951-2962, 1994  
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination  
A:Accession: S46369, MUID:94313975, PMID:8039491  
A:Molecule type: mRNA  
A:Residues: 1-117 <BEN>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:25-99/Domain: immunoglobulin homology <IMV>

Query Match 84.2%; Score 462; DB 2; Length 117;  
Best Local Similarity 84.9%; Pred. No. 2.5e-32;  
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Oy 1 ELTQSPSSVSASVGDVRLTIRASQGISMLAWYQHGKAPKLLIYSASLSQGVPERF 60  
Db 12 QMTQSPSSVSASISGRVLTICRASQDISMLAWIQGKAPKLLIYASLSQGVPLRF 71

Oy 61 SGSGVGTDFSLTISLQFEDSATYCCOANSFPYTFGGTKEIKR 106  
Db 72 SGSGSGTDFLTITISLQPEPATYCCOANSFPRGFGTKEIKR 117

RESULT 2  
S40316  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40316  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312, MUID:94080891, PMID:8258341  
A:Accession: S40316  
A:Status: Preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-125 <KLE>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:31-105/Domain: immunoglobulin homology <IMV>

Query Match 84.2%; Score 462; DB 2; Length 125;  
Best Local Similarity 85.8%; Pred. No. 2.7e-32;

Matches 91; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

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Oy 1 ELTQSPSSVSAVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 18 QLTQSPSSVSAVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYHISLSLQGVPSRF 77
Oy 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSPFYTFGGTKVEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 SSGSGYGTDFSLTISLQFEDPATYCCQANSPFLTFGGTKVEIKR 123
```

## RESULT 3

S40333  
Ig kappa chain V-J region - human  
C/Species: Homo sapiens (man)  
C/Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S40333  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MUID:94080891; PMID:8258341  
A/Accession: S40333  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-125 <KLE>  
A/Cross-references: EMBL:X72443; NID:9441354; PIDN:CAAS1111.1; PID:9441355  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 459; DB 2; Length 125;  
Best Local Similarity 82.9%; Pred. No. 4.8e-32;  
Matches 87; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

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Oy 1 ELTQSPSSVSAVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 QMTQSPETLSASVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYKASSLSQGVPSRF 80
Oy 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSPFYTFGGTKVEIKR 105
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 SSGSGYGTDFSLTISLQFEDPATYCCQANSPFYTFGGTKVEIKR 125
```

## RESULT 4

S40349  
Ig kappa chain V-J region - human  
C/Species: Homo sapiens (man)  
C/Date: 19-May-1994 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C/Accession: S40349  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MUID:94080891; PMID:8258341  
A/Accession: S40349  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-125 <KLE>  
A/Cross-references: EMBL:X72459; NID:9441386; PIDN:CAAS1127.1; PID:9441387  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 455; DB 2; Length 125;  
Best Local Similarity 84.9%; Pred. No. 1e-31;  
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

```
Oy 1 ELTQSPSSVSAVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QLTQSPSSVSAVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYDASSLSQGVPSRF 79
Oy 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSPFYTFGGTKVEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 SSGSGYGTDFSLTISLQFEDPATYCCQANSPFYTFGGTKVEIKR 125
```

RESULT 5  
S40336  
Ig kappa chain V-J region - human  
C/Species: Homo sapiens (man)  
C/Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S40336  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MUID:94080891; PMID:8258341  
A/Accession: S40336  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-124 <KLE>  
A/Cross-references: EMBL:X72446; NID:9441360; PIDN:CAAS1114.1; PID:9441361  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/31-105/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 454.5; DB 2; Length 124;  
Best Local Similarity 84.1%; Pred. No. 1.1e-31;  
Matches 90; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

```
Oy 1 ELTQSPSSVSAVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 18 QLTQSPSSVSAVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYAASTLSQGVPSRF 77
Oy 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSPFYTFGGTKVEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 SSGSGYGTDFSLTISLQFEDPATYCCQANSPFYTFGGTKVEIKR 124
```

## RESULT 6

S40368  
Ig kappa chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S40368  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MUID:94080891; PMID:8258341  
A/Accession: S40368  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-130 <KLE>  
A/Cross-references: EMBL:X72478; NID:9441424; PIDN:CAAS1146.1; PID:9441425  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 82.7%; Score 454; DB 2; Length 130;  
Best Local Similarity 83.0%; Pred. No. 1.3e-31;  
Matches 88; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

```
Oy 1 ELTQSPSSVSAVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QMTQSPETLSASVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYAASTLSQGVPSRF 79
Oy 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSPFYTFGGTKVEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 SSGSGYGTDFSLTISLQFEDPATYCCQANSPFYTFGGTKVEIKR 125
```

## RESULT 7

S46372  
IG light chain variable region (VJ) - human  
C/Species: Homo sapiens (man)  
C/Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C/Accession: S46372  
R/Bensimon, C.; Chastagner, P.; Zouali, M.



EMBO J. 13, 2951-2962, 1994  
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination  
A:Reference number: S46369; MUID:94313975; PMID:8035491  
A:Accession: S46372  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-128 <BEN>  
A:Cross-references: EMBL:Z27173  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 451; DB 2; Length 128;  
Best Local Similarity 83.8%; Pred. No. 2.3e-31;  
Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 2 LTQSPSSVSAVGDRVITTCRASQGISSWLAWYQHOPKAPKLLIYASASSIQGVPSPRS 61  
Db 24 ITQSPSSLSAAGDRVITTCRASQGISSWLAWYQOKPKAPKLLIYASTLIQSGVPSRS 83  
62 GSGVGTDPSSLTISLQFEDSATYTCQANSPPYTFGGGTKEIKR 106  
Db 84 GSGSGTDPSSLTISLQFEDSATYTCQAYSPYTFGGGTKEIKR 128

RESULT 8  
S40352  
Ig kappa chain V-J-C region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40352  
R:Klein, R.; Uenichen, R.; Zachau, H.G.  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40352  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-131 <KLE>  
A:Cross-references: EMBL:X72462; NID:G441392; PIDN:CAAS1130.1; PID:G441393  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterodimer; immunoglobulin  
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 451; DB 2; Length 131;  
Best Local Similarity 83.0%; Pred. No. 2.4e-31;  
Matches 88; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSAVGDRVITTCRASQGISSWLAWYQHOPKAPKLLIYASASSIQGVPSPRS 60  
Db 23 QMTQSPSSLSAAGDRVITTCRASQGISSWLAWYQOKPKAPKLLIYASTLIQSGVPSRS 82  
61 GSGVGTDPSSLTISLQFEDSATYTCQANSPPYTFGGGTKEIKR 106  
Db 83 GSGSGTDPSSLTISLQFEDSATYTCQAYSPYTFGGGTKEIKR 128

RESULT 9  
S36266  
Ig lambda chain V region (clone alpha-TNF-E1) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C:Accession: S36266  
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36255; MUID:93178448; PMID:7679990  
A:Accession: S36266  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-105 <GRI>  
A:Cross-references: EMBL:Z18840; NID:G33423; PIDN:CAA79292.1; PID:G939916  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F.16-90/Domain: immunoglobulin homology <IMM>

Query Match      82.0%; Score 450; DB 2; Length 105;  
Best Local Similarity 85.3%; Pred. No. 2,3e-31;  
Matches 87; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy      2 LTGSPSSVASVAGDRVTITTCRASOGISSWLAWYOHOPGKAPKLIIYSASSLSQGVPSPRF 61  
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
Db      4 LTGSPSSVASVAGDRVTITTCRASOGIRSWLAWYOHOPGKAPKLIIYAASLTLETGVSPSRFS 63

Qy      62 GSAGYGFSLTITSSLQPEDSATFYCCOANSFPPTFGCGTKVE 103  
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
Db      64 GSGSGDTFTLTITSSLQPEDFATFYCCOANSFPLTFGGCTKLE 105

RESULT 10  
S40367  
Ig kappa chain V-J-C region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40367  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; PMID:94080891; PMID:8258341  
A:Accession: S40367  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-127 <KLE>  
A:Cross-references: EMBL:X72477  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F.13-107/Domain: immunoglobulin homology <IMM>

Query Match      81.4%; Score 447; DB 2; Length 127;  
Best Local Similarity 82.1%; Pred. No. 5e-31;  
Matches 87; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Qy      1 ELTPSPSSVASVAGDRVTITTCRASOGISSWLAWYOHOPGKAPKLIIYSASSLSQGVPSPRF 60  
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
Db      20 QMTQSSTSLIASVAGDRVTITTCRASOGISNLTWYORPKGAPKLIIYAASSLSQGVPSPRF 79

Qy      61 SGSGYGTDFSLTITSSLQFEDSATFYCCOANSPPYTFGCGTKVEIKR 106  
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
Db      80 SGSGSGTDFTLTITSSLQPEDFATFYCCOANSYNTPTWTFGCGTKVEIKR 125

RESULT 11  
S19674  
Ig kappa chain V region (clone alpha-TEU9) - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
C:Accession: S19674  
R:Harks, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,  
J. Mol. Biol. 222, 581-597, 1991  
A>Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage.  
A:Reference number: S19663; PMID:92085276; PMID:1748994  
A:Accession: S19674  
A:Molecule type: mRNA  
A:Residues: 1-108 <VAR>  
A:Cross-references: EMBL:X61642; NID:g37860; PIDN:CA443823.1; PID:g1335386  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F.16-90/Domain: immunoglobulin homology <IMM>

Query Match      81.2%; Score 446; DB 2; Length 108;  
Best Local Similarity 82.9%; Pred. No. 5.2e-31;  
Matches 87; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy      2 LTPSPSSVASVDRTYTITTCRASOGISSWLAWYOHOPGKAPKLIIYSASSLSQGVPSPRF 61  
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
Db      4 LTPSPSSLASVDRYTITTCRASOGISNLTWYOHOPGKAPKLIIYAASLTLETGVSPSRFS 63



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 26, 2005, 08:52:21 ; Search time 66.6515 Seconds

(without alignments)  
814.391 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549  
Sequence: 1 ELTGSPSSVASVGDVRLTIF.....QQANSPFYFGGQTKVEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: Uniprot 03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	88.0	236	2	O6GMX8
2	444	80.9	236	2	O6GMW1
3	443	80.7	236	2	O6PIH7
4	437	79.6	108	2	O9UL70
5	437	79.6	108	2	O9UL77
6	435	79.2	108	1	KV1V_HUMAN
7	434	79.1	108	1	KV1S_HUMAN
8	434	79.1	108	2	O9UL79
9	429	78.1	236	2	O6GMX9
10	427	77.8	244	2	O65ZC8
11	426.5	77.7	107	2	KV1D_HUMAN
12	426.5	77.7	107	2	O96SA9
13	426	77.6	234	2	O7Z473
14	425	77.4	236	2	O7Z3Y4
15	424	77.2	108	1	KV1R_HUMAN
16	424	77.2	236	2	KV1W_HUMAN
17	424	77.2	236	2	O6PIT5
18	423	77.0	108	1	KV1G_HUMAN
19	423	77.0	108	1	KV1H_HUMAN
20	423	77.0	240	2	O65ZC9
21	419	76.3	108	1	KV1F_HUMAN
22	419	76.3	108	1	KV1L_HUMAN
23	416	75.8	108	1	KV1O_HUMAN
24	416	75.8	236	2	O6GMX0
25	416	75.8	236	2	O6PIH4
26	413	75.2	108	1	KV1B_HUMAN
27	411.5	75.0	107	2	O9UL81
28	410	74.7	108	1	KV1M_HUMAN
29	408	74.3	108	1	KV1E_HUMAN
30	406	74.0	108	1	KV1A_HUMAN
31	405	73.8	108	1	KV1P_HUMAN

32	402	73.2	117	1	KV1I_HUMAN	P01601 homo sapien
33	401	73.0	108	1	KV1N_HUMAN	P01606 homo sapien
34	401	73.0	108	1	KV1Y_HUMAN	P80362 homo sapien
35	394	71.8	117	1	KV1J_HUMAN	P01602 homo sapien
36	393	71.6	108	1	KV1C_HUMAN	P01595 homo sapien
37	391	71.2	108	1	KV1K_HUMAN	P01603 homo sapien
38	385	70.1	108	1	KV1Q_HUMAN	P01609 homo sapien
39	385	70.1	129	1	KV1X_HUMAN	P04432 homo sapien
40	383	69.8	108	1	KV5S_MOUSE	P01652 mus musculus
41	382	69.6	108	2	O9UL83	O9UL83 homo sapien
42	380	69.2	108	1	KV5Q_MOUSE	P01650 mus musculus
43	376	68.5	108	1	KV5T_MOUSE	P01653 mus musculus
44	374	68.1	236	2	O7ES98	O7ES98 mus musculus
45	373	67.9	108	1	KV5K_MOUSE	P01644 mus musculus

## ALIGNMENTS

RESULT 1  
O6GMX8 PRELIMINARY; PRT; 236 AA.  
AC O6GMX8;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Bask S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,  
RA Roha S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Kravynetski M.I., Skalska U., Smalins D.B., Scherch A., Schein J.B.,  
RA Jones S.J., Maira M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073764; AAH73764.1; -  
DR InterPro; IPR003599; IG-  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG-MHC.  
DR InterPro; IPR003596; IG-V.  
DR Pfam; PF00654; CI-set; I.  
DR Pfam; PF00047; IG-2;  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IG; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.

Query Match	88.0%	Score 483;	DB 2;	Length 236;
Best Local Similarity	87.7%;	Pred. No. 7.5e-41;		
Matches 93;	Conservative	8;	Mismatches 5;	Indels 0;
				Gaps 0;
QY	1	ELTQSPSSVSAVSGDRTVITTCRASGIGISMTLAWYOHQKAKPKLITYSASSLSQGVPSRF	60	
Db	25	QMTQSPSSVSAVSGDRTVITTCRASGIGISMTLAWYOHQKAKPKLITYSASSLSQGVPSRF	84	
QY	61	SGSGYGTDFSLTISLSQFEDSATYTCQQAHPPTFGGTQVKEIKR	106	
Db	85	SGSGYGTDFSLTISLSQFEDSATYTCQQAHPPTFGGTQVKEIKR	130	
RESULT 2				
Q6GMW1	PRELIMINARY;	PRT;	236	AA.
AC	Q6GMW1;			
DT	05-JUN-2004 (TREMBLrel. 27, Created)			
DT	05-JUN-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUN-2004 (TREMBLrel. 27, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.D., Feingold E.A., Grove L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carrincci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,			
RA	Bosak S.A., McEwen P.J., McKernan K.J., Malek J.G., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalobon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smalins D.E., Schermer A., Schein J.E.,			
RT	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RA	Strausberg R.;			
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.			
DR	EMBL, BC073791, AAH73791.1; ..			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG-cl.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG-V.			
DR	Pfam; PF07654, CI-set; I.			
DR	Pfam; PF00047; Ig; 2.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGcl; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS00835; IG_LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 1.			
DR	Hypothetical protein.			
SO	SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;			

Query Match	Best Local Similarity	Matches	80.7%	Score 443;	DB 2;	Length 236;
88; Conservative	87;	Conservative	80.7%;	Score 444;	DB 2;	Length 236;
			82.1%;	Pred. No. 6.8e-37;		
			10;	Mismatches	9;	Indels
						0;
						Gaps
						0;

```
Qy 1 ELTQSPSSVSVASVGDRTVITTCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 QLTQSPSFLSASVGDRTVITTCRASQGISSWLAWYQOKRKGKAPNLLIYAASLTQGVPSRF 84
Qy 61 SSGSGYGFDFSLTISLQPEDSATYCCOQANSFPYTFGGTVEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 SSGSGSGTFDTLTISLQPEDFATYCCOQLNSSPPTFGGTVEIKR 130

RESULT 4
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70
AC Q9UL70;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DE 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
    (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277133; Pubmed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
    fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IBMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCC437 CRC64;

Query Match 79.6%; Score 437; DB 2; Length 108;
Best Local Similarity 80.2%; Pred. No. 1.5e-36;
Matches 85; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSVASVGDRTVITTCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSFLSASVGDRTVITTCRASQGISSWLAWYQOKRKGKAPNLLIYAASLTQGVPSRF 62
Qy 61 SSGSGYGFDFSLTISLQPEDSATYCCOQANSFPYTFGGTVEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGSGTFDTLTISLQPEDVATYCCQKYNASPTFGGTVEIKR 108

RESULT 5
Q9UL77 PRELIMINARY; PRT; 108 AA.
ID Q9UL77
AC Q9UL77;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DE 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
    (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277133; Pubmed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
RA Young D.C.;
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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
    fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR HSSP; P01607; IBMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 79.6%; Score 437; DB 2; Length 108;
Best Local Similarity 81.1%; Pred. No. 1.5e-36;
Matches 86; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSVASVGDRTVITTCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSFLSASVGDRTVITTCRASQGISSWLAWYQOKRKGKAPNLLIYAASLTQGVPSRF 62
Qy 61 SSGSGYGFDFSLTISLQPEDSATYCCOQANSFPYTFGGTVEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGSGTFDTLTISLQPEDFATYCCQSYSTSWTFGGTVEIKR 108

RESULT 6
KVIV HUMAN STANDARD; PRT; 108 AA.
ID KVIV HUMAN
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=6174817; Pubmed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwyer F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR HSSP; P80362; IMTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KM Amyloid; Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1
FT DOMAIN 23
FT DOMAIN 24
FT DOMAIN 34
FT DOMAIN 35
FT DOMAIN 49
FT DOMAIN 50
FT DOMAIN 56
FT DOMAIN 57
FT DOMAIN 88
FT DOMAIN 89
FT DOMAIN 97
FT DOMAIN 98
FT DISULFID 107
FT NON_TER 108
FT SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 79.2%; Score 435; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 2.4e-36;
Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSVASVGDRTVITTCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
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[illegible]

DE MYosin-reactive immunoglobulin light chain variable region  
 (Fragment)  
 OS Homo sapiens (Human)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98271139; PubMed=9614934; DOI=10.1006/clim.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Beney S.M.,  
 RA Young D.C.,  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035035; RAD56271.1; -.  
 DR PIR; S23638; S23638.  
 DR PIR; S30521; S30521.  
 DR PIR; S34090; S34090.  
 DR HSSP; P01607; IBMW.  
 DR Interpro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT TER 108  
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAE CRC64;  
 Query Match 79.1%; Score 434; DB 2; Length 108;  
 Best Local Similarity 81.0%; Pred. No. 3e-36;  
 Matches 85; Conservative 9; Mismatches 11; Indels 0; Gaps 0;  
 QY 2 LTQSPSSVSAVSGRVTITTCRASGCTSSMLAWOHQGRKPKLLIYASLSQGVSPSRFS 61  
 DB 4 MTQSPSLASTGRTVTCRMVSGISSTYLAWYQQRKGAPELLIYASTLQGVSPSRFS 63  
 QY 62 GSGYGTDFSLTISLSIQFEDSATYCCQOANFPFYFGGTKEIKR 106  
 DB 64 GSGSGTDFTLTISLQSEDPATYCCQYYSFPFPFGGTKEIKR 108  
 RESULT 9  
 O6GMX9 PRELIMINARY; PRT; 236 AA.  
 AC O6GMX9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Primary B-Cells;  
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Fellngold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins T.B., Wagner L., Shmaman C.M., Schuler G.D.,  
 RA Altschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jorde H., Moore T., Max S.I., Wang J., Helel F.,  
 RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Faley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalick D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Maitra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Straubeberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073763; AAH73763.1; -  
DR InterPro; IPR003599; Ig\_1.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-ect; 1.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KM Hypothetical protein.  
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFE7 CRC64;  
  
Query Match 78.1%; Score 429; DB 2; Length 236;  
Best Local Similarity 78.3%; Pred. No. 2.2e-35;  
Matches 83; Conservative 9; Mismatches 14; Indels 0; Gaps 0;  
  
QY 1 ELTQSPSSVSVASVGDRTVITCRASQGISSWLAWYOHQPGKAPKLLIYSASSLSQGVPSRF 60  
DB 25 QMTQSPSSLASVGHRTVITCRASQNVSRWLAWYQGRPEKAPKSLIYATSLHSQGVPSRF 84  
QY 61 SGSGYGDPSLTISLQFEDSATYCCOANSFPTFGGTVEIKR 106  
DB 85 SGSGSGDTFTLTISLQPEDPATYCCQYNTFPLTFGGTVEIKR 130  
  
RESULT 10  
Q65ZC8 PRELIMINARY; PRT; 244 AA.  
AC Q65ZC8; 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE Single-chain Fv (Fragment).  
GN Name=scfv;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=97362799; PubMed=9219263;  
RX Kontesmann R.E., Wing M.G., Winter G.;  
RT "Complement recruitment using bispecific diabodies";  
RL Nat. Biotechnol. 15:628-631(1997).  
DR EMBL; Y13057; CAAT3500.1; -  
DR InterPro; IPR003599; Ig\_1.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 2.  
DR SMART; SM00406; Igv; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
FT NON\_TER 1 1  
FT NON\_TER 244 244  
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;  
  
Query Match 77.8%; Score 427; DB 2; Length 244;  
Best Local Similarity 75.5%; Pred. No. 3.7e-35;  
Matches 80; Conservative 13; Mismatches 13; Indels 0; Gaps 0;  
  
QY 1 ELTQSPSSVSVASVGDRTVITCRASQGISSWLAWYOHQPGKAPKLLIYSASSLSQGVPSRF 60

DB 139 QMTQSPSSLASIGDRVITCRASEGYHMLAWYQGRKAPKLLIYSASSLSGAPSRF 198  
QY 61 SGSGYGDPSLTISLQFEDSATYCCOANSFPTFGGTVEIKR 106  
DB 199 SGSGSGDTFTLTISLQPDPAITYCCQYSNPLTFGGTVEIKR 244  
  
RESULT 11  
KVLD HUMAN STANDARD; PRT; 107 AA.  
ID KVLD HUMAN  
AC P01596;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-I region CAR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75075135; PubMed=4216454;  
RA Milstein C.P., Deverson E.V.;  
RT "Primary structure of kappa light chain from a human myeloma protein";  
RL Eur. J. Biochem. 49:377-391(1974).  
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2) marker.  
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.  
DR PIR; A01864; K1HVAR.  
DR HSSP; P80362; 1WTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Direct protein sequencing; Glycoprotein; Immunoglobulin V region.  
FT CARBOHYD 28 28  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF944C3346 CRC64;  
  
Query Match 77.7%; Score 426.5; DB 1; Length 107;  
Best Local Similarity 76.4%; Pred. No. 1.7e-35;  
Matches 81; Conservative 15; Mismatches 9; Indels 1; Gaps 1;  
  
QY 1 ELTQSPSSVSVASVGDRTVITCRASQGISSWLAWYOHQPGKAPKLLIYSASSLSQGVPSRF 60  
DB 3 QMTQSPSSLASVGDRAVITCRASQNTSSWLAWYQGRKAPKLLIYSASSLSGAPSRF 62  
QY 61 SGSGYGDPSLTISLQFEDSATYCCOANSFPTFGGTVEIKR 106  
DB 63 SGSGSGDTFTLTISLQPBPAITYCCQYNTF-FTFGGTVEIKR 107  
  
RESULT 12  
Q96SA9 PRELIMINARY; PRT; 107 AA.  
ID Q96SA9  
AC Q96SA9;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Anti-streptococcal/anti-mycosin immunoglobulin kappa light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.



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RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL, U96396; AAB68785.1; -.
DR PIR, B49047; B49047.
DR PIR, PH0867; PH0867.
DR PIR, S16840; S16840.
DR PIR, S31977; S31977.
DR PIR, S34083; S34083.
DR PIR, S34086; S34086.
DR HSSP, P01607; 1BWW.
DR InterPro, IPR007110; Ig-like.
DR SMART, SM00406; Ig_v.
DR PROSITE, PSS0835; IG_LIKE; 1.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 77.7%; Score 426.5; DB 2; Length 107;
Best Local Similarity 82.1%; Pred. No. 1.7e-35;
Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSFSASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYAASLSQGVPSRF 62
QY 61 GSGGYGTDFTLTISLSLQPEDSATYTCQANSFPYTFGGGTVEIKR 106
Db 63 GSGSGGTDFTLTISLSLQPEDFATYTCQANS-TLTFGGGTVEIKR 107

RESULT 13
Q72473 PRELIMINARY; PRT; 234 AA.
ID Q72473
AC Q72473;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Valladao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
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RC TISSUE=Lung;
RA Strausberg R.;
RT Submitted (JUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC056256; AAH56256.1; -.
DR HSSP, P01834; 1HEZ.
DR InterPro, IPR007110; Ig-like.
DR InterPro, IPR003597; Ig_c1.
DR InterPro, IPR00306; Ig_MHC.
DR InterPro, IPR003596; Ig_v.
DR Pfam, PF07654; C1-sev; 1.
DR SMART, SM00406; Ig_v; 1.
DR PROSITE, PSS0835; IG_LIKE; 2.
DR PROSITE, PSS0290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 77.6%; Score 426; DB 2; Length 234;
Best Local Similarity 78.1%; Pred. No. 4.5e-35;
Matches 82; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 61
Db 24 MTQSPSSFSASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYAASLSQGVPSRF 63
QY 62 GSGGYGTDFTLTISLSLQPEDSATYTCQANSFPYTFGGGTVEIKR 106
Db 84 GSASGTDFTLTISLSLQPEDFATYTCQANSFPYTFGGGTVEIKR 128

RESULT 14
Q723Y4 PRELIMINARY; PRT; 236 AA.
ID Q723Y4
AC Q723Y4;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Valladao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC005332; AAH05332.1; -.
DR HSSP, P01834; 1HEZ.
DR InterPro, IPR007110; Ig-like.
```





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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: July 26, 2005, 08:50:20 ; Search time 79.3394 Seconds  
(without alignments)  
516.724 Million cell updates/sec

Title: US-10-027-725A-12  
Perfect score: 549  
Sequence: 1 ELTQSPSSVSASVGDVYIT.....QANSPFYFGQTKVEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	527	96.0	106	5	ABG30450 Human IGE
2	518	94.4	233	3	AAB03713 Aab03713 Immunoglob
3	518	94.4	233	7	ADB72874 Human AAA
4	491	89.4	107	8	ADP22406 Human ant
5	487	88.7	107	8	ADP22216 Human ant
6	485	88.3	107	5	ABB07237 Anti-IL-4
7	484	88.2	223	6	ABJ36940 Anti-CD40
8	482	87.8	234	7	Adm47073 Mouse ant
9	479	87.2	107	7	ADP03922 Murine ant
10	479	87.2	107	7	ADP03922 Murine-ex
11	478	87.1	107	4	ADP03994 Murine-ex
12	478	87.1	107	7	ADP03924 Murine-ex
13	478	87.1	107	7	ADP03989 Murine-ex
14	478	87.1	107	7	ADP03921 Murine-ex
15	478	87.1	244	5	ABP45870 Human Bly
16	478	87.1	244	7	ADG96697 Single ch
17	477	86.9	212	8	Adf76324 M16-L 11g
18	475	86.5	236	5	AAU74297 Anti-huma
19	474	86.3	105	5	AAO18424 Anti-CD2
20	474	86.3	107	7	ADK18619 Anti-huma
21	474	86.3	107	7	ADK18794 Anti-huma
22	474	86.3	107	8	ADL25454 Human mab
23	472	86.0	107	7	ADP03920 Murine-ex
24	472	86.0	107	7	ADP03923 Murine-ex
25	470.5	85.7	106	7	ADP03944 Murine-ex

26	468.5	85.3	108	7	ADK18933
27	468	85.2	234	7	ADK28413
28	467	85.1	107	4	AAB72880
29	467	85.1	107	8	AD036490
30	467	85.1	107	8	AD036502
31	467	85.1	107	8	AD036494
32	466	85.1	134	6	ABR55899
33	466	84.9	108	5	AAU76522
34	466	84.9	234	7	ADK28429
35	465	84.7	234	8	ADK28446
36	465	84.7	234	8	ADK28458
37	464.5	84.6	109	4	AAE10815
38	464	84.5	107	8	ADK84378
39	464	84.5	107	8	ADK84386
40	464	84.5	107	8	ADK84384
41	464	84.5	107	8	ADK84520
42	464	84.5	107	8	ADK84528
43	464	84.5	107	8	ADK84526
44	463	84.3	107	4	AAK93597
45	463	84.3	107	6	ABO27404

## ALIGNMENTS

RESULT 1	
ID	ABG30450 standard; protein; 106 AA.
XX	ABG30450;
AC	21-OCT-2002 (first entry)
DT	
XX	
DE	Human IGE Fab clone 100 light chain protein.
XX	
KW	Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;
KW	timothy grass pollen allergen; passive immunotherapy.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Location/Qualifiers
FT	Region
FT	/note= "F1 region"
FT	22..32
FT	/notes= "CDR1 region"
FT	33..47
FT	/note= "FR2 region"
FT	48..54
FT	/note= "CDR2 protein"
FT	55..86
FT	/note= "FR3 region"
FT	Misc-difference 65
FT	/note= "Encoded by TCT"
FT	Region
FT	87..95
FT	/note= "CDR2 region"
FT	96..104
FT	/note= "FR4 region"
XX	
PN	W0200253595-A1.
XX	
PD	11-JUL-2002.
XX	
PF	27-DEC-2001; 2001WO-S0002908.
XX	
PR	29-DEC-2000; 2000SE-00004892.
XX	
PA	(PHAA ) PHARMACIA DIAGNOSTICS AB.
XX	
PI	Flicker S, Steinberger P, Kraft D, Valenta R;
XX	
XX	WPI; 2002-583604/62.
DR	
DR	N-PSDB; ABK89642.

PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
PT variable region of group 2 allergen specific-human IgG Fabs, useful for  
PT diagnosing or passive immunotherapy of type I allergy, for environmental  
PT allergen detection.  
XX  
PS Disclosure; Page 41; 45pp; English.  
XX  
CC This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgG Fabs and methods for their use. The proteins  
CC of the invention may have antiallergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE  
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific Fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The Fabs  
CC - or a vaccine against a type I allergy is useful for diagnosing a type  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific Fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergenic patients  
CC IgG antibodies to Phi p 2. The present sequence represents the human IgG  
CC Fab, clone 100 light chain protein of the invention  
XX  
SQ Sequence 106 AA;  
XX  
Query Match 96.0%; Score 527; DB 5; Length 106;  
Best Local Similarity 97.2%; Pred. No. 6,7e-30;  
Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 1 ELTQSPSSVSASVGDRTYITCRASQGISWLAWYQHQPGRAPKRLITYSASLSQGVPSRF 60  
Db 1 ELTQSPSSVSASVGDRTYITCRASQGISWLAWYQHQPGRAPKRLITYSASLSQGVPSRF 60  
XX  
QY 61 SGSGGYGTFSLTITSLQFEDSATYTCQANSFPYTFGQGTVEIKR 106  
Db 61 SGSGGYGTFSLTITSLQFEDSATYTCQANSFPYTFGQGTVEIKR 106  
XX  
RESULT 2  
AAB03713  
ID AAB03713 standard; protein; 233 AA.  
XX  
AC AAB03713;  
XX  
DT 04-OCT-2000 (first entry)  
XX  
DE Immunoglobulin kappa amino acid sequence fragment.  
XX  
DE Aortic aneurysm-associated antigen protein; AAP; microfibrillar protein;  
KW abdominal aortic aneurysm disease; treatment; detect; tolerance;  
XX immunoglobulin kappa; Igk.  
XX  
OS Unidentified.  
XX  
PN US6048704-A.  
XX  
PD 11-APR-2000.  
XX  
PE 07-MAR-1997; 97US-00812586.  
XX  
PR 07-MAR-1996; 96US-0012976P.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Tilson MD;  
XX  
DR WPI; 2000-316895/27.  
XX  
XX Isolated microfibrillar protein for alleviating abdominal aortic aneurysm  
PT disease is purified from human aortic tissue and binds immunoreactively  
PT with immunoglobulin.  
XX  
PS Example 3; Col 29-31; 70pp; English.

XX  
CC The present invention relates to an isolated microfibrillar protein of  
CC approximately 40kD. The protein is isolated from human aortic tissue and  
CC binds immunoreactively with immunoglobulin purified from human abdominal  
CC aortic aneurysm (AAA) tissue. The protein is referred to as aortic  
CC aneurysm-associated antigenic protein (AAP). The protein is capable of  
CC forming a disulphide bonded dimer. The protein is immunoreactive with  
CC human kappa immunoglobulin. Also included in the invention are  
CC recombinantly produced human AAA proteins. AAP shows regions of homology  
CC with the bovine microfibril associated glycoprotein MFAP-4 and also with  
CC fibrinogen and vitronectin. The isolated microfibrillar protein is useful  
CC for alleviating abdominal aortic aneurysm (AAA) disease and detecting the  
CC presence of AAA-associated immunoglobulin bound to the human aortic  
CC tissue. Antibodies directed against AAP can be used to detect AAA  
CC disease. The recombinant protein can be used to induce tolerance to  
CC antigenic AAA protein in the subject e.g. human. This sequence represents  
CC an immunoglobulin kappa amino acid sequence. The sequence shares homology  
CC with the AAP of the invention, it was used to identify and characterise  
XX AAP  
XX  
SQ Sequence 233 AA;  
XX  
Query Match 94.4%; Score 518; DB 3; Length 233;  
Best Local Similarity 96.2%; Pred. No. 5,7e-29;  
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
XX  
QY 1 ELTQSPSSVSASVGDRTYITCRASQGISWLAWYQHQPGRAPKRLITYSASLSQGVPSRF 60  
Db 23 ELTQSPSSVSASVGDRTYITCRASQGISWLAWYQHQPGRAPKRLITYSASLSQGVPSRF 82  
XX  
QY 61 SGSGGYGTFSLTITSLQFEDSATYTCQANSFPYTFGQGTVEIKR 106  
Db 83 SGSGGYGTFSLTITSLQFEDSATYTCQANSFPYTFGQGTVEIKR 128  
XX  
RESULT 3  
ADB72874  
ID ADB72874 standard; protein; 233 AA.  
XX  
AC ADB72874;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Human AAA-associated immunoglobulin related polypeptide, SEQ ID No:42.  
XX  
KW Human; aortic tissue; immunoreactive; abdominal aortic aneurysm;  
XX AAA-associated immunoglobulin 40kDa protein.  
XX  
OS Homo sapiens.  
XX  
PN US6537769-B1.  
XX  
PD 25-MAR-2003.  
XX  
PE 28-MAR-2000; 2000US-00535832.  
XX  
PR 07-MAR-1996; 96US-0012976P.  
XX  
PR 07-MAR-1997; 97US-00812586.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Tilson MD;  
XX  
DR WPI; 2003-687181/65.  
XX  
XX Purified protein useful in diagnosing abdominal aortic aneurysm disease  
PT in subject, e.g. human, contains specified amino acids.  
XX  
PS Disclosure; Col 73-74; 67pp; English.  
XX  
XX The present invention relates to the isolation of a protein approximately  
CC 40kDa which is purified from human aortic tissue. The protein is  
CC immunoreactive with abdominal aortic aneurysms (AAA)-associated

immunoglobulin. The protein is useful for diagnosing AA disease in a subject, e.g. human, by administering the protein or a composition comprising the protein. The inventive protein is capable of forming a disulphide-bonded dimer of 80 kDa. The present sequence of unknown function is given in the Sequence Listing but is not mentioned elsewhere in the specification.

**SQ Sequence 233 AA;**

Query Match	94.4%	Score 518;	DB 7;	length 233;
Best Local Similarity	96.2%	Pred. No. 5,	7e-29;	
Matches 102;	Conservative	1;	Mismatches 3;	Indels 0;
				Gaps 0;

**OY** 1 ELTGSPSSVASVGDRTYTITCRASQGISLWLAHQHPGAPKLLYSASSLSQGVSRF 60  
|||  
||| : |||  
**D6** 23 ELTGSPSSVASVGDRTYTITCRASQGISLWLAHQHPGAPKLLYSASSLSQGVSRF 82

```
QY      61 SSGSGYDPSLTISSLQFEISATYYCCQANSFPYTFGQGTKEIKR 106
      |||||
      83 SSGSGYDPSLTISSLQFEISATYYCCQANSFPYTFGQGTKEIKR 128
Db
```

RESULT 4  
ADP22406

AC ADP22406;

DT 09-SEP-2004 (first entry)

Human anti-TNFa antibody light chain variable region SEQ ID NO:312

KM eating-disorder: anxiomodulator; immunosuppressive; nephrotropic;  
KM neuroprotective: vasotropic; antiapoptotic; TNF antagonist;  
KM TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer  
KM bladder cancer; lung cancer; glioblastoma; stomach cancer;  
KM endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
KM prostate cancer; immuno-mediated inflammatory disease;  
KM rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
KM retinosis; autoimmune disease; Crohn's disease; graft-host reaction;  
KM septic shock; cachexia; anorexia; multiple sclerosis.

OS Homo sapiens.

PN W02004050683-A2.

PD 17-JUN-2004

PF 02-DEC-2003; 2003WO-US038281.

02-DEC-2002; 2002US-0430722P.

PA (ABGE-) ABGENIX INC.

PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
PI Haak-Frendscho M, Rathanaswami P, Piggott C, Liang ML, Lee R  
PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;

DR WPI; 2004-480601/45.

PT New recombinant human monoclonal antibody that specifically binds to  
Tumor Necrosis Factor- $\alpha$ , useful for treating neoplastic disease such  
PT as cancer, or immuno-mediated inflammatory diseases such as rheumatoid  
PT arthritis.

PS Example 10; SEQ ID NO 312; 213pp; English.

CC The present invention describes a human monoclonal antibody (I) that  
CC specifically binds to tumour necrosis factor- $\alpha$  (TNF $\alpha$ ) and comprises:  
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the

CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
CC (M1) the level of TNFa in a patient sample, comprising contacting with  
CC (1), and detecting the level of binding between the antibody and TNFa in  
CC the sample; (2) a composition comprising the antibody or its functional  
CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
CC animal in need of treatment for the disease by administering the human  
CC monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced  
CC apoptosis in an animal by selecting an animal in need of treatment for  
CC TNFa induced apoptosis by administering the human monoclonal antibody of  
CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,  
CC antibacterial, antiinflammatory, antiposterioric, antirheumatic, eating-  
CC disorders, immunomodulatory, immunosuppressive, nephrotropic,  
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
CC as a TNFa antagonist. The antibody (1) is useful in the preparation of  
CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
CC diseases such as rheumatoid arthritis, glomerulonephritis,  
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
CC multiple sclerosis. The present sequence represents a human anti-TNFA  
CC antibody light chain variable region, which is used in the  
CC exemplification of the present invention.

**SQ** Sequence 107 AA;

Query Match	89.4%	Score 491	DB 8	length 107
Best Local Similarity	90.5%	Pred. NC. 2.3e-27		
Matches 95	Conservative 6	Mismatches 4	Indels 0	Gaps 0

**Qy** 1 ELTSPSSVSASVGDRTITTCRASOGISSWLAWYQHQPCKAPKLLIYSASSLSQGVPSTRF 600  
::| | | | | | | | | | : | | | | | | | | | |  
**Dd** 3 QMTGPSVSASVAGDRTITTCRASOGISSWLAWYQQKKGKAPKLLIYAASSLQSGVPSRF 622

Oy                 61 SSGGYGTDLSLTISSLQFEDSATYYCQAANSFPYTFGGGTKEIK 105  
| | | : | | | | | | | | | |  
Db                 63 SSSGSSTDFTLTIISSLQPEDFATYYCQAANSFWPTFGQGKTVEIK 107

RESULT 5  
ADP22216  
ID ADP22216 standard; protein; 107 AA

AC ADP22216;

DT 09-SEP-2004 (first entry)

DE	Human anti-TNFa antibody heavy chain variable region SEQ ID NO:122
1	1
2	2
3	3
4	4
5	5
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7	7
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10	10
11	11
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171</	

KM human monoclonal antibody; tumour necrosis factor- $\alpha$ ; TNF $\alpha$ ;  
KM anti-TNF $\alpha$  antibody; anabolic; antihypertensive; antihypertensive;  
KM antibacterial; antiinflammatory; antipsoriatic; antineoplastic;  
KM eating-disorder; immunomodulator; immunosuppressive; nephrotoxic;  
KM neuroprotective; vasodilator; antiproliferative; TNF $\alpha$  antagonist;  
KM TNF $\alpha$  induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
KM bladder cancer; lung cancer; glioblastoma; stomach cancer;  
KM endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
KM prostate cancer; immuno-mediated inflammatory disease;  
KM rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
KM osteoporosis; autoimmune disease; Crohn's disease; graft-host reaction;  
KM septic shock; cachexia; anorexia; multiple sclerosis.

OS Homo sapiens.

PN WO2004050683-A2.

PD 17-JUN-2004

PF 02-DEC-2003; 2003WO-US038281.

XX 02-DEC-2002; 2002US-0430729P.  
 XX (ABGE-) ABGENIX INC.  
 XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan US;  
 XX WPI; 2004-480601/45.  
 DR N-PSDB; ADP22215.  
 XX  
 PT New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX  
 PS Example 10; SEQ ID NO 122; 213pp; English.

CC The present invention describes a human monoclonal antibody (I) that  
 CC specifically binds to tumor necrosis factor-alpha (TNFa) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFa in a patient sample, comprising contacting with  
 CC (1), and detecting the level of binding between the antibody and TNFa in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFa induced apoptosis by administering the human monoclonal antibody of  
 CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipneumatic, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody heavy chain variable region, which is used in the  
 CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 88.7%; Score 487; DB 8; Length 107;  
 Best Local Similarity 89.5%; Pred. No. 4,4e-27;  
 Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELRTGSPSSVASVDRVTITCRASQGISSWLAWYQHDPGKPKLLIYSASSLSQGVSRF 60  
 Db 3 QMTQSPSSVASVDRVTITCRASQGISSWLAWYQKRGKPKLLIYAASLSQGVSRF 62  
 QY 61 SSGSGYGVDFSLTITSLQPEDSATYYCOANSFPYTFGGGTVEIK 105  
 Db 63 SSGSGYGVDFSLTITSLQPEDSATYYCOANSFPYTFGGGTVEIK 107

RESULT 6

ABR07237 standard; protein; 107 AA.

XX ABR07237;  
 XX 26-MAR-2002 (first entry)

DE Anti-IL-4 and IL-13 receptors Mab 63 light chain variable region.

XX Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;  
 XX antiarthritic; dermatological; antiulcer; antiinflammatory; cytostatic;  
 XX antiskinking; immunosuppressive; tuberculosstatic; ophthalmological;  
 XX IL-13; antineumatic; antithyroid.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 24..34 /note="complementarity determining region (CDR) 1"

FT Region 50..56 /note="complementarity determining region (CDR) 2"

FT Region 89..97 /note="complementarity determining region (CDR) 3"

XX W0200192340-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US017094.

XX 26-MAY-2000; 2000US-00579808.

XX 19-FEB-2000; 2000US-00665343.

XX 15-FEB-2001; 2001US-00785934.

XX 01-MAY-2001; 2001US-00847816.

XX (IMMV) IMMUNEX CORP.

XX Plueneke JD.

XX WPI; 2002-114332/15.

DR N-PSDB; ABA94337.

PT Novel human antibody which binds human interleukin (IL)-4 receptor and is  
 PT capable of inhibiting IL-4 induced biological activity, functions as IL-4  
 PT antagonist and is useful for treating septic arthritis, scleroderma.

XX Claim 3; Page 82; 85pp; English.

CC The invention relates to a human antibody (an interleukin (IL)-4  
 CC antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of  
 CC inhibiting an IL-4-induced biological activity. (I) is also useful for  
 CC inhibiting both IL-4-induced biological activity and IL-13-induced  
 CC biological activity in vivo in a human, and for treating septic arthritis  
 CC in a human afflicted with septic arthritis. (I) is also used for treating  
 CC conditions such as septic/reactive arthritis, dermatitis herpetiformis,  
 CC urticaria (especially chronic idiopathic urticaria), ulcers, gastric  
 CC inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease,  
 CC inflammatory bowel disease, other disorders of the digestive system in  
 CC which IL-4 plays a role (e.g. IL-4-induced inflammation of part of the  
 CC gastrointestinal tract), conditions in which IL-4-induced barrier  
 CC disruption plays a role (e.g. conditions characterized by decreased  
 CC epithelial barrier function in the lung or gastrointestinal tract),  
 CC scleroderma, hypertrophic scarring, whipple's disease, benign prostrate  
 CC hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to  
 CC medication, Kawasaki disease, sickle cell disease or crisis, Churg-  
 CC Strauss syndrome, Grave's disease, pre-eclampsia, Sjogren's syndrome,  
 CC autoimmune lymphoproliferative syndrome, autoimmune haemolytic anemia,  
 CC Barrett's esophagus, autoimmune uveitis, tuberculosis, nephrosis,  
 CC pemphigus vulgaris or bullous pemphigoid (autoimmune blistering  
 CC diseases), and myasthenia gravis (an autoimmune muscular disorder). IL-4  
 CC antagonists also find use as adjuvants to allergy immunotherapy and as  
 CC vaccine adjuvants, especially when directing the immune response toward a  
 CC TH1 response would be beneficial in treating or preventing the disease.  
 CC The present sequence represents an anti-IL-4 receptor and anti-IL-13  
 CC receptor monoclonal antibody (Mab) 63 light chain variable region  
 XX Sequence 107 AA;

Query Match 88.3%; Score 485; DB 5; Length 107;  
 Best Local Similarity 88.6%; Pred. No. 6e-27;

Matches	93:	Conservative	7:	Mismatches	5:	Indels	0:	Gaps	0:
Qy	1	ELTQSPSSVASVGDGRVTTTCRASQGISWTAWYOHQPKAPKLLIYASSLSQGVPSRF	60						
Db	3	QMTQSPSSVSASVGDGRVTTTCRASQGISWTAWYOHKKGKAPKLLIYASSLSQGVPSRF	62						
Qy	61	SGSGGTDPSLTISLSQFEDSATYVCOQANSPRYFGGTVEIK	105						
Db	63	SGSGGTDPTLTISLSQFEDPATYVCOQANSPRYFGGTVEIK	107						
RESULT 7									
ABJ36940									
ID	ABJ36940	standard; protein, 223 AA.							
XX	ABJ36940;								
AC									
XX									
DT	01-MAY-2003	(first entry)							
XX									
DE	Anti-CD40 monoclonal antibody related protein SEQ ID NO 66.								
XX									
KW	Antiallergic; haemostatic; immunomodulator; cyostatic; antibody;								
KW	human CD40; IL-12; IPS; lipopolysaccharide; IFNgamma; interferon gamma;								
KW	dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;								
KW	immunocytotoxic; anti-tumour agent; immunosuppressant; allergy;								
KW	autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.								
XX									
OS	Unidentified.								
XX									
PN	WO20028186-A1.								
PD									
XX	07-NOV-2002.								
PF	26-APR-2002; 2002WO-JP004292.								
XX									
PR	27-APR-2001; 2001WO-US013672.								
PR	11-MAY-2001; 2001JP-00142482.								
PR	05-OCT-2001; 2001JP-00310535.								
PR	26-OCT-2001; 2001US-00040244.								
XX									
PA	(KIRI ) KIRIN BEER KK.								
XX									
PI	Mikayama T, Yoshida H, Force WR, Chen X, Takahashi N;								
DR	WP1; 2003-120463/11.								
XX	N-PSDB; ABT31882.								
PT	Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,								
PT	or functional fragment, is useful in the treatment of e.g. autoimmune								
XX	diseases or cancer.								
PS	Claim 15; Page 60; 94pp; Japanese.								
XX									
CC	The invention relates to an antibody to human CD40, or its functional								
CC	fragment, has at least one of the following properties: acting on								
CC	dendritic cells to produce IL-12 in the presence of IPS								
CC	(lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic								
CC	cells to activate maturity of the dendritic cells with high G28-5								
CC	antibody; and activating CD95 expression with high G28-5 antibody against								
CC	B cell line. Such antibodies or functional fragments can be used as								
CC	immunocytotoxic, anti-tumour agents, immunosuppressants, and as remedies								
CC	for autoimmune diseases, allergy or coagulation factor VIII inhibitors								
CC	syndrome. This sequence represents a protein relating to the anti-CD40								
XX	monoclonal antibody of the invention								
XX									
SQ	Sequence 223 AA;								
Query Match	88.2%;	Score 484;	DB 6;	Length 223;					
Best Local Similarity	87.7%;	Pred. No. 1.4e-26;							
Matches	93;	Conservative	7;	Mismatches	5;	Indels	0;	Gaps	0;
1	ELTQSPSSVASVGDGRVTTTCRASQGISWTAWYOHQPKAPKLLIYASSLSQGVPSRF	60							
3	QMTQSPSSVSASVGDGRVTTTCRASQGISWTAWYOHKKGKAPKLLIYASSLSQGVPSRF	62							
61	SGSGGTDPSLTISLSQFEDSATYVCOQANSPRYFGGTVEIK	105							
63	SGSGGTDPTLTISLSQFEDPATYVCOQANSPRYFGGTVEIK	107							

Db	25	QMTQSPSSVSASVDGRVTITTRAGSGISWLMAYQKRGKAPKLLIYAGSLQSGVPSRF	84
Qy	61	SGSGGTDFTLTISLSLOFEDSATYTCQANSPFYTGCGTKEIKR	106
Db	85	SGSGFGTDFLTITISLSLOPEDPATYTCQANSSFPRTGCGTKEIKR	130
RESULT 8			
ID	ADM47073		
AC	ADM47073	standard; protein; 234 AA.	
XX	ADM47073;		
DT	03-JUN-2004	(first entry)	
DE	Mouse anti-human G-CSF antibody light chain protein.		
KW	methyloctroph yeast; mammalian sugar chain; OCH1; alpha-1;		
KW	6-mannosyl transferase; alpha-1; 2-mannosidase;		
KW	orotidin-5'-phosphate decarboxylase; URA3;		
KW	phosphoribosyl-5'-amino-imidazole succinocarboxamide synthase; ADE1;		
KW	imidazole-glycerol-phosphate dehydratase; HIS3;		
KW	3-isopropyl malate dehydrogenase; LEU2; proteinase A; proteinase B; PRB1;		
KW	PEP4; YPS1; KTR1; MNN9; AOX; GAPDH; mannosyl transferase;		
KW	glyceralddehyde 3-phosphate dehydrogenase; mannosyl glycoprotein.		
OS	Mus sp.		
XX			
PN	WO2003091431-A1.		
PD	06-NOV-2003.		
XX			
XX	28-APR-2003; 2003WO-JP005464.		
PF	26-APR-2002; 2002JP-00127677.		
PR			
XX			
PA	(KIRI ) KIRIN BEER KK.		
PA	(NMAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.		
XX			
XX	Kobayashi K, Kitagawa Y, Komeda T, Kawashima N, Ujigami Y;		
PI	Chiba Y;		
XX			
XX	WPI; 2003-854401/79.		
XX			
PT	Producing methyloctroph yeast that expresses mammalian sugar chains by		
PT	disrupting the OCH1 gene and inserting an alpha-1,2-mannosidase gene.		
XX			
PS	Example 28; SEQ ID NO 92; 247pp; Japanese.		
XX			
CC	The invention relates to the production of a methyloctroph yeast that		
CC	produces mammalian sugar chains, comprising disrupting the OCH1 gene in		
CC	the yeast that encodes for alpha-1,6-mannosyl transferase and inserting		
CC	and expressing the alpha-1,2-mannosidase gene. The specification also		
CC	includes DNA sequences encoding: (a) orotidin-5'-phosphate decarboxylase		
CC	(URA3); (b) phosphoribosyl-amino-imidazole succinocarboxamide synthase		
CC	(ADE1); (c) imidazole-glycerol-phosphate dehydratase (HIS3); (d) 3-		
CC	isopropyl malate dehydrogenase (LEU2); (e) alpha-1,6-mannosyl transferase		
CC	(OCH1); (f) proteinase A (PEP4); (g) proteinase B (PRB1); and (h)		
CC	aspartic protease (YPS1), mannosyl transferase (KTR1 or MNN9), alcohol		
CC	sequence (AOX) and glyceralddehyde 3-phosphate dehydrogenase (GAPDH) gene		
CC	sequences. The yeast is used for the production of human and mammalian		
CC	high mannose glycoproteins with high yield and purity. The method is also		
CC	useful for producing hybrid or complex sugar chains containing mammalian		
CC	type chains. This sequence represents a mouse anti-human G-CSF antibody		
CC	light chain used in the invention.		
XX			
XX	Sequence 234 AA:		
XX			
Query Match	87.8%;	Score 482; DB 7; Length 234;	
Best Local Similarity	89.6%;	Pred. No. 1.9e-26;	
Matches	95;	Conservative 5; Mismatches 6; Indels 0; Gaps 0	
Qy	1	ELTQSPSSVSASVDGRVTITTRAGSGISWLMAYQKRGKAPKLLIYAGSLQSGVPSRF	60

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Db      23 QMTQSPSSVSASVGDRTITTCRASQVTSWLAWYQQRGKAPKLLIYAASLSGVSRRF 82
QY      61 SSGSGYGFDFSLTISLQFEDSATYYCOQANSFPYTFGQGTKEIKR 106
Db      83 SSGSGGTDFTLTISLQPEDPATYYCOQANSFPPTFGQGTKEIKR 128

RESULT 9
ADP03922
ID      ADP03922 standard; protein; 107 AA.
XX
AC      ADP03922;
XX
DT      29-JUL-2004 (first entry)
XX
DE      Murine-expressed anti-human CA IX monoclonal antibody VL protein -SEQ 62.
XX
KW      monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW      cytoskeletal; colorectal neoplasm; renal cell carcinoma;
KW      cervical intraepithelial squamous neoplasia;
KW      cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KW      gene therapy; murine; mouse; human; light chain variable domain.
XX
OS      Unidentified.
XX
PN      WO2003046328-A2.
XX
PD      12-JUN-2003.
XX
PF      02-DEC-2002; 2002MO-US038550.
XX
PR      03-DEC-2001; 2001US-0337275P.
XX
PA      (ABGE-) ABGENIX INC.
XX
PI      Gudas J, Foltz I, Handa M, Gallo M;
XX
DR      WPI; 2003-523295/49.
XX
PT      New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT      colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT      intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS      Claim 3; SEQ ID NO 62; 89pp; English.
XX
CC      The invention relates to a novel isolated monoclonal antibody (mAb)
CC      comprising a heavy chain polypeptide and light chain polypeptide having a
CC      sequence chosen from one of 53 fully defined amino acid sequences given
CC      in the specification, where the antibody specifically binds carbonic
CC      anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC      demonstrates cytoskeletal activity and may be useful for treating a tumour,
CC      such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC      cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC      tumour or breast cancer, possibly via gene therapy. The current sequence
CC      is that of a murine-expressed anti-human CA IX monoclonal antibody VL
CC      (light chain variable domain) protein of the invention. The protein was
CC      generated via the introduction of the human CA IX protein into a
CC      transgenic mouse strain.
XX
SQ      Sequence 107 AA;

Query Match      87.2%; Score 479; DB 7; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.6e-26;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY      1 ELTQSPSSVSASVGDRTITTCRASQGISWLAWYQHQPGRAPKLLIYASLSGVSRRF 60
Db      3 QMTQSPSSVSASVGDRTITTCRASQGISWLAWYQQRGKAPKLLIYAASLSGVSRRF 62

QY      61 SSGSGYGFDFSLTISLQFEDSATYYCOQANSFPYTFGQGTKEIKR 105
Db      63 SSGSGGTDFTLTISLQPEDPATYYCOQANSFPPTFGQGTKEIKR 107

RESULT 10
ADP03994
ID      ADP03994 standard; protein; 107 AA.
XX
AC      ADP03994;
XX
DT      29-JUL-2004 (first entry)
XX
DE      Murine-expressed anti-human CA IX monoclonal antibody VL protein SEQ 164.
XX
KW      monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW      cytoskeletal; colorectal neoplasm; renal cell carcinoma;
KW      cervical intraepithelial squamous neoplasia;
KW      cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KW      gene therapy; murine; mouse; human; light chain variable domain.
XX
OS      Unidentified.
XX
PN      WO2003046328-A2.
XX
PD      12-JUN-2003.
XX
PF      02-DEC-2002; 2002MO-US038550.
XX
PR      03-DEC-2001; 2001US-0337275P.
XX
PA      (ABGE-) ABGENIX INC.
XX
PI      Gudas J, Foltz I, Handa M, Gallo M;
XX
DR      WPI; 2003-523295/49.
XX
PT      New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT      colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT      intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS      Example 2; SEQ ID NO 164; 89pp; English.
XX
CC      The invention relates to a novel isolated monoclonal antibody (mAb)
CC      comprising a heavy chain polypeptide and light chain polypeptide having a
CC      sequence chosen from one of 53 fully defined amino acid sequences given
CC      in the specification, where the antibody specifically binds carbonic
CC      anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC      demonstrates cytoskeletal activity and may be useful for treating a tumour,
CC      such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC      cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC      tumour or breast cancer, possibly via gene therapy. The current sequence
CC      is that of a murine-expressed anti-human CA IX monoclonal antibody VL
CC      (light chain variable domain) protein of the invention. The protein was
CC      generated via the introduction of the human CA IX protein into a
CC      transgenic mouse strain.
XX
SQ      Sequence 107 AA;

Query Match      87.2%; Score 479; DB 7; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.6e-26;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY      1 ELTQSPSSVSASVGDRTITTCRASQGISWLAWYQHQPGRAPKLLIYASLSGVSRRF 60
Db      3 QMTQSPSSVSASVGDRTITTCRASQGISWLAWYQQRGKAPKLLIYAASLSGVSRRF 62

QY      61 SSGSGYGFDFSLTISLQFEDSATYYCOQANSFPYTFGQGTKEIKR 105
Db      63 SSGSGGTDFTLTISLQPEDPATYYCOQANSFPPTFGQGTKEIKR 107

RESULT 11
AA65571
ID      AA65571 standard; protein; 107 AA.
XX

```



AC AAG65571;  
 XX 30-NOV-2001 (first entry)  
 XX  
 XX Amino acid sequence of protein seq Id No. 96.  
 DE  
 XX Gene library; immunoglobulin; antibody library; human.  
 XX  
 XX Homo sapiens.  
 OS  
 XX MO200162907-A1.  
 PN  
 XX 30-AUG-2001.  
 PD  
 XX 22-FEB-2001; 2001WO-JP001298.  
 PF  
 XX 22-FEB-2000; 2000JP-00050543.  
 PR  
 XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.  
 PA  
 XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;  
 PI Okuno Y, Shiraki K;  
 XX WPI; 2001-565420/63.  
 DR N-PSDB; AAH47735.  
 XX  
 XX Producing gene libraries and antibody libraries, involves selecting a  
 PT light chain that binds to a heavy chain product to produce a functional  
 PT formation, and producing a gene library of the light chain variable  
 PT regions.  
 XX  
 PS Examples; p 172; 181pp; Japanese.  
 XX  
 CC The invention relates to producing gene libraries, comprising  
 CC immunoglobulin light and heavy variable region. The method involves  
 CC selecting light chain that binds with the heavy chain product to produce  
 CC a functional conformation, producing a gene library comprising a  
 CC collection of these light chain variable genes, and combining with gene  
 CC library of heavy chain variable genes. The method is used for production  
 CC of gene and antibody libraries  
 CC  
 XX  
 SQ Sequence 107 AA;  
 Query Match 87.1%; Score 478; DB 4; Length 107;  
 Best Local Similarity 88.6%; Pred. No. 1.9e-26;  
 Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAWYOHQPGKAPKLLIYSASSLSQGVPSRF 60  
 Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLAWYOHQPGKAPKLLIYASSLSQGVPSRF 62  
 QY 61 SSGSGYGFDTSLTISLSLQFEDSATYTCQANSFPYTFGGTIVEIK 105  
 Db 63 SSGSGYGFDTSLTISLSLQFEDSATYTCQANSFPYTFGGTIVEIK 107  
 RESULT 12  
 ADP03924  
 ID ADP03924 standard; protein; 107 AA.  
 XX  
 XX ADP03924;  
 XX  
 XX 29-JUN-2004 (first entry)  
 XX  
 XX Murine-expressed anti-human CA IX monoclonal antibody VL protein -SEQ 64.  
 DE  
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; light chain variable domain.  
 XX  
 OS Unidentified.

XX  
 PN MO2003048328-A2.  
 XX  
 XX 12-JUN-2003.  
 PD  
 XX  
 XX 02-DEC-2002; 2002WO-US038550.  
 PF  
 XX 03-DEC-2001; 2001US-0337275P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX Gudas J, Foltz I, Handa M, Gallo M;  
 PI WPI; 2003-523295/49.  
 DR  
 XX  
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 XX Claim 3; SEQ ID NO 64; 89pp; English.  
 PS  
 XX The invention relates to a novel isolated monoclonal antibody (mab)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytosolic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VL  
 CC (light chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 CC  
 XX  
 SQ Sequence 107 AA;  
 Query Match 87.1%; Score 478; DB 7; Length 107;  
 Best Local Similarity 87.6%; Pred. No. 1.9e-26;  
 Matches 92; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAWYOHQPGKAPKLLIYSASSLSQGVPSRF 60  
 Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLAWYOHQPGKAPKLLIYASSLSQGVPSRF 62  
 QY 61 SSGSGYGFDTSLTISLSLQFEDSATYTCQANSFPYTFGGTIVEIK 105  
 Db 63 SSGSGYGFDTSLTISLSLQFEDSATYTCQANSFPYTFGGTIVEIK 107  
 RESULT 13  
 ADP03989  
 ID ADP03989 standard; protein; 107 AA.  
 XX  
 XX ADP03989;  
 XX  
 XX 29-JUN-2004 (first entry)  
 XX  
 XX Murine-expressed anti-human CA IX monoclonal antibody VL protein SEQ 159.  
 DE  
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; light chain variable domain.  
 XX  
 OS Unidentified.  
 XX  
 XX WO2003048328-A2.  
 PN  
 XX 12-JUN-2003.  
 PD  
 XX  
 XX 02-DEC-2002; 2002WO-US038550.  
 PF  
 XX 03-DEC-2001; 2001US-0337275P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX Gudas J, Foltz I, Handa M, Gallo M;  
 PI WPI; 2003-523295/49.  
 DR  
 XX  
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 XX Claim 3; SEQ ID NO 64; 89pp; English.  
 PS  
 XX The invention relates to a novel isolated monoclonal antibody (mab)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytosolic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VL  
 CC (light chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 CC  
 XX  
 SQ Sequence 107 AA;  
 Query Match 87.1%; Score 478; DB 7; Length 107;  
 Best Local Similarity 87.6%; Pred. No. 1.9e-26;  
 Matches 92; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAWYOHQPGKAPKLLIYSASSLSQGVPSRF 60  
 Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLAWYOHQPGKAPKLLIYASSLSQGVPSRF 62  
 QY 61 SSGSGYGFDTSLTISLSLQFEDSATYTCQANSFPYTFGGTIVEIK 105  
 Db 63 SSGSGYGFDTSLTISLSLQFEDSATYTCQANSFPYTFGGTIVEIK 107  
 RESULT 13  
 ADP03989  
 ID ADP03989 standard; protein; 107 AA.  
 XX  
 XX ADP03989;  
 XX  
 XX 29-JUN-2004 (first entry)  
 XX  
 XX Murine-expressed anti-human CA IX monoclonal antibody VL protein SEQ 159.  
 DE  
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; light chain variable domain.  
 XX  
 OS Unidentified.  
 XX  
 XX WO2003048328-A2.  
 PN  
 XX 12-JUN-2003.  
 PD  
 XX  
 XX 02-DEC-2002; 2002WO-US038550.  
 PF

XX 03-DEC-2001; 2001US-0337275P.  
XX (ABGE-) ABGENIX INC.  
XX Gudas J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
XX Example 2; SEQ ID NO 159; 89pp; English.  
XX  
XX The invention relates to a novel isolated monoclonal antibody (mAb)  
XX comprising a heavy chain polypeptide and light chain polypeptide having a  
XX sequence chosen from one of 53 fully defined amino acid sequences given  
XX in the specification, where the antibody specifically binds carbonic  
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
XX demonstrates cytostatic activity and may be useful for treating a tumour,  
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal  
XX tumour or breast cancer, possibly via gene therapy. The current sequence  
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VL  
XX (light chain variable domain) protein of the invention. The protein was  
XX generated via the introduction of the human CA IX protein into a  
XX transgenic mouse strain.  
XX  
XX Sequence 107 AA;  
XX  
XX  
XX Query Match 87.1%; Score 478; DB 7; Length 107;  
XX Best Local Similarity 87.6%; Pred. No. 1.9e-26;  
XX Matches 92; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
XX  
XX 1 ELTQSPSSVASVGVDRVTITCRASQGISWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 60  
XX 3 QMTQSPSSVASVGVDRVTITCRASQGISWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 62  
XX  
XX 61 SSGSGYGFDFSLTITSLQFEDSATYTCQANSFPYTFGGQTKVEIK 105  
XX 63 SSGSGSGTFEFLTITSLQPEDFATYTCQANSFPITFGGTRLEIK 107  
XX  
XX  
XX RESULT 14  
XX ADP03921  
XX ID ADP03921 standard; protein; 107 AA.  
XX  
XX AC ADP03921;  
XX  
XX DT 29-JUL-2004 (first entry)  
XX  
XX DE Murine-expressed anti-human CA IX monoclonal antibody VL protein -SEQ 61.  
XX  
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX cytostatic; colorectal neoplasm; renal cell carcinoma;  
XX cervical intraepithelial squamous neoplasia;  
XX cervical intraepithelial glandular neoplasia;  
XX gene therapy; murine; mouse; human; light chain variable domain.  
XX  
XX OS Unidentified.  
XX  
XX PN WO2003048328-A2.  
XX  
XX PD 12-JUN-2003.  
XX  
XX PF 02-DEC-2002; 2002WO-US038550.  
XX  
XX PR 03-DEC-2001; 2001US-0337275P.  
XX  
XX PA (ABGE-) ABGENIX INC.  
XX  
XX PI Gudas J, Foltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.  
XX  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
XX Claim 3; SEQ ID NO 61; 89pp; English.  
XX  
XX The invention relates to a novel isolated monoclonal antibody (mAb)  
XX comprising a heavy chain polypeptide and light chain polypeptide having a  
XX sequence chosen from one of 53 fully defined amino acid sequences given  
XX in the specification, where the antibody specifically binds carbonic  
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
XX demonstrates cytostatic activity and may be useful for treating a tumour,  
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal  
XX tumour or breast cancer, possibly via gene therapy. The current sequence  
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VL  
XX (light chain variable domain) protein of the invention. The protein was  
XX generated via the introduction of the human CA IX protein into a  
XX transgenic mouse strain.  
XX  
XX Sequence 107 AA;  
XX  
XX  
XX Query Match 87.1%; Score 478; DB 7; Length 107;  
XX Best Local Similarity 87.6%; Pred. No. 1.9e-26;  
XX Matches 92; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
XX  
XX 1 ELTQSPSSVASVGVDRVTITCRASQGISWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 60  
XX 3 QMTQSPSSVASVGVDRVTITCRASQGISWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 62  
XX  
XX 61 SSGSGYGFDFSLTITSLQFEDSATYTCQANSFPYTFGGQTKVEIK 105  
XX 63 SSGSGSGTFEFLTITSLQPEDFATYTCQANSFPITFGGTRLEIK 107  
XX  
XX  
XX RESULT 15  
XX ABP45870  
XX ID ABP45870 standard; protein; 244 AA.  
XX  
XX AC ABP45870;  
XX  
XX DT 19-AUG-2002 (first entry)  
XX  
XX DE Human BlyS binding scFv SEQ ID 1881.  
XX  
XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antitumematic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200202641-A1.  
XX  
XX PD 10-JAN-2002.  
XX  
XX PF 15-JUN-2001; 2001WO-US019110.  
XX  
XX PR 16-JUN-2000; 2000US-0212210P.  
XX 17-OCT-2000; 2000US-0240816P.  
XX 16-MAR-2001; 2001US-0276248P.  
XX 21-MAR-2001; 2001US-0277379P.  
XX 25-MAY-2001; 2001US-0293499P.  
XX  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:26:32 ; Search time 67.4545 Seconds

(without alignments)  
611.274 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELTQSPSSVSAVSDRVITF.....COANSFPYTGQTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/prodata/2/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/2/pubppaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/prodata/2/pubppaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/prodata/2/pubppaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/2/pubppaa/US07\_NEW\_PUB.pep:\*
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- 11: /cgn2\_6/prodata/2/pubppaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/prodata/2/pubppaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/prodata/2/pubppaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/prodata/2/pubppaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/prodata/2/pubppaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/prodata/2/pubppaa/US10E\_PUBCOMB.pep:\*
- 18: /cgn2\_6/prodata/2/pubppaa/US10F\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/prodata/2/pubppaa/US11\_PUBCOMB.pep:\*
- 20: /cgn2\_6/prodata/2/pubppaa/US11\_NEW\_PUB.pep:\*
- 21: /cgn2\_6/prodata/2/pubppaa/US60\_NEW\_PUB.pep:\*
- 22: /cgn2\_6/prodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	100.0	106	US-10-027-725A-12	Sequence 12, Appl
2	493	89.8	107	US-10-891-658-80	Sequence 80, Appl
3	491	89.4	107	US-10-727-155-312	Sequence 312, Appl
4	491	89.4	129	US-10-910-901-20	Sequence 20, Appl
5	489	89.1	236	US-10-910-901-12	Sequence 12, Appl
6	488	88.9	108	US-10-938-353-109	Sequence 109, Appl
7	487	88.7	107	US-10-727-155-122	Sequence 122, Appl
8	486	88.5	107	US-10-938-353-117	Sequence 117, Appl
9	484	88.2	223	US-10-982-359-67	Sequence 67, Appl
10	484	88.2	223	US-10-693-629-66	Sequence 66, Appl
11	483	88.0	129	US-10-910-901-19	Sequence 19, Appl

12	482	87.8	107	15	US-10-309-762-159	Sequence 159, Appl
13	481	87.6	107	15	US-10-292-088-105	Sequence 105, Appl
14	481	87.6	129	17	US-10-910-901-17	Sequence 17, Appl
15	479	87.2	107	15	US-10-309-762-62	Sequence 62, Appl
16	479	87.2	107	15	US-10-309-762-164	Sequence 164, Appl
17	478	87.1	107	15	US-10-309-762-61	Sequence 61, Appl
18	478	87.1	107	15	US-10-309-762-64	Sequence 64, Appl
19	478	87.1	107	15	US-09-880-748-1881	Sequence 1881, Ap
20	478	87.1	244	15	US-10-293-418-1881	Sequence 1881, Ap
21	477	86.9	107	17	US-10-638-265-76	Sequence 76, Appl
22	477	86.9	107	17	US-10-893-576-177	Sequence 177, Appl
23	477	86.9	129	17	US-10-893-576-24	Sequence 24, Appl
24	477	86.9	212	18	US-10-513-725-7	Sequence 7, Appl
25	475	86.5	236	9	US-09-859-053-30	Sequence 30, Appl
26	475	86.5	236	16	US-10-625-105-30	Sequence 30, Appl
27	475	86.5	236	18	US-10-800-250-30	Sequence 30, Appl
28	474	86.3	107	14	US-10-041-860-43	Sequence 43, Appl
29	474	86.3	107	14	US-10-041-860-218	Sequence 218, Appl
30	474	86.3	107	16	US-10-665-383-64	Sequence 64, Appl
31	474	86.3	236	17	US-10-910-901-16	Sequence 16, Appl
32	473.5	86.2	106	15	US-10-309-762-84	Sequence 84, Appl
33	472	86.0	107	15	US-10-309-762-60	Sequence 60, Appl
34	472	86.0	107	15	US-10-309-762-63	Sequence 63, Appl
35	471	85.8	236	17	US-10-910-901-4	Sequence 4, Appl
36	468.5	85.3	108	14	US-10-041-860-357	Sequence 357, Appl
37	468	85.2	234	15	US-10-292-088-24	Sequence 24, Appl
38	467	85.1	107	16	US-10-703-714-4	Sequence 4, Appl
39	467	85.1	107	16	US-10-703-714-8	Sequence 8, Appl
40	467	85.1	107	16	US-10-703-714-16	Sequence 16, Appl
41	467	85.1	134	16	US-10-473-287-47	Sequence 47, Appl
42	466	84.9	108	10	US-09-920-262A-8	Sequence 8, Appl
43	466	84.9	108	17	US-10-912-994-8	Sequence 8, Appl
44	466	84.9	108	17	US-10-975-683-8	Sequence 8, Appl
45	466	84.9	109	16	US-10-835-641-3	Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-10-027-725A-12  
; Sequence 12, Application US/10027725A  
; Publication No. US20030082659A1  
GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-12

Query Match 100.0%; Score 549; DB 14; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.4e-40;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAVSDRVITTCRASQGISWLAWOHPGKAPKLLIYSASSLSQGVSRF 60  
DB 1 ELTQSPSSVSAVSDRVITTCRASQGISWLAWOHPGKAPKLLIYSASSLSQGVSRF 60

QY 61 SSGSGYGFSLITISLQFEDSATYCCOANSFPYTGQTKVEIKR 106  
DB 61 SSGSGYGFSLITISLQFEDSATYCCOANSFPYTGQTKVEIKR 106

RESULT 2

US-10-891-658-80  
; Sequence 80, Application US/10891658  
; Publication No. US20050074821A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth, Wild  
; APPLICANT: Treanor, James  
; APPLICANT: Huang, Haichun  
; APPLICANT: Inoue, Heather  
; APPLICANT: Zhang, Tie J.  
; APPLICANT: Martin, Frank  
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway  
; FILE REFERENCE: 02-1240  
; CURRENT APPLICATION NUMBER: US/10/891,658  
; CURRENT FILING DATE: 2004-07-15  
; PRIOR APPLICATION NUMBER: US 60/487,431  
; PRIOR FILING DATE: 2003-07-15  
; NUMBER OF SEQ ID NOS: 138  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 80  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-10-891-658-80

Query Match 89.8%; Score 493; DB 17; Length 107;  
Best Local Similarity 90.5%; Pred. No. 1.1e-35;  
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISSWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 60  
Db 3 QMTQSPSSVSAVGDRTVITTCRASQGISSWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 62  
61 SSGSGYGFDTLTITSLQFEDSATYCCQANSFPYTFGGGTVEIK 105  
63 SSGSGYGFDTLTITSLQFEDPATYCCQANSFPWTFGGGTVEIK 107

## RESULT 3

US-10-727-155-312  
; Sequence 312, Application US/10727155  
; Publication No. US20050049402A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. Babcock  
; APPLICANT: Jaspal S. Kang  
; APPLICANT: Larry Green  
; APPLICANT: Xiao Feng  
; APPLICANT: Scott Klakamp  
; APPLICANT: Mary Haak-Frendescho  
; APPLICANT: Palaniswami Rathanaswami  
; APPLICANT: Craig Pigott  
; APPLICANT: Meina Liang  
; APPLICANT: Rozanne Lee  
; APPLICANT: Kathy Manchulenko  
; APPLICANT: Rafiaella Faggioli  
; APPLICANT: Giorgio Senaldi  
; APPLICANT: Olajuan Jane Su  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
; FILE REFERENCE: AGENIX.073A  
; CURRENT APPLICATION NUMBER: US/10/727,155  
; CURRENT FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: 60/430729  
; PRIOR FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 320  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 312  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-727-155-312

Query Match 89.4%; Score 491; DB 17; Length 107;  
Best Local Similarity 90.5%; Pred. No. 1.6e-35;  
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISSWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 60  
Db 3 QMTQSPSSVSAVGDRTVITTCRASQGISSWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 62  
61 SSGSGYGFDTLTITSLQFEDSATYCCQANSFPYTFGGGTVEIK 105  
63 SSGSGYGFDTLTITSLQFEDPATYCCQANSFPWTFGGGTVEIK 107

## RESULT 4

US-10-910-901-20  
; Sequence 20, Application US/10910901  
; Publication No. US20050054019A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHAUD, NEIL R., et al.  
; TITLE OF INVENTION: ANTIBODIES TO C-MET  
; FILE REFERENCE: ABX-PF5  
; CURRENT APPLICATION NUMBER: US/10/910,901  
; CURRENT FILING DATE: 2004-08-03  
; PRIOR APPLICATION NUMBER: US 60/492,432  
; PRIOR FILING DATE: 2003-08-04  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 20  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-910-901-20

Query Match 89.4%; Score 491; DB 17; Length 129;  
Best Local Similarity 90.5%; Pred. No. 2e-35;  
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISSWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 60  
Db 25 QMTQSPSSVSAVGDRTVITTCRASQGISSWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 84  
61 SSGSGYGFDTLTITSLQFEDSATYCCQANSFPYTFGGGTVEIK 105  
85 SSGSGYGFDTLTITSLQFEDPATYCCQANSFPWTFGGGTVEIK 129

## RESULT 5

US-10-910-901-12  
; Sequence 12, Application US/10910901  
; Publication No. US20050054019A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHAUD, NEIL R., et al.  
; TITLE OF INVENTION: ANTIBODIES TO C-MET  
; FILE REFERENCE: ABX-PF5  
; CURRENT APPLICATION NUMBER: US/10/910,901  
; CURRENT FILING DATE: 2004-08-03  
; PRIOR APPLICATION NUMBER: US 60/492,432  
; PRIOR FILING DATE: 2003-08-04  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 12  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-910-901-12

Query Match 89.1%; Score 489; DB 17; Length 236;  
Best Local Similarity 89.6%; Pred. No. 5.3e-35;  
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISSWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 60  
Db 25 QMTQSPSSVSAVGDRTVITTCRASQGISSWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 84

QY 61 SGGSGTDFSLTISLQFEDSATYCCOANSFPYTFQGTKEIKR 106  
DB 85 SGGSGTDFSLTISLQSEDFATYCCOANSFPITFGTKVEIKR 130

## RESULT 6

US-10-938-353-109  
; Sequence 109, Application US/10938353  
; Publication No. US20050059113A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA  
; APPLICANT: FOLTZ, IAN  
; APPLICANT: HAAK-FRENDSCHO, MARY  
; APPLICANT: KELLERMANN, SIRID-AIMEE  
; APPLICANT: LOW, JOSEPH EDWIN  
; APPLICANT: MOBLEY, JAMES LESLIE  
; TITLE OF INVENTION: ANTIBODIES TO M-CSF  
; FILE REFERENCE: ABX-PF4  
; CURRENT APPLICATION NUMBER: US/10/938,353  
; CURRENT FILING DATE: 2004-09-09  
; PRIOR APPLICATION NUMBER: 60/502,163  
; PRIOR FILING DATE: 2003-09-10  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 109  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-938-353-109

Query Match 88.9%; Score 488; DB 17; Length 108;  
Best Local Similarity 88.7%; Pred. No. 3e-35;  
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYOHOPGKAPKLLIYASASSLQSGVPSRF 60  
DB 3 QMTQSPSSVASVGDRTVITTCRASQGISWLAHYOHOPGKAPKLLIYASASSLQSGVPSRF 62  
QY 61 SGGSGTDFSLTISLQFEDSATYCCOANSFPYTFQGTKEIKR 106  
DB 63 SGGSGTDFSLTISLQSEDFATYCCOANSFPITFGTKVEIKR 108

## RESULT 7

US-10-727-155-122  
; Sequence 122, Application US/10727155  
; Publication No. US20050049402A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. Babcock  
; APPLICANT: Jaspal S. Kang  
; APPLICANT: Orit Foord  
; APPLICANT: Larry Green  
; APPLICANT: Xiao Feng  
; APPLICANT: Scott Klakamp  
; APPLICANT: Mary Haak-Frendescho  
; APPLICANT: Palaniswami Rathnaswami  
; APPLICANT: Craig Pigot  
; APPLICANT: Meina Liang  
; APPLICANT: Rozanne Lee  
; APPLICANT: Kathy Marchulenchio  
; APPLICANT: Ralfaela Faggioli  
; APPLICANT: Giorgio Senaldi  
; APPLICANT: Qiaojuan Jane Su  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
; FILE REFERENCE: ARGENIX 073A  
; CURRENT APPLICATION NUMBER: US/10/727,155  
; CURRENT FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: 60/430729  
; PRIOR FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 320

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 122  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-727-155-122

Query Match 88.7%; Score 487; DB 17; Length 107;  
Best Local Similarity 89.5%; Pred. No. 3.7e-35;  
Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYOHOPGKAPKLLIYASASSLQSGVPSRF 60  
DB 3 QMTQSPSSVASVGDRTVITTCRASQGISWLAHYOHOPGKAPKLLIYASASSLQSGVPSRF 62  
QY 61 SGGSGTDFSLTISLQFEDSATYCCOANSFPYTFQGTKEIKR 105  
DB 63 SGGSGTDFSLTISLQSEDFATYCCOANSFPITFGTKVEIKR 107

## RESULT 8

US-10-938-353-117  
; Sequence 117, Application US/10938353  
; Publication No. US20050059113A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA  
; APPLICANT: FOLTZ, IAN  
; APPLICANT: HAAK-FRENDSCHO, MARY  
; APPLICANT: KELLERMANN, SIRID-AIMEE  
; APPLICANT: LOW, JOSEPH EDWIN  
; APPLICANT: MOBLEY, JAMES LESLIE  
; TITLE OF INVENTION: ANTIBODIES TO M-CSF  
; FILE REFERENCE: ABX-PF4  
; CURRENT APPLICATION NUMBER: US/10/938,353  
; CURRENT FILING DATE: 2004-09-09  
; PRIOR APPLICATION NUMBER: 60/502,163  
; PRIOR FILING DATE: 2003-09-10  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 117  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-938-353-117

Query Match 88.5%; Score 486; DB 17; Length 108;  
Best Local Similarity 89.6%; Pred. No. 4.5e-35;  
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYOHOPGKAPKLLIYASASSLQSGVPSRF 60  
DB 3 QMTQSPSSVASVGDRTVITTCRASQGISWLAHYOHOPGKAPKLLIYASASSLQSGVPSRF 62  
QY 61 SGGSGTDFSLTISLQFEDSATYCCOANSFPYTFQGTKEIKR 106  
DB 63 SGGSGTDFSLTISLQSEDFATYCCOANSFPITFGTKVEIKR 108

## RESULT 9

US-10-982-359-67  
; Sequence 67, Application US/10982359  
; Publication No. US20050112694A1  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Zhou, Hongxing  
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR  
; FILE REFERENCE: 3492-A  
; CURRENT APPLICATION NUMBER: US/10/982,359  
; CURRENT FILING DATE: 2004-11-04  
; PRIOR APPLICATION NUMBER: 60/518,166  
; PRIOR FILING DATE: 2003-11-07  
; NUMBER OF SEQ ID NOS: 77

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; SOFTWARE: Patentin version 3.2
; SEQ ID NO 67
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: 63 light chain variable region
US-10-982-359-67

Query Match      88.3%; Score 485; DB 17; Length 107;
Best Local Similarity 88.6%; Pred. No. 5.5e-35;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYGFDFSLTISLQFEDSATYTCQOANSFPYTFGQGTVEIKR 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGYGFDFTLTISLQPEDFATYTCQOANSFPYTFGQGTVEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
US-10-693-629-66
; Sequence 66, Application US/10693629
; Publication No. US20040120948A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: MIKAYAMA, Toshifumi
; APPLICANT: YOSHIDA, Hitoshi
; APPLICANT: FORCE, Walker, R.
; APPLICANT: CHEN, Xingjie
; APPLICANT: TAKAHASHI, Nobuaki
; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
; FILE REFERENCE: 021286-0306473
; CURRENT APPLICATION NUMBER: US/10/693,629
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US09/844,684
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP2001/142482
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: JP2001/310535
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US10/040,244
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 66
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-693-629-66

Query Match      88.2%; Score 484; DB 16; Length 223;
Best Local Similarity 87.7%; Pred. No. 1.4e-34;
Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 QMTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 84
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYGFDFSLTISLQFEDSATYTCQOANSFPYTFGQGTVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 SSGSGYGFDFTLTISLQPEDFATYTCQOANSFPYTFGQGTVEIKR 130
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-10-910-901-19
; Sequence 19, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
```

```
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO C-MET
; FILE REFERENCE: ABX-BF5
; CURRENT APPLICATION NUMBER: US/10/910,901
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 19
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-901-19

Query Match      88.0%; Score 483; DB 17; Length 129;
Best Local Similarity 88.6%; Pred. No. 9.8e-35;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 QMTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 84
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYGFDFSLTISLQFEDSATYTCQOANSFPYTFGQGTVEIKR 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 SSGSGYGFDFTLTISLQPEDFATYTCQOANSFPYTFGQGTVEIKR 129
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
US-10-309-762-159
; Sequence 159, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Handa, Masahisa
; APPLICANT: Poltz, Ian
; APPLICANT: Gallio, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-159

Query Match      87.8%; Score 482; DB 15; Length 107;
Best Local Similarity 88.6%; Pred. No. 1e-34;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYGFDFSLTISLQFEDSATYTCQOANSFPYTFGQGTVEIKR 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGYGFDFTLTISLQPEDFATYTCQOANSFPYTFGQGTVEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
US-10-292-088-105
; Sequence 105, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
```



```

; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-105

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```

Query Match      87.6%; Score 481; DB 15; Length 107;
Best Local Similarity 89.5%; Pred. No. 1.2e-34;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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QY 1 ELTQSPSSVASVGDRTVITCRASQGISWLAHYQHOGKAPKLLIYASASSLQGVPSRF 60
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DB 3 QMTQSPSSVASVGDRTVITCRASQGISWLAHYQHOGKAPKLLIYASASSLQGVPSRF 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQTKVEIK 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 SGSGSGTDFLTITISLQPEDPATYCCQANSFPLTFGGTKVEIK 107
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```

```

RESULT 14
US-10-910-901-17
; Sequence 17; Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO C-MET
; FILE REFERENCE: ABX-PF5
; CURRENT APPLICATION NUMBER: US/10/910,901
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-901-17

```

```

Query Match      87.6%; Score 481; DB 17; Length 129;
Best Local Similarity 89.5%; Pred. No. 1.5e-34;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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QY 1 ELTQSPSSVASVGDRTVITCRASQGISWLAHYQHOGKAPKLLIYASASSLQGVPSRF 60
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DB 25 QMTQSPSSVASVGDRTVITCRASQGISWLAHYQHOGKAPKLLIYASASSLQGVPSRF 84
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQTKVEIK 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 85 SGSGSGTDFLTITISLQPEDPATYCCQANSFPLTFGGTKVEIK 129
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RESULT 15
US-10-309-762-62
; Sequence 62; Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Folitz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

```

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; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-62

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Query Match      87.2%; Score 479; DB 15; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.8e-34;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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QY 1 ELTQSPSSVASVGDRTVITCRASQGISWLAHYQHOGKAPKLLIYASASSLQGVPSRF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 QMTQSPSSVASVGDRTVITCRASQGISWLAHYQHOGKAPKLLIYASASSLQGVPSRF 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQTKVEIK 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 SGSGSGTDFLTITISLQPEDPATYCCQANSFPLTFGGTKVDIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Search completed: July 26, 2005, 10:05:21  
Job time : 68.6212 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 09:09:56 ; Search time 20.0758 Seconds  
(without alignments)  
394.147 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547  
Sequence: 1 ELTQSPSSLSASVCDRTVIT.....QQSTTYLTFRSGTKLEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484	88.5	107	1	US-08-276-852-104
2	484	88.5	107	1	US-08-899-575-104
3	484	88.5	107	1	US-08-899-575-104
4	484	88.5	107	5	PCT-US95-08743-104
5	483	88.3	107	3	US-09-240-274-33
6	480	87.8	107	3	US-09-240-274-156
7	476	87.0	107	1	US-08-276-852-105
8	476	87.0	107	1	US-08-899-575-105
9	476	87.0	107	1	US-08-899-575-105
10	476	87.0	107	5	PCT-US95-08743-105
11	475	86.8	107	3	US-09-240-274-115
12	475	86.8	107	3	US-09-240-274-176
13	474	86.7	107	3	US-09-240-274-179
14	473.5	86.6	108	3	US-09-240-274-32
15	473.5	86.6	108	3	US-09-240-274-41
16	473	86.5	107	3	US-09-240-274-37
17	472.5	86.4	108	3	US-09-240-274-167
18	472	86.3	107	3	US-09-240-274-38
19	472	86.3	107	3	US-09-240-274-39
20	472	86.3	107	3	US-09-240-274-162
21	471	86.1	107	3	US-09-240-274-158
22	469	85.7	107	3	US-09-240-274-44
23	468	85.6	108	2	US-08-379-057-29
24	467	85.4	240	4	US-09-192-854-2
25	464.5	84.9	108	3	US-09-240-274-163
26	463	84.6	104	1	US-08-276-852-106
27	463	84.6	104	1	US-08-899-575-106

28	463	84.6	104	1	US-08-899-575-106	Sequence 106, App
29	463	84.6	104	5	PCT-US95-08743-106	Sequence 106, App
30	461	84.3	108	3	US-09-025-769B-14	Sequence 14, App1
31	461	84.3	108	4	US-09-490-070A-14	Sequence 14, App1
32	461	84.3	108	4	US-09-490-153-14	Sequence 14, App1
33	461	84.3	108	4	US-09-490-324-14	Sequence 14, App1
34	459	83.9	107	1	US-08-300-386A-66	Sequence 66, App1
35	459	83.9	107	3	US-08-931-645-66	Sequence 66, App1
36	459	83.9	107	3	US-09-240-274-168	Sequence 168, App
37	459	83.9	107	5	PCT-US95-11235-66	Sequence 66, App1
38	457	83.5	107	3	US-09-240-274-36	Sequence 36, App1
39	457	83.5	109	3	US-09-157-370-3	Sequence 71, App1
40	457	83.5	214	4	US-09-472-087-71	Sequence 71, App1
41	456.5	83.5	108	1	US-08-276-852-109	Sequence 109, App
42	456.5	83.5	108	1	US-08-899-575-109	Sequence 109, App
43	456.5	83.5	108	1	US-08-899-575-109	Sequence 109, App
44	456.5	83.5	108	3	US-09-240-274-41	Sequence 41, App1
45	456.5	83.5	108	5	PCT-US95-08743-109	Sequence 109, App

## ALIGNMENTS

RESULT 1  
US-08-276-852-104  
Sequence 104, Application US/08276852  
Patent No. 5652138  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESS: The Scripps Research Institute, Office of  
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,852  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRI452P  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-852-104

Query Match 88.5%; Score 484; DB 1; Length 107;  
Best Local Similarity 88.7%; Pred. No. 2e-36;  
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCRASQISTYLNWYQOKGKAPKLLIYASNLQSGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITTCRASQISTYLNWYQOKGKAPKLLIYASNLQSGVPSRF 60

Qy 61 SGSGSGTEFTLTISNLQPEDFASYYCOQSYTTLTYTFSGGTLEIKR 106  
Db 61 SGSGSGTDFTLTISLQPEDFATYYCOQSYSTPYTFGGTLEIKR 106

RESULT 2  
US-08-899-575-104  
; Sequence 104, Application US/08899575  
; Patent No. 5770440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbos, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCR1452P  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-899-575-104

Query Match 88.5%; Score 484; DB 1; Length 107;  
Best Local Similarity 88.7%; Pred. No. 2e-36;  
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCRASQISTYLNWYQOKGKAPKLLIYASNLQSGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITTCRASQISTYLNWYQOKGKAPKLLIYASNLQSGVPSRF 60

Qy 61 SGSGSGTEFTLTISNLQPEDFASYYCOQSYTTLTYTFSGGTLEIKR 106  
Db 61 SGSGSGTDFTLTISLQPEDFATYYCOQSYSTPYTFGGTLEIKR 106

RESULT 3  
US-08-899-575-104  
; Sequence 104, Application US/08899575  
; Patent No. 5804440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbos, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCR1452P  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-899-575-104

Query Match 88.5%; Score 484; DB 1; Length 107;  
Best Local Similarity 88.7%; Pred. No. 2e-36;  
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCRASQISTYLNWYQOKGKAPKLLIYASNLQSGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITTCRASQISTYLNWYQOKGKAPKLLIYASNLQSGVPSRF 60

Qy 61 SGSGSGTEFTLTISNLQPEDFASYYCOQSYTTLTYTFSGGTLEIKR 106  
Db 61 SGSGSGTDFTLTISLQPEDFATYYCOQSYSTPYTFGGTLEIKR 106

RESULT 4  
PCT-US95-08743-104  
; Sequence 104, Application PC/TUS9508743

```

; GENERAL INFORMATION:
; APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-104

Query Match 88.5%; Score 484; DB 5; Length 107;
Best Local Similarity 88.7%; Pred. No. 2e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTOSPSLSASVGDRTVITTCRASQISITVLMWYQOKRGKAPKLLIYASNLQSGVPSRF 60
Db 1 ELTOSPSLSASVGDRTVITTCRASQISITVLMWYQOKRGKAPKLLIYASNLQSGVPSRF 60
Qy 61 SSGSGGTFTLTISLQPEDPASYCCOOSYTTLYTFSGGTLEIKR 106
Db 61 SSGSGGTFTLTISLQPEDPASYCCOOSYTTLYTFSGGTLEIKR 106

RESULT 5
US-09-240-274-33
; Sequence 33, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-33

Query Match 88.3%; Score 483; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.4e-36;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ELTOSPSLSASVGDRTVITTCRASQISITVLMWYQOKRGKAPKLLIYASNLQSGVPSRF 60
Db 2 ELTOSPSLSASVGDRTVITTCRASQISITVLMWYQOKRGKAPKLLIYASNLQSGVPSRF 61
Qy 61 SSGSGGTFTLTISLQPEDPASYCCOOSYTTLYTFSGGTLEIKR 106
Db 62 SSGSGGTFTLTISLQPEDPASYCCOOSYTTLYTFSGGTLEIKR 107
```

```

RESULT 6
US-09-240-274-156
; Sequence 156, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-156

Query Match 87.8%; Score 480; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 4.5e-36;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTOSPSLSASVGDRTVITTCRASQISITVLMWYQOKRGKAPKLLIYASNLQSGVPSRF 60
Db 2 ELTOSPSLSASVGDRTVITTCRASQISITVLMWYQOKRGKAPKLLIYASNLQSGVPSRF 61
Qy 61 SSGSGGTFTLTISLQPEDPASYCCOOSYTTLYTFSGGTLEIKR 106
Db 62 SSGSGGTFTLTISLQPEDPASYCCOOSYTTLYTFSGGTLEIKR 107

RESULT 7
US-08-276-852-105
; Sequence 105, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESS: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRI452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-852-105

Query Match 87.0%; Score 476; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1e-35;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNMYQOKPGKAPKLLIWSASNLQGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNMYQOKPGKAPKLLIYAASSLQGVPSRF 60  
QY 61 SGGSGGTFFLTITISNLQFEDFASYCCOQSYTTLVTFSGTKLEIKR 106  
Db 61 SGGSGGTDFLTITISLQPEDFATYCCOQSYSTPQTFGGTLEIKR 106

RESULT 8  
US-08-899-575-105  
Sequence 105, Application US/08899575  
Patent No. 5770440  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbias, Carlos F  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
STREET: Mail Drop TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,575  
FILING DATE: 24-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRI452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-899-575-105

Query Match 87.0%; Score 476; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1e-35;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNMYQOKPGKAPKLLIWSASNLQGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNMYQOKPGKAPKLLIYAASSLQGVPSRF 60  
QY 61 SGGSGGTFFLTITISNLQFEDFASYCCOQSYTTLVTFSGTKLEIKR 106  
Db 61 SGGSGGTDFLTITISLQPEDFATYCCOQSYSTPQTFGGTLEIKR 106

RESULT 9  
US-08-899-575-105  
Sequence 105, Application US/08899575  
Patent No. 5804440  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbias, Carlos F  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
STREET: Mail Drop TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,575  
FILING DATE: 24-JUL-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRI452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-899-575-105

Query Match 87.0%; Score 476; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1e-35; Indels 0; Gaps 0;  
Matches 93; Conservative 8; Mismatches 5;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 60  
QY 61 SGGSGGTEFTLTISNLOPEDFASYYCOQSYTTLYTFSGTYKLEIKR 106  
DB 61 SGGSGGTEFTLTISNLOPEDFASYYCOQSYTTLYTFSGTYKLEIKR 106

RESULT 10  
PCT-US95-08743-105  
Sequence 105, Application PC/TUS9508743  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08743  
FILING DATE: 11-JUL-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-08743-105

Query Match 87.0%; Score 476; DB 5; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1e-35; Indels 0; Gaps 0;  
Matches 93; Conservative 8; Mismatches 5;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 60  
QY 61 SGGSGGTEFTLTISNLOPEDFASYYCOQSYTTLYTFSGTYKLEIKR 106  
DB 61 SGGSGGTEFTLTISNLOPEDFASYYCOQSYTTLYTFSGTYKLEIKR 106

RESULT 11  
US-09-240-274-175  
Sequence 175, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
EARLIER FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 175  
LENGTH: 107

TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH49  
US-09-240-274-175

Query Match 86.8%; Score 475; DB 3; Length 107;  
Best Local Similarity 85.8%; Pred. No. 1.3e-35; Indels 0; Gaps 0;  
Matches 91; Conservative 11; Mismatches 4;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 61  
QY 61 SGGSGGTEFTLTISNLOPEDFASYYCOQSYTTLYTFSGTYKLEIKR 106  
DB 62 SGGSGGTEFTLTISNLOPEDFASYYCOQSYTTLYTFSGTYKLEIKR 107

RESULT 12  
US-09-240-274-176  
Sequence 176, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
EARLIER FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 176  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH50  
US-09-240-274-176

Query Match 86.8%; Score 475; DB 3; Length 107;  
Best Local Similarity 85.8%; Pred. No. 1.3e-35; Indels 0; Gaps 0;  
Matches 91; Conservative 11; Mismatches 4;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 61  
QY 61 SGGSGGTEFTLTISNLOPEDFASYYCOQSYTTLYTFSGTYKLEIKR 106  
DB 62 SGGSGGTEFTLTISNLOPEDFASYYCOQSYTTLYTFSGTYKLEIKR 107

RESULT 13  
US-09-240-274-179  
Sequence 179, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
EARLIER FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
NUMBER OF SEQ ID NOS: 224

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-179
```

```
Query Match      86.6%; Score 474; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.5e-35;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSLSASVGDVTTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 ELTQSPSSLSASVGDVTTITCRASQISIGTYLMWYQKPGKAPKLLIYAASSLQGVPSRF 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SSGSGGTFTLTISNLFQEDFASYYCOQSYTT-LYTFGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 SSGSGGTFTLTISLQPEDFATYYCOQSYSTPTPTFGQGTKEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

## RESULT 14

```
US-09-240-274-32
; Sequence 32, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 101
US-09-240-274-32
```

```
Query Match      86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.7e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;
```

```
QY 1 ELTQSPSSLSASVGDVTTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 ELTQSPSSLSASVGDVTTITCRASQISISTYLMWYQKPGKAPKLLIYAASSLQGVPSRF 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SSGSGGTFTLTISNLFQEDFASYYCOQSYTT-LYTFGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 SSGSGGTFTLTISLQPEDFATYYCOQSYSTPTPTFGQGTKEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

## RESULT 15

```
US-09-240-274-43
; Sequence 43, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
```

```
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 112
US-09-240-274-43
```

```
Query Match      86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.7e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;
```

```
QY 1 ELTQSPSSLSASVGDVTTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 ELTQSPSSLSASVGDVTTITCRASQISISTYLMWYQKPGKAPKLLIYAASSLQGVPSRF 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SSGSGGTFTLTISNLFQEDFASYYCOQSYTT-LYTFGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 SSGSGGTFTLTISLQPEDFATYYCOQSYSTPTPTFGQGTKEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
Search completed: July 26, 2005, 09:30:01
Job time : 21.0758 secs
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Result No.	Score	Query Match	Length	DB	ID	Description
1	468	85.6	108	2	B49047	Ig kappa chain V r
2	465	85.0	108	2	S47182	Ig kappa chain - h
3	465	85.0	127	2	S40367	Ig kappa chain V-J
4	464	84.8	109	2	S31998	Ig kappa chain - h
5	462	84.5	123	2	S40331	Ig kappa chain - h
6	457	83.5	122	2	S40370	Ig kappa chain - h
7	455	83.2	108	2	S44122	Ig kappa chain V r
8	454	83.0	108	2	S31977	Ig kappa chain - h
9	453	82.8	129	1	K1HWK	Ig kappa chain pre
10	451	82.4	109	2	S31981	Ig kappa chain - h
11	451	82.4	109	2	S31978	Ig kappa chain - h
12	449	82.1	108	1	K1HDE	Ig kappa chain V-I
13	447	81.7	108	2	S19674	Ig kappa chain V r
14	446	81.5	119	2	S40317	Ig kappa chain V r
15	438	80.1	127	2	S46371	Ig kappa chain V-J
16	437.5	80.0	106	2	PC3297	anti-tetanus toxin
17	437	79.9	107	2	S36264	Ig lambda chain V
18	437	79.9	108	1	K1HBU	Ig kappa chain V-I
19	437	79.9	120	2	S46370	Ig kappa chain V-J
20	436	79.7	109	2	S31979	Ig kappa chain - h
21	434	79.3	129	2	S52793	Ig kappa chain V r
22	433	79.2	128	2	S46372	Ig light chain vari
23	432	79.0	109	2	S31980	Ig kappa chain - h
24	432	79.0	125	2	S40350	Ig kappa chain - h
25	431	78.8	109	2	S31983	Ig kappa chain - h
26	429	78.4	129	2	S52792	Ig kappa chain V r
27	429	78.4	132	2	S40334	Ig kappa chain - h
28	428	78.2	109	2	S32001	Ig kappa chain - h
29	428	78.2	122	2	S40314	Ig kappa chain - h

30	428	78.2	132	2	S38646	Ig kappa chain V
31	427.5	78.1	125	2	S40315	Ig kappa chain - h
32	427	78.1	125	2	S40349	Ig kappa chain V-J
33	425.5	77.8	124	2	S40336	Ig kappa chain V-J
34	424.5	77.6	107	2	S36275	Ig lambda chain V
35	424	77.5	108	1	K1HU0U	Ig kappa chain V-I
36	424	77.5	125	2	S40333	Ig kappa chain V-I
37	421.5	77.1	108	2	S30521	Ig kappa chain V
38	419	76.6	116	2	A27594	Ig kappa chain pre
39	419	76.6	117	2	S24206	Ig kappa chain V r
40	418	76.4	109	2	JUN296	Ig kappa chain V-J
41	418	76.4	129	2	S40369	Ig kappa chain - h
42	417.5	76.3	108	2	S34007	Ig kappa chain V r
43	417	76.2	126	2	S40335	Ig kappa chain V-I
44	416	76.1	108	1	K1HU4U	Ig kappa chain V-I
45	416	76.1	108	1	K1HU9E	Ig kappa chain V-I

ig kappa chain V region (monoclonal stratiational autoantibody strAB SA-1A) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: B49047  
R/Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.  
Eur. J. Immunol. 22, 2231-2236, 1992  
A>Title: Human monoclonal stratiational autoantibodies isolated from thymic B lymphocytes  
A/Reference number: A49047, PMID:92387224, PMID:1516616  
A/Accession: B49047  
A/Status: preliminary  
A/Molecule type: nucleic acid  
A/Residues: 1-108 <VIC>  
A/Cross-references: UNIPROT:O96SA9; UNIPROT:O9UL77  
A/Experimental source: thymic B lymphocytes  
A/Note: sequence extracted from NCBI backbone (NCBI:113208, NCBI:113209)  
C/Superfamily: Immunoglobulin V region; Immunoglobulin Homology  
/16-90/Domain: Immunoglobulin homology <IMH>

Query Match 85.6%; Score 468; DB 2; length 108;  
 Best Local Similarity 84.9%; Pred.No. 4,1e-34;  
 Matches 90; Conservative 11; Mismatches 5; Indels 0; Gaps 0.

QY 1 ELTSPSSLSASVDRVTITCRARQSISTYLNMYQQRGKAPKLLIWSASNIQSGVPSRF 60  
 ::  
 Db 3 QMTDPSPLSASVDRVTITCRARQSISTYLNMYQQRGKAPKLLIYAASLSQSGVPSRF 62

QY 61 SGGSGGTEFTLLTISNLQFEDFASYTCOOSYTTLLTFGSGTKLEIKR 106  
 ::  
 Db 63 SGGSSGTDFTLLTISLQPEDPATYTCOOSYSTPLTFGGTQVLEIKR 108

IG kappa chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C/Accession: S47182  
R/McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.  
submitted to the EMBL Data Library, June 1994  
A/Description: Cloning and analysis of IGM anti-thyroglobulin autoantibodies from patient  
A/Reference number: S47181  
A/Accession: S47182  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-108 <K1>  
A/Cross-references: EMBL:X79786; NID:G506422; PIDN:CA56182.1; PID:G506423  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
#16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 465; DB 2; Length 108;  
Best Local Similarity 85.8%; Pred. No. 7.5e-34;  
Matches 91; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Query 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPKGAPKLLIWSASNLQSGVPSRF 60  
Db 3 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPKGAPKLLIWAASLQSGVPSRF 62  
Qy 61 SSGSGGTEFTLITISNLQPEDFASYCCOQSYTTLYTFGSGTKLEIKR 106  
Db 63 SSGSGGTEFTLITISNLQPEDFASYCCOQSYTTLYTFGSGTKLEIKR 108

RESULT 3  
S40367  
Ig kappa chain V-J-C region - human  
C/Species: Homo sapiens (man)  
C/Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S40367  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MUID:94080891; PMID:8258341  
A/Accession: S40367  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-127 <KLE>  
A/Cross-references: EMBL:X72477  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 465; DB 2; Length 127;  
Best Local Similarity 84.0%; Pred. No. 8.8e-34;  
Matches 89; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Query 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPKGAPKLLIWSASNLQSGVPSRF 60  
Db 20 QMTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPKGAPKLLIWAASLQSGVPSRF 79  
Qy 61 SSGSGGTEFTLITISNLQPEDFASYCCOQSYTTLYTFGSGTKLEIKR 106  
Db 80 SSGSGGTEFTLITISNLQPEDFASYCCOQSYTTLYTFGSGTKLEIKR 125

RESULT 4  
S31998  
Ig kappa chain - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C/Accession: S31998  
R/Portiano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
A/Reference number: S31977  
A/Accession: S31998  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-109 <POR>  
A/Cross-references: EMBL:Z15081; NID:G38501; PIDN:CAA78790.1; PID:G38502  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 464; DB 2; Length 109;  
Best Local Similarity 85.7%; Pred. No. 9.3e-34;  
Matches 90; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Query 2 LTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPKGAPKLLIWSASNLQSGVPSRF 61  
Db 4 MTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPKGAPKLLIWAASLQSGVPSRF 63  
Qy 62 SSGSGTEFTLITISNLQPEDFASYCCOQSYTTLYTFGSGTKLEIKR 106

Db 64 SSGSGTEFTLITISNLQPEDFASYCCOQSYTTLYTFGSGTKLEIKR 108

RESULT 5  
S40331  
Ig kappa chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S40331  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MUID:94080891; PMID:8258341  
A/Accession: S40331  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-123 <KLE>  
A/Cross-references: EMBL:X72441; NID:G441350; PIDN:CAA51109.1; PID:G441351  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 462; DB 2; Length 123;  
Best Local Similarity 84.8%; Pred. No. 1.6e-33;  
Matches 89; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Query 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPKGAPKLLIWSASNLQSGVPSRF 60  
Db 19 QMTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPKGAPKLLIWAASLQSGVPSRF 78  
Qy 61 SSGSGGTEFTLITISNLQPEDFASYCCOQSYTTLYTFGSGTKLEIKR 105  
Db 79 SSGSGGTEFTLITISNLQPEDFASYCCOQSYTTLYTFGSGTKLEIKR 123

RESULT 6  
S40370  
Ig kappa chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S40370  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MUID:94080891; PMID:8258341  
A/Accession: S40370  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-122 <KLE>  
A/Cross-references: EMBL:X72480; NID:G441428; PIDN:CAA51148.1; PID:G441429  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/30-104/Domain: immunoglobulin homology <IMM>

Query Match 83.5%; Score 457; DB 2; Length 122;  
Best Local Similarity 84.9%; Pred. No. 4.2e-33;  
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Query 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPKGAPKLLIWSASNLQSGVPSRF 60  
Db 17 QMTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPKGAPKLLIWAASLQSGVPSRF 76  
Qy 61 SSGSGGTEFTLITISNLQPEDFASYCCOQSYTTLYTFGSGTKLEIKR 106  
Db 77 SSGSGGTEFTLITISNLQPEDFASYCCOQSYTTLYTFGSGTKLEIKR 122

RESULT 7  
S44122  
Ig kappa chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001





Best Local Similarity 80.6%; Pred. No. 1.8e-31;  
Matches 87; Conservative 10; Mismatches 9; Indels 2; Gaps 1;

Qy	1	ELTQSPSSLSASVGRVYITTCRAROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF	60
Db	10	QMTQSPSTLSASVGRVYITTCRASRISITWLAWYQOKPGKAPKLLIYKASTLESVPSRF	69
Qy	61	SGSGSGTEFTLTISNLOFEDFASYCOO--SYTLYTFGSGSTKLEIKR	106
Db	70	SGSGSGTEFTLTISLQPDDEATYCCQYNSYFPPTFGGCTKLEIKR	117

Search completed: July 26, 2005, 09:27:50  
Job time : 13.6515 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 26, 2005, 08:52:21 ; Search time 66.6515 Seconds

(without alignments)  
814.391 Million cell updates/sec

Title: US-10-027-725a-11

Sequence: 1 ELTQSPSSLSASVGDRTYIT.....QQSYTTLTYFGSGTKLEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt 03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	85.4	108	Q9UL77	Q9UL77 homo sapien
2	465.5	85.1	107	Q96SA9	Q96SA9 homo sapien
3	453	82.8	129	KV1W_HUMAN	P04433 homo sapien
4	449	82.0	108	KV1E_HUMAN	P01597 homo sapien
5	448.5	82.0	107	Q9UL81	P01597 homo sapien
6	437	79.9	108	KV1H_HUMAN	P01600 homo sapien
7	433	79.2	236	Q6GMX8	Q6GMX8 homo sapien
8	431	78.8	236	Q6GMW1	Q6GMW1 homo sapien
9	430	78.6	236	Q6GMX0	Q6GMX0 homo sapien
10	428	78.2	236	Q6PIH7	Q6PIH7 homo sapien
11	424	77.5	108	KV1N_HUMAN	P01606 homo sapien
12	423	77.3	234	Q7Z473	Q7Z473 homo sapien
13	416	76.1	108	KV1B_HUMAN	P01594 homo sapien
14	416	76.1	108	KV1O_HUMAN	P01607 homo sapien
15	414	75.7	108	Q9UL70	Q9UL70 homo sapien
16	413.5	75.6	107	KV1D_HUMAN	P01596 homo sapien
17	413	75.3	129	Q9UL79	Q9UL79 homo sapien
18	412	75.3	109	KV1X_HUMAN	P04432 homo sapien
19	411.5	75.2	109	KV1T_HUMAN	P01612 homo sapien
20	411	75.1	108	KV1S_HUMAN	P01611 homo sapien
21	408	74.6	108	KV1V_HUMAN	P04430 homo sapien
22	408	74.6	236	Q7Z3Y4	Q7Z3Y4 homo sapien
23	407	74.4	108	KV1F_HUMAN	P01598 homo sapien
24	403	73.7	108	KV1P_HUMAN	P01608 homo sapien
25	402	73.5	108	KV1G_HUMAN	P01593 homo sapien
26	402	73.5	108	KV1I_HUMAN	P01604 homo sapien
27	401	73.3	108	KV1L_HUMAN	P01604 homo sapien
28	401	73.3	108	KV1Y_HUMAN	P01610 homo sapien
29	401	73.3	236	Q6PIT5	Q6PIT5 homo sapien
30	399	72.9	108	KV1R_HUMAN	P01610 homo sapien
31	398	72.8	236	Q6GMX9	Q6GMX9 homo sapien

32	397	72.6	244	2	Q65ZC8	Q65ZC8 homo sapien
33	396	72.4	108	1	KV1C_HUMAN	P01595 homo sapien
34	395	72.2	108	1	KV1M_HUMAN	P01605 homo sapien
35	395	72.2	236	2	Q6PIH4	Q6PIH4 homo sapien
36	394	72.0	240	2	Q65ZC9	Q65ZC9 homo sapien
37	393	71.8	108	1	KV1K_HUMAN	P01603 homo sapien
38	387	70.7	238	2	Q9QYF0	Q9QYF0 synthetic c
39	384	70.2	108	1	KV1Q_HUMAN	P01609 homo sapien
40	384	70.2	108	1	KV5M_MOUSE	P01646 mus musculu
41	383	70.0	117	1	KV1J_HUMAN	P01602 homo sapien
42	377	68.9	117	1	KV1I_HUMAN	P01601 homo sapien
43	375	68.6	108	1	KV5N_MOUSE	P01647 mus musculu
44	374	68.4	108	1	KV5K_MOUSE	P01644 mus musculu
45	374	68.4	116	2	Q96PF6	Q96PF6 homo sapien

## ALIGNMENTS

RESULT 1									
ID	Q9UL77	PRELIMINARY;	PRT;	108	AA.				
AC	Q9UL77								
DT	01-MAY-2000 (TREMBlrel. 13, Created)								
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)								
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)								
DE	Myosin-reactive immunoglobulin light chain variable region (Fragment).								
OS	Homo sapiens (human).								
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.								
OX	NCBI_Taxid:9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE:98277139; PubMed:9614934; DOI:10.1006/clin.1998.4531;								
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,								
RT	Young D.C.;								
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."								
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).								
DR	EMBL; AF035037; AAD56273.1; -.								
DR	PIR; B49047; B49047.								
DR	PIR; S34083; S34083.								
DR	HSSP; P01607; IBMW.								
DR	InterPro; IPR007110; Ig-like.								
DR	InterPro; IPR003596; Ig_v.								
DR	SMART; SM00406; IG_v.1.								
DR	PROSITE; PS50835; IG_LIKE; 1.								
FT	NON_TER								
FT	SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;								
SO	SEQUENCE								
Query Match									
Best Local Similarity 84.0%; Pred. No. 7.1e-41;									
Matches 89; Conservative 12; Mismatches 5; Indels 0; Gaps 0;									
Qy	1	ELTQSPSSLSASVGDRTYITTCRAQOSTIYNTQYQPGKPKLLMSASNLGCVSRF	60						
Db	3	QMTQSPSSLSASVGDRTYITTCRASQSTSYIYNTYQKRGKAPNLLIYAASLSGVSRRF	62						
Qy	61	SGSGSGEFTLTISNLFQEDPASYYCOASYTTLTYFGSGTKLEIKR	106						
Db	63	SGSGSGFTLTITSSLSQPEDPATYCCQASTSTMTFSGTKVEIKR	108						
RESULT 2									
ID	Q96SA9	PRELIMINARY;	PRT;	107	AA.				
AC	Q96SA9								
DT	01-DEC-2001 (TREMBlrel. 19, Created)								
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)								
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)								
DE	Anti-streptococcal/anti-myosin immunoglobulin kappa light chain								

```

DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic arthritis: human anti-N-acetylglucosamine/anti-mycosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AB86785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; 1BMW.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IG_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 85.1%; Score 465.5; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 1e-40; 3; Indels 1; Gaps 1;
Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTITICRAQSISTYLNWYQKPKGAPKLLIWSASNLGVSRSF 60
Db 3 QMTQSPSSLSASVGDRTITICRAQSISTYLNWYQKPKGAPKLLIWSASNLGVSRSF 62
QY 61 SSGSGGTFTLTISNLOPEDPASYCCOQSTTYTTPSGSKLEIKR 106
Db 63 SSGSGGTFTLTISNLOPEDPASYCCOQSTTYTTPSGSKLEIKR 107

RESULT 3
KVLE_HUMAN STANDARD; PRT; 129 AA.
ID KVLE_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G.; Combracio G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1HDWK.
DR HSSP; P01607; 1BMW.

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DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 23 129
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
FT DOMAIN 79 110
FT DOMAIN 111 119
FT DOMAIN 120 129
FT DISULFID 45 110
FT NON_TER 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07DAFC2F9 CRC64;

Query Match 82.8%; Score 453; DB 1; Length 129;
Best Local Similarity 83.8%; Pred. No. 2.5e-39; 7; Indels 0; Gaps 0;
Matches 88; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTITICRAQSISTYLNWYQKPKGAPKLLIWSASNLGVSRSF 60
Db 25 QMTQSPSSLSASVGDRTITICRAQSISTYLNWYQKPKGAPKLLIWSASNLGVSRSF 84
QY 61 SSGSGGTFTLTISNLOPEDPASYCCOQSTTYTTPSGSKLEIKR 105
Db 85 SSGSGGTFTLTISNLOPEDPASYCCOQSTTYTTPSGSKLEIKR 129

RESULT 4
KVLE_HUMAN STANDARD; PRT; 108 AA.
ID KVLE_HUMAN STANDARD; PRT; 108 AA.
AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Mistein C.P.; Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain.";
RL Biochem. J. 123:945-958(1971).
CC 1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -----
DR PIR; A01865; K1HDEU.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88

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FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6350017F1E51 CRC64;

Query March
Best Local Similarity 82.1%; Score 449; DB 1; Length 108;
Matches 88; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQQRKPKLLMSASNLQSGVPSRF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 ZMTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQQRKPKPKYLIFASLSKGVPSRF 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGSTGFLLTISNLOPEDFASVYCOQSYTTLTTPSGSTKLEIKR 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGSTGFLLTISNLOPEDFATVYCOQSYTTPYFGGTKEVETR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Betney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -
DR HSP; P01607; IBMW
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query March
Best Local Similarity 82.0%; Score 448.5; DB 2; Length 107;
Matches 87; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQQRKPKLLMSASNLQSGVPSRF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 ZMTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQQRKPKPKYLIFASLSKGVPSRF 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGSTGFLLTISNLOPEDFASVYCOQSYTTLTTPSGSTKLEIKR 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGSTGFLLTISNLOPEDFATVYCOQSYTTPYFGGTKEVETR 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
KV1H HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hirschman N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01868; KIHUHU.
DR PDB; 1F6U; X-ray; L=1-108.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query March
Best Local Similarity 79.9%; Score 437; DB 1; Length 108;
Matches 83; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQQRKPKLLMSASNLQSGVPSRF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 ZMTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQQRKPKPKYLIFASLSKGVPSRF 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGSTGFLLTISNLOPEDFASVYCOQSYTTLTTPSGSTKLEIKR 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGSTGFLLTISNLOPEDFATVYCOQSYTTPYFGGTKEVETR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q6GMX8 PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Cavani P., Prange C.,
RA Raha S.S., Loguailano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073764; AAH73764.1; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003066; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-sec; 1.  
 DR Pfam; PF07654; Ig; 2.  
 DR SMART; SM00409; IgC1; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PSS0835; IG LIKE; 2.  
 DR PROSITE; PSS0230; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25707 MW; 4FC8E1AB6559EFC9 CRC64;

Query Match 79.2%; Score 433; DB 2; Length 236;  
 Best Local Similarity 77.4%; Pred. No. 6,1e-37;  
 Matches 82; Conservative 17; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVYITTCRAQOSISTYLMNYOQKPGKAPKLLIWSASNLQSGVPSRF 60  
 Db 25 QMTQSPSSLSASVGDVYITTCRAQOSISTYLMNYOQKPGKAPKLLIWSASNLQSGVPSRF 84  
 QY 61 SSGSGGTFTLTISNLOFEDPASYCCOQSYTTLTYFGSGTKLEIKR 106  
 Db 85 SSGSGGTFTLTISNLOFEDPASYCCOQSYTTLTYFGSGTKLEIKR 130

RESULT 8  
 Q6GKM1 PRELIMINARY; PRT; 236 AA.  
 AC Q6GKM1;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Beseck S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Blakesley R.W., Touchman J.W., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073791; AAH73791.1; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003066; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-sec; 1.  
 DR Pfam; PF07654; Ig; 2.  
 DR SMART; SM00409; IgC1; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PSS0835; IG LIKE; 2.  
 DR PROSITE; PSS0230; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25751 MW; 5BFB6A087APAC437 CRC64;

Query Match 78.8%; Score 431; DB 2; Length 236;  
 Best Local Similarity 79.2%; Pred. No. 9,8e-37;  
 Matches 84; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVYITTCRAQOSISTYLMNYOQKPGKAPKLLIWSASNLQSGVPSRF 60  
 Db 25 QMTQSPSSLSASVGDVYITTCRAQOSISTYLMNYOQKPGKAPKLLIWSASNLQSGVPSRF 84  
 QY 61 SSGSGGTFTLTISNLOFEDPASYCCOQSYTTLTYFGSGTKLEIKR 106  
 Db 85 SSGSGGTFTLTISNLOFEDPASYCCOQSYTTLTYFGSGTKLEIKR 130

RESULT 9  
 Q6GKM1 PRELIMINARY; PRT; 236 AA.  
 AC Q6GKM1;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Beseck S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Blakesley R.W., Touchman J.W., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strauberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073775; AAH3775.1; -  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00047; IG; 2.  
 DR SMART; SM00407; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KM Hypothetical protein\_1.  
 SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8 CRC64;  
 Query Match 78.6%; Score 430; DB 2; Length 236;  
 Best Local Similarity 77.4%; Pred. No. 1,3e-36;  
 Matches 82; Conservative 13; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 ELTQSPSLASVGDRTVITTCRAQOSISTYLNMYQKRGKAPKLLMSASNLQSGVSRF 60  
 DB 25 QLTQSPFLSASVGDRTVITTCRAQOSISTYLNMYQKRGKAPKLLMSASNLQSGVSRF 84  
 QY 61 SGSSGSGTEFLTITSLQPEDPASYCCOQSYTTLTPSGGTLEIKR 106  
 DB 85 SGSSGSGTEFLTITSLQPEDPASYCCOQSYTTLTPSGGTLEIKR 130  
 RESULT 10  
 ID Q6PIH7 PRELIMINARY; PRT; 236 AA.  
 AC Q6PIH7;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg H., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uscid T.B., Toshlyuk S., Carlini P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,  
 RA Kizylinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Maitra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strauberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC034141; AAH34141.1; -  
 DR HSSP; P01607; IAK2.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;  
 Query Match 78.2%; Score 428; DB 2; Length 236;  
 Best Local Similarity 80.2%; Pred. No. 2e-36;  
 Matches 85; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 ELTQSPSLASVGDRTVITTCRAQOSISTYLNMYQKRGKAPKLLMSASNLQSGVSRF 60  
 DB 25 QLTQSPFLSASVGDRTVITTCRAQOSISTYLNMYQKRGKAPKLLMSASNLQSGVSRF 84  
 QY 61 SGSSGSGTEFLTITSLQPEDPASYCCOQSYTTLTPSGGTLEIKR 106  
 DB 85 SGSSGSGTEFLTITSLQPEDPASYCCOQSYTTLTPSGGTLEIKR 130  
 RESULT 11  
 ID KVIN HUMAN STANDARD; PRT; 108 AA.  
 AC P01606;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig kappa chain V-I region OU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=70201507; PubMed=5447531;  
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;  
 RT "Macroglobulin structure: variable sequence of light and heavy  
 chains".  
 RL Science 169:56-59(1970).  
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
 CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's  
 macroglobulin.  
 DR PIR; A01872; KIHUOU.  
 DR HSSP; P01607; IEMW.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 2 34 Complementarity-determining-1.  
 FT DOMAIN 3 35 Framework-2.  
 FT DOMAIN 4 49 Complementarity-determining-2.  
 FT DOMAIN 5 56 Complementarity-determining-3.  
 FT DOMAIN 6 88 Complementarity-determining-4.  
 FT DOMAIN 7 97 Framework-4.  
 FT DOMAIN 8 107 Framework-4.

FT DISULFID 23 88 By similarity.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24105827E CRC64;  
Query Match 77.5%; Score 424; DB 1; Length 108;  
Best Local Similarity 68.9%; Pred. No. 2.2e-36;  
Matches 73; Conservative 25; Mismatches 8; Indels 0; Gaps 0;  
QY 1 ELTPSPSSLSASVGDRTVITTCRAQOSISTYLMWYQKPGKAPKLLIWSASNLGSPSRF 60  
DB 3 QMTZSPSSLSASVGBRVITTCRASZITSSYLBWZZKRGKAPBILIIYAASBLHSGVPSRF 62  
QY 61 GSGSGTFFLTITSLNLOFEDFASYYCOOSTTTLTPSSGRTLEIKR 106  
DB 63 GSGSGTFFLTITSLNLOFEDFASYYCOOSTTTLTPSSGRTLEIKR 108  
RESULT 12  
Q72473 PRELIMINARY; PRT; 234 AA.  
AC Q72473;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=23388257; Pubmed=12477932; DOI=10.1073/pnas.2426038999;  
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatzenko L., Marusik K., Farmer A.A., Rubin G.W., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshitsuki S., Carninci P., Prange C.,  
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McGean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fehey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywnicki M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC056256; AAH56256.1; -;  
DR HSSP: P01834; 1HEZ.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003597; Ig-cl.  
DR InterPro: IPR003066; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF07654; C1-sect. 1.  
DR SMART: SM00406; IGV. 1.  
DR PROSITE: PSS0835; IG\_LIKE; 2.  
DR PROSITE: PSS0290; IG\_MHC; UNKNOWN\_1.  
KM Hypothetical protein.  
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BCOF CRC64;  
Query Match 77.3%; Score 423; DB 2; Length 234;  
Best Local Similarity 78.1%; Pred. No. 6.6e-36;

Matches 82; Conservative 10; Mismatches 13; Indels 0; Gaps 0;  
QY 2 LTQSPSSLSASVGDRTVITTCRAQOSISTYLMWYQKPGKAPKLLIWSASNLGSPSRF 61  
DB 24 MTQSPSSLSASVGDRTVITTCRAQOSIGSYLMWYQKPGKAPKLLIYAASBLHSGVPSRF 83  
QY 62 GSGSGTFFLTITSLNLOFEDFASYYCOOSTTTLTPSSGRTLEIKR 106  
DB 84 GSGSGTFFLTITSLNLOFEDFASYYCOOSTTTLTPSSGRTLEIKR 128  
RESULT 13  
KV1B\_HUMAN STANDARD; PRT; 108 AA.  
ID KV1B\_HUMAN  
AC P01594;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ig kappa chain V-I region AU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72189444; Pubmed=5028201;  
RA Schiehl H., Haischmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
RT protein Au).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=77022433; Pubmed=1234024;  
RA Fehlgamer H., Schiffer M., Epp O., Colman P.M., Lattman B.E.,  
RA Schwager P., Steigemann W., Schramm H.J.;  
RT "The structure determination of the variable portion of the Bence-  
RT Jones protein Au.";  
RL Biophys. Struct. Mech. 1:139-146(1975).  
CC -1- MISCELLANEOUS: The structure of the V region was determined by  
CC molecular replacement methods using the known structure of the V  
CC region of the kappa chain REI.  
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
CC PIR: A91653; K1H0AU.  
DR PDB: 1JVS; X-ray; A=1-107.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; IGV. 1.  
DR SMART: SM00406; IGV. 1.  
DR PROSITE: PSS0835; IG\_LIKE; 1.  
KM 3D-structure; Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 2 34 Complementarity-determining-1.  
FT DOMAIN 3 35 Framework-2.  
FT DOMAIN 4 49 Complementarity-determining-2.  
FT DOMAIN 5 56 Complementarity-determining-3.  
FT DOMAIN 6 88 Framework-3.  
FT DOMAIN 7 97 Complementarity-determining-4.  
FT DOMAIN 8 107 Framework-4.  
FT DISULFID 23 88 By similarity.  
FT STRAND 4 5 Strand.  
FT STRAND 10 13 Strand.  
FT TURN 15 16 Turn.  
FT STRAND 19 25 Strand.  
FT TURN 30 31 Turn.  
FT STRAND 33 38 Strand.  
FT TURN 40 41 Turn.  
FT STRAND 44 52 Strand.  
FT TURN 50 52 Turn.

FT STRAND 53 54  
 FT TURN 56 57  
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 FT STRAND 62 67  
 FT TURN 68 69  
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 FT STRAND 80 82  
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 FT STRAND 97 98  
 FT STRAND 102 106  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA, 11939 MW, E801187EE6F6FB9 CRC64;  
 Query Match 76.1%; Score 416; DB 1; Length 108;  
 Best Local Similarity 76.4%; Pred. No. 1.5e-35;  
 Matches 81; Conservative 9; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTVITTCRARQSIQSTYLMWYQKPGKAPKLLIWSASNLQSGVPSRF 60  
 DB 3 QMTQSPSSLSASVGDRTVITTCQASQDIDYLMWYQKPGKAPKLLIYDASNLQSGVPSRF 62  
 QY 61 SGGSSGTEFLTITSLNLFQEDPASVYCCQSYTTLTTPSGGTLEIKR 106  
 DB 63 SGGSSGTEFLTITSLNLFQEDPASVYCCQSYTTLTTPSGGTLEIKR 108  
 RESULT 14  
 ID KVLIO\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01607;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Ig kappa chain V-I region Rel.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76023758; PubMed=809329;  
 RA Palm W., Hilschmann N.;  
 RT "The primary structure of a crystalline monoclonal immunoglobulin  
 RT kappa-type L-chain; subgroup I (Bence-Jones protein Rel); isolation  
 RT and characterization of the tryptic peptides; the complete amino acid  
 RT sequence of the protein; a contribution to the elucidation of the  
 RT three-dimensional structure of antibodies, in particular their  
 RT combining site.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191 (1975).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=76039968; PubMed=1182131;  
 RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;  
 RT "The molecular structure of a dimer composed of the variable portions  
 RT of the Bence-Jones protein REI refined at 2.0-A resolution.";  
 RT Biochemistry 14:4943-4952 (1975).  
 RL Blochmistry 14:4943-4952 (1975).  
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)  
 CC marker.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 DR PIR; A91663; KIHURE.  
 DR PDB; 1AR2; X-ray; @=1-107.  
 DR PDB; 1BMW; X-ray; A/B=1-107.  
 DR PDB; 1REI; X-ray; A/B=1-107.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW 3D-structure; Bence-Jones protein; Direct protein sequencing;  
 KW Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 34 Complementarity-determining-1.  
 FT DOMAIN 35 49 Framework-2.  
 FT DOMAIN 50 56 Complementarity-determining-2.  
 FT DOMAIN 57 88 Framework-3.  
 FT DOMAIN 89 97 Complementarity-determining-3.  
 FT DOMAIN 98 107 Framework-4.  
 FT DISULFID 23 88  
 FT STRAND 4 7  
 FT STRAND 10 13  
 FT STRAND 15 16  
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 FT STRAND 102 106  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA, 11902 MW, 9E8143E1188BCE2A CRC64;  
 Query Match 76.1%; Score 416; DB 1; Length 108;  
 Best Local Similarity 75.5%; Pred. No. 1.5e-35;  
 Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTVITTCRARQSIQSTYLMWYQKPGKAPKLLIWSASNLQSGVPSRF 60  
 DB 3 QMTQSPSSLSASVGDRTVITTCQASQDIDYLMWYQKPGKAPKLLIYDASNLQSGVPSRF 62  
 QY 61 SGGSSGTEFLTITSLNLFQEDPASVYCCQSYTTLTTPSGGTLEIKR 106  
 DB 63 SGGSSGTEFLTITSLNLFQEDPASVYCCQSYTTLTTPSGGTLEIKR 108  
 RESULT 15  
 ID Q9UL70 PRELIMINARY; PRT; 108 AA.  
 AC Q9UL70;  
 DT 01-MAY-2000 (TREMURel. 13, Created)  
 DT 01-MAY-2000 (TREMURel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMURel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RT Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 DR EMBL; AF035044; AAD56280.1; -.  
 DR PIR; PH0863; PH0863.  
 DR HSSP; P01607; 1BMW.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 108 108

SO SEQUENCE 108 AA; 1163 MW; B7BEDC3E41FCCA37 CRC64;

Query Match	75.7%;	Score 414;	DB 2;	Length 108;
Best Local Similarity	77.4%;	Pred NO	2	46-35.

Best Local Similarity 77.4%; Pred. No. 2.4e-35;  
Matches 82; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Matches 82; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

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QY      1 ELTQSSSLASVGDRTITTCARQSTLYLAWYQQPKGAPKLLIWSASNLQGVPSRF 60
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b 3 QMTQSPSSLSASVGDVTTITCRASQGISNYLAWYQQKPKSLIYAASTLQSGVPSRF 62

61 SGGSGTEFTLTISNLQFEDFASYYCQGSYTLTYFGSGTKEIKR 106

Db 63 SGGSGTDFLTITSSLPEDVATYYCQKNSAPRTFGPGTLEIKR 108

Search completed: July 26, 2005, 09:26:20  
Job time: 07:57:55

Job time : 67.6515 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 08:50:20 ; Search time 79.3394 Seconds

(without alignments)  
516.724 Million cell updates/sec

Title: US-10-027-725a-11

Sequence: 1 ELRGSPESLASVGDRTVIT.....QQSYTLTYTGSGTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	537	98.2	106	5	ABG30449 Human IGE
2	484	88.5	107	2	AAR54260 Anti-HIV
3	484	88.5	107	2	AAW01283 VL region
4	484	88.5	107	3	AAV98244 Anti-gp12
5	484	88.5	107	3	AAV95135 Anti-gp12
6	483	88.3	107	4	AAV93590 Human ant
7	483	88.3	107	6	ABO27397 Anti-Rh(D
8	480	87.8	107	4	AAV93644 Human ant
9	480	87.8	107	6	ABO27451 Anti-Rh(D
10	476	87.0	107	2	AAV54261 Anti-HIV
11	476	87.0	107	2	AAW01284 VL region
12	476	87.0	107	3	AAV98245 Anti-gp12
13	476	87.0	107	3	AAV95136 Anti-gp12
14	475	86.8	107	4	AAV93663 Human ant
15	475	86.8	107	4	AAV93664 Human ant
16	475	86.8	107	6	ABO27471 Anti-Rh(D
17	475	86.8	107	6	ABO27470 Anti-Rh(D
18	474	86.7	107	6	AAV93667 Human ant
19	474	86.7	107	6	ABO27474 Anti-Rh(D
20	473.5	86.6	108	4	AAV93589 Human ant
21	473.5	86.6	108	4	AAV93600 Human ant
22	473.5	86.6	108	6	ABO27407 Anti-Rh(D
23	473.5	86.6	108	6	ABO27396 Anti-Rh(D
24	473	86.5	107	4	AAV93594 Human ant
25	473	86.5	107	6	ABO27401 Anti-Rh(D

26	473	86.5	109	8	ADP66620 Anti-RAS
27	473	86.5	109	8	ADP66619 Anti-RAS
28	473	86.5	109	8	ADP66623 Anti-RAS
29	473	86.5	109	8	ADO79347 Anti-RAS
30	473	86.5	109	8	ADO79343 Anti-RAS
31	473	86.5	109	8	ADO79344 Anti-RAS
32	473	86.5	111	6	AAV93656 Human aci
33	473	86.5	111	6	ABJ38615 Hepatitis
34	473	86.5	240	6	ABJ38595 Hepatitis
35	473	86.5	244	8	ADQ75290 Immunoglo
36	473	86.5	299	4	AAV93660 Anti-Rh(D
37	472.5	86.4	108	6	AAV93655 Human ant
38	472.5	86.4	108	6	ABO27462 Anti-Rh(D
39	472	86.3	107	4	AAV93596 Human ant
40	472	86.3	107	4	AAV93650 Human ant
41	472	86.3	107	4	AAV93595 Human ant
42	472	86.3	107	6	ABO27457 Anti-Rh(D
43	472	86.3	107	6	ABO27403 Anti-Rh(D
44	472	86.3	107	6	ABO27402 Anti-Rh(D
45	471	86.1	107	4	AAV93646 Human ant

## ALIGNMENTS

RESULT 1	
ABG30449	ABG30449 standard; protein; 106 AA.
XX	
AC	ABG30449;
XX	
DT	21-OCT-2002 (first entry)
XX	
DE	Human IGE Fab clone 60 light chain protein.
XX	
KW	Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;
KW	timothy grass pollen allergen; passive immunotherapy.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Location/Qualifiers
FT	1..21
FT	/note= "FRL region"
FT	22..32
FT	/note= "CDR1 region"
FT	33..47
FT	/note= "FR2 region"
FT	48..54
FT	/note= "CDR2 protein"
FT	55..86
FT	/note= "FR3 region"
FT	87..95
FT	/note= "CDR2 region"
FT	96..104
FT	/note= "FR4 region"
FT	Misc-difference 98
FT	/note= "Encoded by CCT"
PN	W0200253595-A1.
XX	
PD	11-JUL-2002.
XX	
PD	27-DEC-2001; 2001WO-SE002908.
XX	
PR	29-DEC-2000; 2000SE-00004892.
XX	
PA	(PHAA ) PHARMACIA DIAGNOSTICS AB.
XX	
PI	Flicker S, Steinberger P, Kraft D, Valenta R;
XX	WPI; 2002-583604/62.
DR	N-PSDB; ABK89641.
XX	

PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
PT diagnosing or passive immunotherapy of type I allergy, for environmental  
PT allergen detection.  
XX  
PS Disclosure; Page 40; 45pp; English.  
XX  
CC This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE Fabs and methods for their use. The proteins  
CC of the invention may have antiallergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE  
CC antibodies to Phi P 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific Fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The Fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific Fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergic patients  
CC IgE antibodies to Phi P 2. The present sequence represents the human IgG  
CC Fab, clone 60 light chain protein of the invention  
XX  
SQ Sequence 106 AA:  
Query Match 98.2%; Score 537; DB 5; Length 106;  
Best Local Similarity 99.1%; Pred. No. 5.8e-30;  
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ELTQSPSLASVGDRTYTCRARSISTYLNWYQKPKKLIMASNLQGVPSRF 60  
Db 1 ELTQSPSLASVGDRTYTCRARSISTYLNWYQKPKKLIMASNLQGVPSRF 60  
QY 61 SSGSGSGTEFTLTISNLQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
Db 61 SSGSGSGTEFTLTISNLQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
RESULT 2  
ID AAR54260  
AAAR54260 standard; protein; 107 AA.  
XX  
AC AAR54260;  
XX  
DT 25-MAR-2003 (revised)  
DT 10-NOV-1994 (first entry)  
XX  
DE Anti-HIV gp120 immunoglobulin light chain variable region b22.  
XX  
XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
KM neutralisation; monoclonal antibody; kappa light chain; variable region;  
KM framework; complementarity determining region.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH Region 1..21  
FT /label= FR1  
FT 22..33  
FT /label= CDR1  
FT 34..48  
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FT /label= CDR3  
FT 96..107  
FT /label= FR4  
XX  
PN MO9407922-A1.  
XX

PD 14-APR-1994.  
XX  
XX 30-SEP-1993; 93WO-US009328.  
PF 30-SEP-1992; 92US-00954148.  
PR 30-SEP-1992; 92US-00954148.  
XX  
XX (SCRI ) SCRIIPS RES INST.  
XX  
PI Burton DR, Barbas CF, Lerner RA;  
XX  
XX WPI; 1994-135516/16.  
DR  
XX  
XX New human monoclonal antibodies neutralising HIV - react with gp120 or  
PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro  
PT diagnosis and for passive immuno-therapy.  
XX  
PS Claim 5; Page 189; 248pp; English.  
XX  
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification  
CC using primers specific for heavy and light chain variable regions. The  
CC amplification products were inserted into a dicistronic vector to produce  
CC a library of fragments. E.coli XLI Blue cells were transformed with the  
CC library. Filamentous phage were produced which expressed the Mab regions  
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of  
CC immunoreactive clones. The light chain VK region sequence AAR54260  
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 107 AA:  
Query Match 88.5%; Score 484; DB 2; Length 107;  
Best Local Similarity 88.7%; Pred. No. 2.6e-26;  
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ELTQSPSLASVGDRTYTCRARSISTYLNWYQKPKKLIMASNLQGVPSRF 60  
Db 1 ELTQSPSLASVGDRTYTCRARSISTYLNWYQKPKKLIMASNLQGVPSRF 60  
QY 61 SSGSGSGTEFTLTISNLQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
Db 61 SSGSGSGTEFTLTISNLQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
RESULT 3  
ID AAM01283  
AAM01283 standard; protein; 107 AA.  
XX  
AC AAM01283;  
XX  
DT 29-JAN-1997 (first entry)  
XX  
DE VL region of HIV neutralising Mab, clone b22 and B35.  
XX  
XX Heavy chain; light chain; variable region; VH; monoclonal antibody; Mab;  
KM HIV; human immunodeficiency virus; glycoprotein; gp120; clone;  
KM virus infectivity assay; precursor gp160; immunocompetence; human;  
KM anti-HIV antibody; detection; HIV infection.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH Region 1..21  
FT /label= FR1  
FT 22..32  
FT /label= CDR1  
FT 33..47  
FT /label= FR2  
FT 48..54  
FT /label= CDR2  
FT 55..86  
FT /label= FR3  
FT 87..95  
FT /label= CDR3  
FT 96..107  
FT /label= FR4  
XX  
PN Region  
XX



FT /label= FR4  
 XX MO9602273-A1.  
 XX 01-FEB-1996.  
 XX 11-JUL-1995; 95MO-US008743.  
 XX 18-JUL-1994; 94US-00276852.  
 XX (SCRI ) SCRIPPS RES INST.  
 XX Burton DR, Barbas CF, Lerner RA;  
 XX WPI, 1996-179601/18.  
 XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive  
 XX immuno:therapy and detection of HIV infection.  
 XX Example: Fig 11; 366pp; English.  
 XX The sequences given in AAW01261-92 represent the light chain variable  
 XX regions (VL) of a series of monoclonal antibodies (Mab's) which are  
 XX immunoreactive with HIV glycoprotein gp120 and are capable of  
 XX neutralising HIV. This sequence represents the sequence of the JK2 gene  
 XX clones; b22 and B35. A Mab containing this VL sequence has the capacity  
 XX to reduce HIV infectivity titre in an in vivo virus infectivity assay by  
 XX 50 % at a concentration of less than 700 ng of antibody/ml, and binds  
 XX mature gp120 preferentially over the precursor gp160. The Mab may be used  
 XX for determining immunocompetence of a human anti-HIV antibody and in the  
 XX detection of HIV infection  
 XX SQ Sequence 107 AA;  
 Query Match 88.5%; Score 484; DB 2; Length 107;  
 Best Local Similarity 88.7%; Pred. No. 2.6e-26;  
 Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTVITTCARQSIISTYLNWYQOKRGKAPKLIWASNLQGVPSRF 60  
 DB 1 ELTQSPSSLSASVGDRTVITTCARQSIISTYLNWYQOKRGKAPKLIWASNLQGVPSRF 60  
 QY 61 SSGSGTEFTLTISNLQPEDFASYYCOOSYTTLYTFGSGTKLEIKR 106  
 DB 61 SSGSGGTDFTLTISLQPEDFATYYCOOSYSTPTTFGGTKLEIKR 106  
 RESULT 4  
 AAY98244  
 ID AAY98244 standard; protein; 107 AA.  
 AC AAY98244;  
 XX 04-JUL-2000 (first entry)  
 DT  
 XX Anti-gp120 antibody light chain variable region from clone b22.  
 DE  
 XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;  
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;  
 KW passive immunotherapy; reduce severity; HIV-induced disease;  
 KW immunocompetence; active immunisation.  
 XX Homo sapiens.  
 OS  
 XX AU9948754-A.  
 XX 17-FEB-2000.  
 PD 16-SEP-1999; 99NU-00048754.  
 PF 16-SEP-1999; 99NU-00048754.  
 PR (SCRI ) SCRIPPS RES INST.  
 XX

XX Burton DR, Barbas CF, Lerner RA;  
 XX WPI, 2000-246867/22.  
 XX Human neutralizing monoclonal antibodies to human immunodeficiency virus  
 XX (HIV) used for providing passive immunotherapy to HIV are specific for  
 XX glycoprotein-120.  
 XX Example 9; Fig 11; 374pp; English.  
 XX This sequence represents a fragment of the antibodies of the invention.  
 XX The invention relates to the production of an anti-HIV (human  
 XX immunodeficiency virus) glycoprotein (gp) -120 monoclonal antibody capable  
 XX of reducing an HIV infectivity titre in an in vitro virus infectivity  
 XX assay by 50% at a concentration of less than 70 ng/ml. The method for the  
 XX production of the antibody comprises: (a) providing a first  
 XX polynucleotide encoding a heavy chain immunoglobulin amino acid sequence  
 XX (which does not comprise the sequence represented by AAY98206) and a  
 XX second polynucleotide encoding a light chain immunoglobulin amino acid  
 XX sequence; (b) inserting the first and second polynucleotide sequences  
 XX into a host cell; (c) maintaining the host cell in conditions which allow  
 XX the amino acid sequences encoded by the polynucleotides to be expressed  
 XX in the host cell; and (d) isolating the antibody comprising the heavy and  
 XX light chain immunoglobulin amino acid sequences from the host cell. The  
 XX anti-HIV gp-120 monoclonal antibody is used for providing passive  
 XX immunotherapy to HIV in a human. They can be administered to high-risk  
 XX patients to reduce the likelihood and/or severity of HIV-induced disease  
 XX and to patients who are already HIV-infected. The antibodies are used for  
 XX neutralising field isolates which provides information about the  
 XX immunocompetence of an immune response in HIV patients, for detecting HIV  
 XX in a biological fluid or tissue sample e.g. by radioimmunoassay, for  
 XX producing anti-idiotype antibodies which can be used for active  
 XX immunisation and to screen human monoclonal antibodies to identify those  
 XX with the same binding specificity and to monitor the course of HIV  
 XX disease therapy by measuring the changes in concentration of HIV present  
 XX in the body or in body fluids by immunoassay. The anti-HIV gp-120  
 XX monoclonal antibodies are encoded by a human polynucleotide sequence and  
 XX when used in vivo for diagnosis and immunotherapy of HIV-induced disease  
 XX reduce the problems of significant host immune response to the antibodies  
 XX associated with monoclonal antibodies of xenogeneic or chimeric  
 XX derivation  
 XX SQ Sequence 107 AA;  
 Query Match 88.5%; Score 484; DB 3; Length 107;  
 Best Local Similarity 88.7%; Pred. No. 2.6e-26;  
 Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTVITTCARQSIISTYLNWYQOKRGKAPKLIWASNLQGVPSRF 60  
 DB 1 ELTQSPSSLSASVGDRTVITTCARQSIISTYLNWYQOKRGKAPKLIWASNLQGVPSRF 60  
 QY 61 SSGSGTEFTLTISNLQPEDFASYYCOOSYTTLYTFGSGTKLEIKR 106  
 DB 61 SSGSGGTDFTLTISLQPEDFATYYCOOSYSTPTTFGGTKLEIKR 106  
 RESULT 5  
 AAY95135  
 ID AAY95135 standard; protein; 107 AA.  
 AC AAY95135;  
 XX 30-JUN-2000 (first entry)  
 DT  
 XX Anti-gp120 antibody light chain variable region from clone b22.  
 DE  
 XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;  
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;  
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.  
 XX Homo sapiens.  
 OS

```
XX AU9948756-A.
PN
XX
XX 17-FEB-2000.
PD
XX
XX 16-SEP-1999; 99AU-00048756.
PF
XX
XX 16-SEP-1999; 99AU-00048756.
PR
XX
XX (SCRI ) SCRIPPS RES INST.
PA
XX
XX Burton DR, Barbas CF, Lerner RA;
PI
XX WPI; 2000-293393/26.
DR
XX
XX Novel human monoclonal antibodies which immunoreact with and neutralize
PT human immunodeficiency virus useful for treating HIV infections.
XX
XX Example 9; Fig 11; 36pp; English.
PS
XX
XX The present sequence represents a fragment of an anti-human
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
CC in vitro virus infectivity assay by 50%, at a concentration of less than
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
CC immunotherapy of HIV induced disease. They are useful as neutralising
CC field isolates and provide useful information regarding the
CC immunocompetence of an immune response in HIV infected patients. The
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
CC which can be used to screen human monoclonal antibodies to identify
CC whether the antibody has the same binding specificity as the antibodies
CC of the invention. The neutralising antibodies define new epitopes on the
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
CC immunotherapeutic human monoclonal antibodies. A major advantage of the
CC monoclonal antibodies derives from the fact that they are encoded by a
CC human polynucleotide sequence. Thus in vivo use of the monoclonal
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
CC reduces the problems of significant host immune response to the passively
CC administered antibodies which is a problem commonly encountered when
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
CC An additional major advantage of the monoclonal antibodies described
CC derives from the fact that they immunoreact with a unique determinant
CC present on mature HIV glycoprotein gp120. This class of antibodies is
CC particularly effective at neutralising field isolates of HIV
CC
XX
XX Sequence 107 AA;
SQ
Query Match 88.5%; Score 484; DB 3; Length 107;
Best Local Similarity 88.7%; Pred. No. 2.6e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 ELTQSPSLASVGDRTVITTCRARSISTYLNWYQKRGKAPKLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSLASVGDRTVITTCRARSISTYLNWYQKRGKAPKLIWAASSLQSGVPSRF 60
QY 61 SSGSGTEFTLTISNLQFEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
DB 61 SSGSGGIDFTLTISLQPEDPATYCCOOSYSTLTWTFGQTKLEIKR 106
RESULT 6
AAG93590
ID AAG93590 standard; protein; 107 AA.
AC AAG93590;
XX
XX 14-SEP-2001 (first entry)
XX
XX Human anti-Rh(D) chain I02 protein sequence.
DE
XX Human, anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW
```

```
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
XX Homo sapiens.
OS
XX US6255455-B1.
XX
XX 03-JUL-2001.
PD
XX
XX 29-JAN-1999; 99US-00240274.
PF
XX
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Siegel DL;
PI
XX WPI; 2001-386931/41.
DR N-PSDB; AAH68647.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Claim 1; Col 43; 162pp; English.
XX
XX The present invention describes an isolated Rh(D) binding protein.
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (II) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determining the Rh phenotype of human red blood cells.
CC AA68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
XX Sequence 107 AA;
SQ
Query Match 88.3%; Score 483; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 3.1e-26;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
QY 1 ELTQSPSLASVGDRTVITTCRARSISTYLNWYQKRGKAPKLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSLASVGDRTVITTCRARSISTYLNWYQKRGKAPKLIWAASSLQSGVPSRF 61
QY 61 SSGSGTEFTLTISNLQFEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
DB 62 SSGSGGIDFTLTISLQPEDPATYCCOOSYSTLTWTFGQTKLEIKR 107
RESULT 7
ABO27397
ID ABO27397 standard; protein; 107 AA.
AC ABO27397;
XX
XX 12-SEP-2003 (first entry)
XX
XX Anti-Rh(D) chain I02.
DE
XX Human, Rh(D) binding protein; blood typing; blood product; antibody;
KW magnetically activated cell sorting.
XX
XX Homo sapiens.
XX
XX US2003040605-A1.
XX
XX 27-FEB-2003.
XX
```

PF 04-MAY-2001; 2001US-00848798.  
XX  
XX 11-OCT-1996; 96US-0028550P.  
PR 27-JUN-1997; 97US-0088404S.  
PR 10-APR-1998; 98US-0081380P.  
PR 29-JAN-1999; 99US-00240274.  
XX  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX  
XX Siegel DL;  
XX  
XX WPI; 2003-512273/48.  
DR N-PSDB; ACD4531L.  
XX  
XX New human Rh(D)-binding protein useful for various diagnostic and  
PT therapeutic applications, including typing of blood or blood products.  
XX  
XX  
XX Claim 4; Page 26; 187pp; English.  
XX  
XX The invention relates to an isolated Rh(D) binding protein. The protein  
CC can be used for magnetically activated cell sorting. The protein is  
CC useful in various diagnostic and therapeutic applications in humans,  
CC including typing of blood or blood products. The present sequence  
CC represents the amino acid sequence of a human anti-Rh(D) chain  
XX  
SQ Sequence 107 AA;

Query Match 88.3%; Score 483; DB 6; Length 107;  
Best Local Similarity 87.7%; Pred. No. 3,1e-26;  
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ELTQSPSLASVGDRTITTCRAQSISTYLNWYQKRGKAPKLLINSASNLQSGVPSRF 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 2 ELTQSPSLASVGDRTITTCRAQSISTYLNWYQKRGKAPKLLIYAASLRGVSFRF 61  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
62 SGSGSGTDFLTITSLQPEDFATYCCQSYSTLTWTFGGTKEIKR 107

RESULT 8  
AAG93644  
ID AAG93644 standard; protein; 107 AA.  
XX  
XX AAG93644;  
XX  
XX 14-SEP-2001 (first entry)  
XX  
XX Human anti-Rh(D) antibody clone SH13 protein sequence.  
XX  
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
KW red blood cell; Rh phenotype; diagnosis; therapeutic.  
XX  
XX Homo sapiens.  
XX  
XX US6255455-B1.  
XX  
XX 03-JUL-2001.  
XX  
XX 29-JAN-1999; 99US-00240274.  
XX  
XX 11-OCT-1996; 96US-0028550P.  
PR 27-JUN-1997; 97US-0088404S.  
PR 10-APR-1998; 98US-0081380P.  
XX  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX  
XX Siegel DL;  
XX  
XX WPI; 2001-388931/41.  
DR N-PSDB; AAH68701.  
XX  
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in

PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine.

PS Claim 1; Col 68; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,  
CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
CC immunostimulant activity, and can be used as an immune system stimulant.  
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
CC chain CDS amino acid sequences which are given in the exemplification of  
CC the present invention  
XX  
XX

SQ Sequence 107 AA;

Query Match 87.8%; Score 480; DB 4; Length 107;  
Best Local Similarity 87.7%; Pred. No. 5e-26;  
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ELTQSPSLASVGDRTITTCRAQSISTYLNWYQKRGKAPKLLINSASNLQSGVPSRF 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 2 ELTQSPSLASVGDRTITTCRAQSISTYLNWYQKRGKAPKLLIYAASLRGVSFRF 61  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
62 SGSGSGTDFLTITSLQPEDFATYCCQSYSTPYTFGGTKEIKR 107

RESULT 9  
ABO27451  
ID ABO27451 standard; protein; 107 AA.  
XX  
XX ABO27451;  
XX  
XX 12-SEP-2003 (first entry)  
XX  
XX Anti-Rh(D) light chain SH13.  
XX  
XX Human; RH(D) binding protein; blood typing; blood product; antibody;  
KW magnetically activated cell sorting.  
XX  
XX Homo sapiens.  
XX  
XX US2003040605-A1.  
XX  
XX 27-FEB-2003.  
XX  
XX 04-MAY-2001; 2001US-00848798.  
XX  
XX 11-OCT-1996; 96US-0028550P.  
PR 27-JUN-1997; 97US-0088404S.  
PR 10-APR-1998; 98US-0081380P.  
PR 29-JAN-1999; 99US-00240274.  
XX  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX  
XX Siegel DL;  
XX  
XX WPI; 2003-512273/48.  
DR N-PSDB; ACD45365.  
XX  
XX New human Rh(D)-binding protein useful for various diagnostic and  
PT therapeutic applications, including typing of blood or blood products.  
XX  
XX Claim 4; Page 50; 187pp; English.  
XX  
XX The invention relates to an isolated Rh(D) binding protein. The protein  
CC can be used for magnetically activated cell sorting. The protein is  
CC useful in various diagnostic and therapeutic applications in humans,

CC including typing of blood or blood products. The present sequence  
CC represents the amino acid sequence of a human anti-Rh(D) chain  
XX  
SQ Sequence 107 AA;

Query Match 87.8%; Score 480; DB 6; Length 107;  
Best Local Similarity 87.7%; Pred. No. 5e-26;  
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISITVLMWYQOKPGKAPKLLIMASNLQSGVPSRF 60  
Db 2 ELTQSPSSLSASVGDRTVITTCRASQISITVLMWYQOKPGKAPKLLITVAASLSRGSVPSRF 61

QY 61 SGGSGGTFTLLTISNLFQEDFPASYCCQSYTTLYTFSGGTLKEIKR 106  
Db 62 SGGSGGTFTLLTISNLFQEDFPATYCCQSYSTPTPTFGGTLKEIKR 107

RESULT 10  
AAR54261  
ID AAR54261 standard; protein; 107 AA.

AC AAR54261;  
DT 25-MAR-2003 (revised)  
DT 10-NOV-1994 (first entry)

XX Anti-HIV gp120 immunoglobulin light chain variable region b27.

XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
KW neutralisation; monoclonal antibody; kappa light chain; variable region;  
KW framework; complementarity determining region.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..21  
FT /label= FR1  
FT Region 22..33  
FT /label= CDR1  
FT Region 34..48  
FT /label= FR2  
FT Region 49..55  
FT /label= CDR2  
FT Region 56..87  
FT /label= FR3  
FT Region 88..95  
FT /label= CDR3  
FT Region 96..107  
FT /label= FR4

XX MO9407922-A1.

XX 14-APR-1994.

XX 30-SEP-1993; 93WO-US0093328.

XX 30-SEP-1992; 92US-00954148.

XX (SCRI ) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;

XX WPI; 1994-135516/16.

XX New human monoclonal antibodies neutralising HIV - react with gp120 or  
PT gp1 and nucleic acid encoding them, useful for in vivo or in vitro  
PT diagnosis and for passive immuno-therapy.

XX Claim 5; Page 190; 248pp; English.

XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification  
CC using primers specific for heavy and light chain variable regions. The

CC amplification products were inserted into a dicistronic vector to produce  
CC a library of fragments. E.coli XL1 Blue cells were transformed with the  
CC library. Filamentous phage were produced which expressed the Mab regions  
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of  
CC immunoreactive clones. The light chain VK region sequence AAR54261  
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 107 AA;

Query Match 87.0%; Score 476; DB 2; Length 107;  
Best Local Similarity 87.7%; Pred. No. 9.4e-26;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISITVLMWYQOKPGKAPKLLIMASNLQSGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITTCRASQISITVLMWYQOKPGKAPKLLITVAASLSRGSVPSRF 60

QY 61 SGGSGGTFTLLTISNLFQEDFPASYCCQSYTTLYTFSGGTLKEIKR 106  
Db 61 SGGSGGTFTLLTISNLFQEDFPATYCCQSYSTPTPTFGGTLKEIKR 106

RESULT 11  
AAW01284  
ID AAW01284 standard; protein; 107 AA.

XX AAW01284;

XX 29-JAN-1997 (first entry)

XX VL region of HIV neutralising Mab, clone b27.

XX Heavy chain; light chain; variable region; VH; monoclonal antibody; Mab;  
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;  
KW virus infectivity assay; precursor gp160; immunocompetence; human;  
KW anti-HIV antibody; detection; HIV infection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..21  
FT /label= FR1  
FT Region 22..32  
FT /label= CDR1  
FT Region 33..47  
FT /label= FR2  
FT Region 48..54  
FT /label= CDR2  
FT Region 55..86  
FT /label= FR3  
FT Region 87..95  
FT /label= CDR3  
FT Region 96..107  
FT /label= FR4

XX WO9602273-A1.

XX 01-FEB-1996.

XX 11-JUL-1995; 95WO-US008743.

XX 18-JUL-1994; 94US-00276852.

XX (SCRI ) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;

XX WPI; 1996-179601/18.

XX Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in passive  
PT immuno-therapy and detection of HIV infection.

XX Example; Fig 11; 366pp; English.

XX The sequences given in AAW01261-92 represent the light chain variable  
CC regions (VL) of a series of monoclonal antibodies (Mab's) which are  
CC immunoreactive with HIV glycoprotein gp120 and are capable of  
CC neutralising HIV. This sequence represents the sequence of the JK2 gene  
CC clone, b27. A Mab containing this VL sequence has the capacity to reduce  
CC HIV infectivity titre in an in vitro virus infectivity assay by 50 % at a  
CC concentration of less than 700 ng of antibody/ml, and binds mature gp120  
CC preferentially over the precursor gp160. The Mab may be used for  
CC determining immunocompetence of a human anti-HIV antibody and in the  
CC detection of HIV infection  
CC  
XX Sequence 107 AA;  
SQ  
Query Match 87.0%; Score 476; DB 2; Length 107;  
Best Local Similarity 87.7%; Pred. No. 9.4e-26;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
Dy 1 ELTQSPSSLASVGVDRVTITCRAROSISTYLNWYQKRGKAPKLLIMASNLQSGVPSRF 60  
1 ELTQSPSSLASVGVDRVTITCRAROSISTYLNWYQKRGKAPKLLIMASNLQSGVPSRF 60  
Db 1 ELTQSPSSLASVGVDRVTITCRAROSISTYLNWYQKRGKAPKLLIMASNLQSGVPSRF 60  
61 SGSGSGTEFTLTITSNLQPEDPASYCCOQSYTTLTYTPSGTKLEIKR 106  
61 SGSGSGTEFTLTITSNLQPEDPASYCCOQSYTTLTYTPSGTKLEIKR 106  
Db 61 SGSGSGTEFTLTITSNLQPEDPASYCCOQSYTTLTYTPSGTKLEIKR 106  
RESULT 12  
AA98245  
ID AAY98245 standard; protein; 107 AA.  
XX  
AC AAY98245;  
XX  
DT 04-JUN-2000 (first entry)  
DE Anti-gp120 antibody light chain variable region from clone B27.  
XX  
KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;  
KW human immunodeficiency virus type 1; HIV-1; infectivity titre;  
KW passive immunotherapy; reduce severity; HIV-induced disease;  
KW immunocompetence; active immunisation.  
XX  
OS Homo sapiens.  
XX  
PN AU9948754-A.  
XX  
PD 17-FEB-2000.  
XX  
PF 16-SEP-1999; 99AU-00048754.  
XX  
PR 16-SEP-1999; 99AU-00048754.  
XX  
PA (SCRI ) SCRIPPS RES INST.  
XX  
PI Burton DR, Barbas CF, Lerner RA;  
XX  
DR WPI; 2000-246667/22.  
XX  
PT Human neutralizing monoclonal antibodies to human immunodeficiency virus  
PT (HIV) used for providing passive immunotherapy to HIV are specific for  
PT glycoprotein-120.  
XX  
PS Example 9; Fig 11; 374bp; English.  
XX  
CC This sequence represents a fragment of the antibodies of the invention.  
CC The invention relates to the production of an anti-HIV (human  
CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable  
CC of reducing an HIV infectivity titre in an in vitro virus infectivity  
CC assay by 50% at a concentration of less than 70 ng/ml. The method for the  
CC production of the antibody comprises: (a) providing a first  
CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence  
CC (which does not comprise the sequence represented by AAY98206) and a  
CC second polynucleotide encoding a light chain immunoglobulin amino acid

CC sequence; (b) inserting the first and second polynucleotide sequences  
CC into a host cell; (c) maintaining the host cell in conditions which allow  
CC the amino acid sequences encoded by the polynucleotides to be expressed  
CC in the host cell; and (d) isolating the antibody comprising the heavy and  
CC light chain immunoglobulin amino acid sequences from the host cell. The  
CC anti-HIV gp-120 monoclonal antibody is used for providing passive  
CC immunotherapy to HIV in a human. They can be administered to high-risk  
CC patients to reduce the likelihood and/or severity of HIV-induced disease  
CC and to patients who are already HIV-infected. The antibodies are used for  
CC neutralising field isolates which provides information about the  
CC immunocompetence of an immune response in HIV patients, for detecting HIV  
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for  
CC producing anti-idiotypic antibodies which can be used for active  
CC immunisation and to screen human monoclonal antibodies to identify those  
CC with the same binding specificity and to monitor the course of HIV  
CC disease therapy by measuring the changes in concentration of HIV present  
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120  
CC monoclonal antibodies are encoded by a human polynucleotide sequence and  
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease  
CC reduce the problems of significant host immune response to the antibodies  
CC associated with monoclonal antibodies of xenogeneic or chimeric  
CC derivation  
CC  
XX Sequence 107 AA;  
SQ  
Query Match 87.0%; Score 476; DB 3; Length 107;  
Best Local Similarity 87.7%; Pred. No. 9.4e-26;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
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1 ELTQSPSSLASVGVDRVTITCRAROSISTYLNWYQKRGKAPKLLIMASNLQSGVPSRF 60  
Db 1 ELTQSPSSLASVGVDRVTITCRAROSISTYLNWYQKRGKAPKLLIMASNLQSGVPSRF 60  
61 SGSGSGTEFTLTITSNLQPEDPASYCCOQSYTTLTYTPSGTKLEIKR 106  
61 SGSGSGTEFTLTITSNLQPEDPASYCCOQSYTTLTYTPSGTKLEIKR 106  
Db 61 SGSGSGTEFTLTITSNLQPEDPASYCCOQSYTTLTYTPSGTKLEIKR 106  
RESULT 13  
AA95136  
ID AAY95136 standard; protein; 107 AA.  
XX  
AC AAY95136;  
XX  
DT 30-JUN-2000 (first entry)  
DE Anti-gp120 antibody light chain variable region from clone B27.  
XX  
KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;  
KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;  
KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.  
XX  
OS Homo sapiens.  
XX  
PN AU9948756-A.  
XX  
PD 17-FEB-2000.  
XX  
PF 16-SEP-1999; 99AU-00048756.  
XX  
PR 16-SEP-1999; 99AU-00048756.  
XX  
PA (SCRI ) SCRIPPS RES INST.  
XX  
PI Burton DR, Barbas CF, Lerner RA;  
XX  
DR WPI; 2000-293393/26.  
XX  
PT Novel human monoclonal antibodies which immunoreact with and neutralize  
PT human immunodeficiency virus useful for treating HIV infections.  
XX  
PS Example 9; Fig 11; 366bp; English.  
XX

CC The present sequence represents a fragment of an anti-human  
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to  
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV  
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein  
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an  
CC in vitro virus infectivity assay by 50% at a concentration of less than  
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and  
CC immunotherapy of HIV induced disease. They are useful as neutralising  
CC field isolates and provide useful information regarding the  
CC immunocompetence of an immune response in HIV infected patients. The  
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies  
CC which can be used to screen human monoclonal antibodies to identify  
CC whether the antibody has the same binding specificity as the antibodies  
CC of the invention. The neutralising antibodies define new epitopes on the  
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new  
CC immunotherapeutic human monoclonal antibodies. A major advantages of the  
CC monoclonal antibodies derives from the fact that they are encoded by a  
CC human polynucleotide sequence. Thus in vivo use of the monoclonal  
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly  
CC reduces the problems of significant host immune response to the passively  
CC administered antibodies which is a problem commonly encountered when  
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.  
CC An additional major advantage of the monoclonal antibodies described  
CC derives from the fact that they immunoreact with a unique determinant  
CC present on mature HIV glycoprotein gp120. This class of antibodies is  
CC particularly effective at neutralising field isolates of HIV

CC Sequence 107 AA;

Query Match 87.0%; Score 476; DB 3; Length 107;

Best Local Similarity 87.7%; Pred. No. 9,4e-26; Mismatches 5; Gaps 0;

Matches 93; Conservative 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPGKAPKLLIWSASNLQGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPGKAPKLLIWAASLQGVPSRF 60

Qy 61 SSGSSGTEFTLTISNLOPEDFASYYCOQSYTTLYTFSGGTKLEIKR 106  
Db 61 SSGSSGTDFTLTISLQPEDFATYYCOQSYSTPTQFGGTKLEIKR 106

RESULT 14

AAG93663 ID AAG93663 standard; protein; 107 AA.

AC AAG93663;

DT 14-SEP-2001 (first entry)

XX Human anti-Rh(D) antibody clone SH49 protein sequence.

KM Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
KW red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens.

PN US6255455-B1.

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

XX (UTPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

XX WPI: 2001-388931/41.

DR N-PSDB; AAH68720.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine.

PS Claim 1; Col 69; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,  
CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
CC immunostimulant activity, and can be used as an immune system stimulant.  
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAH6815 to AAH68726 represent the nucleotide sequence which encode  
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
CC chain CDR3 amino acid sequences which are given in the exemplification of  
CC the present invention

XX Sequence 107 AA;

Query Match 86.8%; Score 475; DB 4; Length 107;

Best Local Similarity 85.8%; Pred. No. 1,1e-25; Mismatches 4; Indels 0; Gaps 0;

Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPGKAPKLLIWSASNLQGVPSRF 60  
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Qy 61 SSGSSGTEFTLTISNLOPEDFASYYCOQSYTTLYTFSGGTKLEIKR 106  
Db 62 SSGSSGTDFTLTISLQPEDFATYYCOQSYSTPTQFGGTKLEIKR 107

RESULT 15

AAG93664 ID AAG93664 standard; protein; 107 AA.

AC AAG93664;

DT 14-SEP-2001 (first entry)

XX Human anti-Rh(D) antibody clone SH50 protein sequence.

KM Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
KW red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens.

PN US6255455-B1.

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

XX (UTPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

XX WPI: 2001-388931/41.

DR N-PSDB; AAH68721.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine.

PS Claim 1; Col 69; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,

CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AA693558 to AA693669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AA68615 to AA68726 represent the nucleotide sequence which encode  
 CC AA693558 to AA693669. AA693670 to AA693697 represent anti-Rh (D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification of  
 CC the present invention  
 CC  
 XX  
 SQ Sequence 107 AA;

Query Match 86.8%; Score 475; DB 4; Length 107;  
 Best Local Similarity 85.8%; Pred. No. 1.1e-25;  
 Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;  
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 Db 2 ELTQSPSSLSASVGDVVTTCRAQOSISTYLNWYQOKPKAPKLLIYAASLQSGVPSRF 61  
 QY 61 SGGSGGTBFTLTISNLQPEDPASTYCCQSYTTLVTFSGTKLEIKR 106  
 Db 62 SGGSGGTBFTLTISNLQPEDPASTYCCQSYTTLVTFSGTKLEIKR 107

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## OM protein - protein search, using sw model

Run on: July 26, 2005, 09:26:32 ; Search time 67.4545 Seconds

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Title: US-10-027-725A-11

Perfect score: 547  
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Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0  
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Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCR\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
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- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US10F\_PUBCOMB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US10G\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	547	100.0	106	US-10-027-725A-11	Sequence 11, Appl
2	484	88.5	107	US-10-016-986-104	Sequence 104, Appl
3	483	88.3	107	US-09-848-798-33	Sequence 33, Appl
4	480	87.8	107	US-09-848-798-156	Sequence 156, Appl
5	476	87.0	107	US-10-016-986-105	Sequence 105, Appl
6	475	86.8	107	US-09-848-798-175	Sequence 175, Appl
7	475	86.8	107	US-09-848-798-176	Sequence 176, Appl
8	474	86.7	107	US-09-848-798-179	Sequence 179, Appl
9	473.5	86.6	108	US-09-848-798-32	Sequence 32, Appl
10	473.5	86.6	108	US-09-848-798-43	Sequence 43, Appl
11	473	86.5	107	US-09-848-798-37	Sequence 37, Appl

12	473	86.5	111	14	US-10-203-754A-57	Sequence 57, Appl
13	472.5	86.4	108	10	US-09-848-798-167	Sequence 167, Appl
14	472	86.3	107	10	US-09-848-798-38	Sequence 38, Appl
15	472	86.3	107	10	US-09-848-798-39	Sequence 39, Appl
16	472	86.3	107	10	US-09-848-798-162	Sequence 162, Appl
17	472	86.3	116	17	US-10-783-311-198	Sequence 198, Appl
18	471	86.1	107	10	US-09-848-798-158	Sequence 158, Appl
19	469	85.7	107	10	US-09-848-798-44	Sequence 44, Appl
20	468	85.6	108	17	US-10-726-332-209	Sequence 209, Appl
21	468	85.6	111	14	US-10-203-754A-36	Sequence 56, Appl
22	467	85.4	108	16	US-10-409-814A-4	Sequence 4, Appl
23	467	85.4	108	16	US-10-477-830-90	Sequence 90, Appl
24	467	85.4	240	9	US-09-192-854-2	Sequence 2, Appl
25	467	85.4	240	9	US-09-968-561A-2	Sequence 2, Appl
26	467	85.4	240	10	US-09-968-561A-2	Sequence 2, Appl
27	467	85.4	240	11	US-09-968-561A-2	Sequence 2, Appl
28	467	85.4	240	16	US-10-744-774-1	Sequence 1, Appl
29	466	85.2	107	10	US-09-791-153A-67	Sequence 67, Appl
30	466	85.2	108	17	US-10-726-332-214	Sequence 214, Appl
31	466	85.2	108	17	US-10-805-177-64	Sequence 64, Appl
32	465.5	85.1	107	15	US-10-460-595-9	Sequence 9, Appl
33	465	85.0	107	15	US-10-309-762-89	Sequence 89, Appl
34	465	85.0	108	16	US-10-744-774-15	Sequence 15, Appl
35	465	85.0	108	17	US-10-726-332-28	Sequence 28, Appl
36	464.5	84.9	108	10	US-09-848-798-163	Sequence 163, Appl
37	464	84.8	108	17	US-10-726-332-18	Sequence 18, Appl
38	463	84.6	104	14	US-10-016-986-106	Sequence 106, Appl
39	463	84.6	107	15	US-10-309-762-88	Sequence 88, Appl
40	463	84.6	107	17	US-10-727-155-308	Sequence 308, Appl
41	463	84.6	107	17	US-10-938-353-103	Sequence 103, Appl
42	462	84.5	108	17	US-10-805-177-20	Sequence 20, Appl
43	462	84.5	127	15	US-10-309-762-101	Sequence 101, Appl
44	460.5	84.2	107	15	US-10-363-349-4	Sequence 4, Appl
45	460.5	84.2	288	15	US-10-363-349-7	Sequence 7, Appl

## ALIGNMENTS

RESULT 1  
US-10-027-725A-11  
; Sequence 11, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-11

Query Match 100.0%; Score 547; DB 14; Length 106;  
Best Local Similarity 100.0%; Pred. No. 3.6e-40;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 SGSGSGTEFTLTISNQFEDFASYCOQSYTLTYRSGTKLEIKR 106  
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RESULT 2

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US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbás, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-104

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Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRARSISITLNMVYQKPGKAPKLLIWSASNLQSGVPSRF 60
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QY 61 SSGSGTEFTLTISNLOFEDFASVYCOQSYTTLTYTSGGKLEIKR 106
Db 61 SSGSGTEFTLTISNLOFEDFASVYCOQSYTTLTYTSGGKLEIKR 106

Db 61 SSGSGTEFTLTISNLOFEDFASVYCOQSYTTLTYTSGGKLEIKR 106

RESULT 3
US-09-848-798-33
; Sequence 33, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR APPLICATION NUMBER: 2001-05-04
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-33

Query Match      88.3%; Score 483; DB 10; Length 107;
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Best Local Similarity 87.7%; Pred. No. 1.3e-34;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

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QY 61 SSGSGTEFTLTISNLOFEDFASVYCOQSYTTLTYTSGGKLEIKR 106
Db 62 SSGSGTEFTLTISNLOFEDFASVYCOQSYTTLTYTSGGKLEIKR 107

RESULT 4
US-09-848-798-156
; Sequence 156, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR APPLICATION NUMBER: 2001-05-04
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-156

Query Match      87.8%; Score 480; DB 10; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.4e-34;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

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Db 2 ELTQSPSSLSASVGDVVTITTCRARSISITLNMVYQKPGKAPKLLIWSASNLQSGVPSRF 61

QY 61 SSGSGTEFTLTISNLOFEDFASVYCOQSYTTLTYTSGGKLEIKR 106
Db 62 SSGSGTEFTLTISNLOFEDFASVYCOQSYTTLTYTSGGKLEIKR 107

RESULT 5
US-10-016-986-105
; Sequence 105, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbás, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
```

PRIOR APPLICATION NUMBER: US 07/954,148  
PRIOR FILING DATE: 1992-09-30  
NUMBER OF SEQ ID NOS: 176  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 105  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized  
US-10-016-986-105

Query Match 87.0%; Score 476; DB 14; Length 107;  
Best Local Similarity 87.7%; Pred. No. 5.5e-34;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQISITVLYNMYQQRKAPKLLIWSASNLGSPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITCRARQISITVLYNMYQQRKAPKLLIWSASNLGSPSRF 60  
QY 61 SSGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTRKLEIKR 106  
DB 61 SSGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTRKLEIKR 106

## RESULT 6

US-09-848-798-175  
Sequence 175, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/848,798  
CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 175  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH49  
US-09-848-798-175

Query Match 86.8%; Score 475; DB 10; Length 107;  
Best Local Similarity 85.8%; Pred. No. 6.7e-34;  
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQISITVLYNMYQQRKAPKLLIWSASNLGSPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITCRARQISITVLYNMYQQRKAPKLLIWSASNLGSPSRF 61  
QY 61 SSGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTRKLEIKR 106  
DB 62 SSGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTRKLEIKR 107

## RESULT 7

US-09-848-798-176  
Sequence 176, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/848,798

CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: 09/240,274  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 176  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH50  
US-09-848-798-176

Query Match 86.8%; Score 475; DB 10; Length 107;  
Best Local Similarity 85.8%; Pred. No. 6.7e-34;  
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQISITVLYNMYQQRKAPKLLIWSASNLGSPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITCRARQISITVLYNMYQQRKAPKLLIWSASNLGSPSRF 61  
QY 61 SSGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTRKLEIKR 106  
DB 62 SSGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTRKLEIKR 107

## RESULT 8

US-09-848-798-179  
Sequence 179, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/848,798  
CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 179  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH54  
US-09-848-798-179

Query Match 86.7%; Score 474; DB 10; Length 107;  
Best Local Similarity 85.8%; Pred. No. 8.1e-34;  
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQISITVLYNMYQQRKAPKLLIWSASNLGSPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITCRARQISITVLYNMYQQRKAPKLLIWSASNLGSPSRF 61  
QY 61 SSGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTRKLEIKR 106  
DB 62 SSGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTRKLEIKR 107

## RESULT 9

US-09-848-798-32  
Sequence 32, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

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; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-848-798-32

Query Match      86.6%; Score 473.5; DB 10; Length 108;
Best Local Similarity 87.9%; Pred. No. 9,1e-34;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQOKPGKAPKLLIWAASLSQGVPSRF 61

QY 61 SSGSGGTFTLTISNLOPEDFASYCCOOSYTT-LYTGSGGTKEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGGTDFLTITISLQPEDFATYCCOOSYSTPYTGGGTKEIKR 108

RESULT 10
US-09-848-798-43
; Sequence 43, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-848-798-43

Query Match      86.6%; Score 473.5; DB 10; Length 108;
Best Local Similarity 87.9%; Pred. No. 9,1e-34;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQOKPGKAPKLLIWAASLSQGVPSRF 61

QY 61 SSGSGGTFTLTISNLOPEDFASYCCOOSYTT-LYTGSGGTKEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGGTDFLTITISLQPEDFATYCCOOSYSTPYTGGGTKEIKR 108

RESULT 11
US-09-848-798-37
; Sequence 37, Application US/09848798
; Publication No. US20030040605A1
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; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I06
US-09-848-798-37

Query Match      86.5%; Score 473; DB 10; Length 107;
Best Local Similarity 86.7%; Pred. No. 1e-33;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
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Db 2 ELTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQOKPGKAPKLLIWAASLSQGVPSRF 61

QY 61 SSGSGGTFTLTISNLOPEDFASYCCOOSYTTLYTGSGGTKEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGGTDFLTITISLQPEDFATYCCOOSYSTPYTGGGTKEIKR 107

RESULT 12
US-10-203-754A-57
; Sequence 57, Application US/10203754A
; Publication No. US20050157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSURA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuro
; APPLICANT: YOTSUMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: anti-Rh(D) chain I12
US-10-203-754A-57

Query Match      86.5%; Score 473; DB 14; Length 111;
Best Local Similarity 86.7%; Pred. No. 1e-33;
Matches 91; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 MTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQOKPGKAPKLLIWAASLSQGVPSRF 63

QY 62 SSGSGGTFTLTISNLOPEDFASYCCOOSYTTLYTGSGGTKEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 SSGSGGTDFLTITISLQPEDFATYCCOOSYSTPYTGGGTKEIKR 108

RESULT 13
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US-09-848-798-167  
: Sequence 167, Application US/09848798  
: Publication No. US20030040605A1  
: GENERAL INFORMATION:  
: APPLICANT: Siegel, Donald L.  
: TITLE OF INVENTION: R(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
: TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
: FILE REFERENCE: 09596-42U2  
: CURRENT APPLICATION NUMBER: US/09/848,798  
: CURRENT FILING DATE: 2001-05-04  
: PRIOR APPLICATION NUMBER: 09/240,274  
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
: PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
: NUMBER OF SEQ ID NOS: 224  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 167  
: LENGTH: 108  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
: FEATURE:  
: OTHER INFORMATION: anti-Rh(D) antibody clone SH34  
US-09-848-798-167

	Query Match	86.4%	Score 472.5;	DB 10;	Length 108;
	Best Local Similarity	87.9%	Pred. No. 1.le-33;		
	Matches	94;	Conservative	7;	Mismatches 5; Indels 1; Gaps 1.
QY	1	ELTSPSSLSASVGDRTVTTCRAROSISTYLNWYOOKGPKLTIWASNLQGVSRRF	60		
			:	:	:
DB	2	ELTSPSSLASVGDRVTITTCRASGISISYLNWYOOKGKAPKLITIYAAGLGQSVSRF	61		
			:	:	:
QY	61	SGSGSGTEFTLTISNLFQEDPASYCCOQSYYT-LTFPSGGTLEIKR	106		
			:	:	:
DB	62	SGSGSGNDFTLTISSLQPEDPATIYYCCOQSISTPTTPPTFGCGTKLEIKR	108		

RESULT 14  
US-09-848-798-38  
Sequence 38, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLULAR  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-42U2  
CURRENT APPLICATION NUMBER: US/09/848,798  
CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 38  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain I07  
US-09-848-798-38

Query Match	86.3%	Score 472	DB 10	Length 107	
Best Local Similarity	86.8%	Pred. NO. 1.2e-33			
Matches 92	Conservative 9	Mismatches 5	Indels 0	Gaps 0	

Qy 1 ELTQSPSLSLASVSDRVTITICRAQOSITSLTINMYQOKPGAPKLLTWSASNLQSGVSPF 60  
Db 2 ELTQSPSLSLASVSDRVTITICRAQOSITSLTINMYQOKPGAPKLLTWSASNLQSGVSPF 61  
Qy 61 SGSSSGTEFTLTITINLQEDPASPASYCOOSYTTLLTIFSGSTKLEIKR 106  
Db 62 SGSSSGTDFLTITISLQPEDPATARYCOOSYSTPTPTFGGKVEIKR 107

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RESULT 15
US-09-848-798-39
; Sequence 39, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLULOSE
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ. ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 108
US-09-848-798-39

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Query Match	86.3%	Score 472	DB 10	Length 107
Best Local Similarity	86.8%	Pred. No. 1.2e-33		
Matches 92	Conservative 9	Mismatches 5	Indels 0	Gaps 0
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Db	2	ELTSPSSLSASVGDRTVITTCRAQOSISTYINMTYQOKRGKAPKLLIWAASLSQGVPSRF	61	
Qy	61	SGSSSGTEFTLTISNLOFEDFASYYCOOSYTLTLVTFSGTDLKIR	106	
Db	62	SGSSSGTDFLTITISNLOFEDFATYYCOOSISTPTTFGGTIVKIR	107	

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Job time : 67.6212 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:09:56 ; Search time 20.0758 Seconds  
(without alignments)  
394.147 Million cell updates/sec

Title: US-10-027-725A-10  
Perfect score: 543  
Sequence: 1 ELRTSPSSLSASVGDRTYIS.....QESLSAGYTFQGRKVEIKR 106

Scoring table:  
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	475	87.5	107	US-08-276-852-104	Sequence 104, App
2	475	87.5	107	US-08-899-575-104	Sequence 104, App
3	475	87.5	107	US-08-899-575-104	Sequence 104, App
4	475	87.5	107	PCT-US95-08743-104	Sequence 104, App
5	474	87.3	107	US-09-240-274-179	Sequence 179, App
6	472	86.9	107	US-09-240-274-33	Sequence 33, App
7	472	86.9	107	US-09-240-274-175	Sequence 175, App
8	472	86.9	107	US-09-240-274-176	Sequence 176, App
9	471	86.7	107	US-09-240-274-156	Sequence 156, App
10	468	86.2	107	US-09-240-274-36	Sequence 36, App
11	467	86.0	107	US-08-276-852-105	Sequence 105, App
12	467	86.0	107	US-08-899-575-105	Sequence 105, App
13	467	86.0	107	US-08-899-575-105	Sequence 105, App
14	467	86.0	107	PCT-US95-08743-105	Sequence 105, App
15	464.5	85.5	108	US-09-240-274-32	Sequence 32, App
16	464.5	85.5	108	US-09-240-274-43	Sequence 43, App
17	464	85.5	107	US-09-240-274-37	Sequence 37, App
18	464	85.5	107	US-09-192-854-2	Sequence 37, App
19	462	85.1	107	US-09-240-274-38	Sequence 38, App
20	462	85.1	107	US-09-240-274-39	Sequence 39, App
21	461	84.9	107	US-09-240-274-158	Sequence 158, App
22	460.5	84.8	108	US-09-240-274-167	Sequence 167, App
23	459.5	84.6	108	US-09-240-274-163	Sequence 163, App
24	458	84.3	107	US-09-240-274-35	Sequence 35, App
25	458	84.3	107	US-09-240-274-173	Sequence 173, App
26	458	84.3	108	US-08-379-057-29	Sequence 29, App
27	457	84.2	104	US-08-276-852-106	Sequence 106, App

28	457	84.2	104	1	US-08-899-575-106	Sequence 106, App
29	457	84.2	104	1	US-08-899-575-106	Sequence 106, App
30	457	84.2	104	5	PCT-US95-08743-106	Sequence 40, App
31	457	84.2	107	3	US-09-240-274-40	Sequence 44, App
32	457	84.2	214	4	US-09-472-087-71	Sequence 71, App
33	456	84.0	107	3	US-09-240-274-14	Sequence 17, App
34	452	83.2	107	3	US-09-240-274-172	Sequence 17, App
35	452	83.2	107	3	US-09-240-274-174	Sequence 17, App
36	451.5	83.1	108	1	US-08-276-852-109	Sequence 109, App
37	451.5	83.1	108	1	US-08-899-575-109	Sequence 109, App
38	451.5	83.1	108	1	US-08-899-575-109	Sequence 109, App
39	451.5	83.1	108	3	US-09-240-274-41	Sequence 41, App
40	451.5	83.1	108	3	PCT-US95-08743-109	Sequence 109, App
41	451	83.1	107	3	US-09-240-274-168	Sequence 168, App
42	451	83.1	108	3	US-09-025-7698-14	Sequence 14, App
43	451	83.1	108	4	US-09-490-070A-14	Sequence 14, App
44	451	83.1	108	4	US-09-490-153-14	Sequence 14, App
45	451	83.1	108	4	US-09-490-324-14	Sequence 14, App

ALIGNMENTS

RESULT 1  
US-08-276-852-104  
Sequence 104, Application US/08276852

Patent No. 5652138

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R

APPLICANT: Barbas, Carlos F

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 170

CORRESPONDENCE ADDRESS:

ADDRESS: The Scripps Research Institute, Office of

ADDRESS: Patent Counsel

STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,

STREET: Mail Drop TPC8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/276,852

FILING DATE: 18-JUL-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/178,302

FILING DATE: 30-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/954,148

FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SCRI452P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 104:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-276-852-104

Query Match 87.5%; Score 475; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.3e-38;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAKPLIYAASSLSQGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAKPLIYAASSLSQGVPSRF 60

Qy 61 SSGSGTDFLTITSSLOPEDFASYYCOESLSASTYFGQGTVEIKR 106  
Db 61 SSGSGTDFLTITSSLOPEDFATYYCOQSYSTPYTFQGTLEIKR 106

RESULT 2  
US-08-899-575-104  
; Sequence 104, Application US/08899575  
; Patent No. 5770440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbos, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCRL452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.3e-38;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAKPLIYAASSLSQGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAKPLIYAASSLSQGVPSRF 60

Qy 61 SSGSGTDFLTITSSLOPEDFASYYCOESLSASTYFGQGTVEIKR 106  
Db 61 SSGSGTDFLTITSSLOPEDFATYYCOQSYSTPYTFQGTLEIKR 106

RESULT 3  
US-08-899-575-104  
; Sequence 104, Application US/08899575  
; Patent No. 5804440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbos, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCRL452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.3e-38;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAKPLIYAASSLSQGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAKPLIYAASSLSQGVPSRF 60

Qy 61 SSGSGTDFLTITSSLOPEDFASYYCOESLSASTYFGQGTVEIKR 106  
Db 61 SSGSGTDFLTITSSLOPEDFATYYCOQSYSTPYTFQGTLEIKR 106

RESULT 4  
PCT-US95-08743-104  
; Sequence 104, Application PC/TUS9508743



GENERAL INFORMATION:  
APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08743  
FILING DATE: 11-JUL-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-08743-104

Query Match 87.5%; Score 475; DB 5; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.3e-38;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTSPSSLSASVGDVDTISCRASORINTYNTYQHKRGKAPKLLIYAASSLGVSRRF 60  
DB 1 ELTSPSSLSASVGDVDTITCRASQSISSYNTMYQKRGKAPKLLIYAASSLGVSRRF 60  
QY 61 SGGSGYDFTLTISLQPEDFASYCOESLSASTFFGQGTVEIKR 106  
DB 61 SGGSGYDFTLTISLQPEDFATYCCQSYSTPYTFFGQGTVEIKR 106

## RESULT 5

US-09-274-179  
Sequence 179, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 179  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH54  
US-09-240-274-179

Query Match 87.3%; Score 474; DB 3; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.6e-38;  
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTSPSSLSASVGDVDTISCRASORINTYNTYQHKRGKAPKLLIYAASSLGVSRRF 60  
DB 2 ELTSPSSMSASVGDVDTITCRASQSICTYNTMYQKRGKAPKLLIYAASSLGVSRRF 61  
QY 61 SGGSGYDFTLTISLQPEDFASYCOESLSASTFFGQGTVEIKR 106  
DB 62 SGGSGYDFTLTISLQPEDFATYCCQSYSTPYTFFGQGTVEIKR 107

RESULT 6  
US-09-240-274-33  
Sequence 33, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 33  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain 102  
US-09-240-274-33

Query Match 86.9%; Score 472; DB 3; Length 107;  
Best Local Similarity 87.7%; Pred. No. 2.6e-38;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTSPSSLSASVGDVDTISCRASORINTYNTYQHKRGKAPKLLIYAASSLGVSRRF 60  
DB 2 ELTSPSSLSASVGDVDTITCRASQSISSYNTMYQKRGKAPKLLIYAASSLGVSRRF 61  
QY 61 SGGSGYDFTLTISLQPEDFASYCOESLSASTFFGQGTVEIKR 106  
DB 62 SGGSGYDFTLTISLQPEDFATYCCQSYSTLTMTFFGQGTVEIKR 107

## RESULT 7

US-09-240-274-175  
Sequence 175, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 175  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH49  
US-09-240-274-175

Query Match 86.9%; Score 472; DB 3; Length 107;  
Best Local Similarity 86.8%; Pred. No. 2.6e-38;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTSPSSLSASVGDVDTISCRASORINTYNTYQHKRGKAPKLLIYAASSLGVSRRF 60  
DB 2 ELTSPSSLSASVGDVDTITCRASQSISSYNTMYQKRGKAPKLLIYAASSLGVSRRF 61



FILING DATE: 18-JUL-1994  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/178,302  
 FILING DATE: 30-SEP-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/954,148  
 FILING DATE: 30-SEP-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fitting, Thomas  
 REGISTRATION NUMBER: 34,163  
 REFERENCE/DOCKET NUMBER: SCR1452P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-554-2937  
 TELEFAX: 619-554-6312  
 INFORMATION FOR SEQ ID NO: 105:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 107 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-276-852-105

Query Match 86.0%; Score 467; DB 1; Length 107;  
 Best Local Similarity 86.8%; Pred. No. 7.7e-38;  
 Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTYISGRASQRIINTYINWYQKRGKAPKLLIYAASLSQGVPSRF 60  
 DB 1 ELTQSPSLASVGDRTYISGRASQRIINTYINWYQKRGKAPKLLIYAASLSQGVPSRF 60  
 QY 61 SGSGYGTDFLTITSLQFEDPASYCOESLSASYTFQGTVEIKR 106  
 DB 61 SGSGYGTDFLTITSLQFEDPASYCOESLSASYTFQGTVEIKR 106

RESULT 12  
 US-08-899-575-105  
 Sequence 105, Application US/08899575  
 Patent No. 5770440  
 GENERAL INFORMATION:  
 APPLICANT: Burton, Dennis R  
 APPLICANT: Barbias, Carlos F  
 APPLICANT: Lerner, Richard A  
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 NUMBER OF SEQUENCES: 170  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: The Scripps Research Institute, Office of  
 STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/899,575  
 FILING DATE: 24-JUL-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/276,852  
 FILING DATE: 18-JUL-1994  
 APPLICATION NUMBER: US 08/178,302  
 FILING DATE: 30-SEP-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/954,148  
 FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:  
 NAME: Fitting, Thomas  
 REGISTRATION NUMBER: 34,163  
 REFERENCE/DOCKET NUMBER: SCR1452P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-554-2937  
 TELEFAX: 619-554-6312  
 INFORMATION FOR SEQ ID NO: 105:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 107 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-899-575-105

Query Match 86.0%; Score 467; DB 1; Length 107;  
 Best Local Similarity 86.8%; Pred. No. 7.7e-38;  
 Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTYISGRASQRIINTYINWYQKRGKAPKLLIYAASLSQGVPSRF 60  
 DB 1 ELTQSPSLASVGDRTYISGRASQRIINTYINWYQKRGKAPKLLIYAASLSQGVPSRF 60  
 QY 61 SGSGYGTDFLTITSLQFEDPASYCOESLSASYTFQGTVEIKR 106  
 DB 61 SGSGYGTDFLTITSLQFEDPASYCOESLSASYTFQGTVEIKR 106

RESULT 13  
 US-08-899-575-105  
 Sequence 105, Application US/08899575  
 Patent No. 5804440  
 GENERAL INFORMATION:  
 APPLICANT: Burton, Dennis R  
 APPLICANT: Barbias, Carlos F  
 APPLICANT: Lerner, Richard A  
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 NUMBER OF SEQUENCES: 170  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: The Scripps Research Institute, Office of  
 STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/899,575  
 FILING DATE: 24-JUL-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/276,852  
 FILING DATE: 18-JUL-1994  
 APPLICATION NUMBER: US 08/178,302  
 FILING DATE: 30-SEP-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/954,148  
 FILING DATE: 30-SEP-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fitting, Thomas  
 REGISTRATION NUMBER: 34,163  
 REFERENCE/DOCKET NUMBER: SCR1452P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-554-2937  
 TELEFAX: 619-554-6312  
 INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-899-575-105

Query Match 86.0%; Score 467; DB 1; Length 107;  
Best Local Similarity 86.8%; Pred. No. 7.7e-38;  
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60

QY 61 SSGSGYDFTLTISLQPEDFASYYCQESLSASYTFGGGTVEIKR 106  
DB 61 SSGSGYDFTLTISLQPEDFATYYCQGSYSTPTFGGTVEIKR 106

RESULT 14  
PCT-US95-08743-105  
Sequence 105, Application PC/TUS9508743

GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08743  
FILING DATE: 11-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-08743-105

Query Match 86.0%; Score 467; DB 5; Length 107;  
Best Local Similarity 86.8%; Pred. No. 7.7e-38;  
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60

QY 61 SSGSGYDFTLTISLQPEDFASYYCQESLSASYTFGGGTVEIKR 106  
DB 61 SSGSGYDFTLTISLQPEDFATYYCQGSYSTPTFGGTVEIKR 106

RESULT 15  
US-09-240-274-32  
Sequence 32, Application US/09240274

GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-42U2  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 32  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain 101  
US-09-240-274-32

Query Match 85.5%; Score 464.5; DB 3; Length 108;  
Best Local Similarity 86.9%; Pred. No. 1.4e-37;  
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SSGSGYDFTLTISLQPEDFASYYCQESLSA-SYTFGGGTVEIKR 106  
DB 62 SSGSGYDFTLTISLQPEDFATYYCQGSYSTPTFGGTVEIKR 108

Search completed: July 26, 2005, 09:30:00  
Job time : 20.0758 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:07:26 ; Search time 13.6515 Seconds

(without alignments)  
747.095 Million cell updates/sec

Title: US-10-027-725A-10

Sequence: 1 ELTQSPSSLSASVGDRTVTS.....QESLSASYTFGQGTKEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	464	85.5	127	2	S40367
2	459	84.5	123	2	S40331
3	458	84.3	108	2	B49047
4	456	84.0	108	2	S47182
5	452	83.2	109	2	S31998
6	452	83.2	109	2	S31979
7	448	82.5	109	2	S31980
8	446	82.1	108	2	S44122
9	445	82.0	109	2	S32001
10	441	81.2	108	2	S19674
11	439	80.8	109	2	S31981
12	439	80.8	129	2	S52793
13	438	80.7	107	2	S36264
14	437	80.5	108	2	S31973
15	436	80.3	109	2	S31983
16	436	80.3	122	2	S40370
17	436	80.3	129	1	K1HUK
18	436	80.3	129	2	S40317
19	435	80.1	128	2	S46372
20	434	79.9	120	2	S46370
21	433.5	79.8	125	2	S40315
22	433	79.7	108	1	K1HUK
23	432	79.6	132	2	S40334
24	431	79.4	109	2	S31978
25	430	79.2	108	1	K1HUK
26	430	79.2	132	2	S36646
27	425	78.3	122	2	S40314
28	425	78.3	129	2	S40369
29	424.5	78.2	106	2	PC2397

30	423.5	78.0	124	2	S40336	Ig kappa chain V-J
31	422.5	77.8	107	2	S36275	Ig lambda chain V
32	422	77.7	125	2	S40333	Ig kappa chain V-J
33	422	77.7	131	2	S40352	Ig kappa chain V-J
34	420	77.3	108	1	K1HUK	Ig kappa chain V-I
35	420	77.3	125	2	S40349	Ig kappa chain V-J
36	420	77.3	126	2	S40335	Ig kappa chain V-J
37	419	77.2	125	2	S40350	Ig kappa chain - h
38	418	77.0	117	2	S46371	Ig kappa chain V-J
39	418	77.0	129	2	S52792	Ig kappa chain V r
40	417	76.8	117	2	S46376	Ig kappa chain V-J
41	416	76.6	108	1	K1HUK	Ig kappa chain V-I
42	414	76.2	107	2	JL0139	Ig kappa chain V r
43	414	76.2	107	2	S36262	Ig kappa chain V
44	414	76.2	108	1	K1HUK	Ig lambda chain V
45	413.5	76.2	108	2	S30521	Ig kappa chain V r

## ALIGNMENTS

```
RESULT 1
S40367
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40367
R:Klein, R.; Jaenichen, R.; Zachau, H. G.
Bur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40367
A:Status: Preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-127 <KLE>
A:Cross-references: EMBL:X72477
C:Keywords: heterotetramer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match      85.5%; Score 464; DB 2; Length 127;
Best Local Similarity 84.9%; Pred. No. 2.9e-34;
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY      1 ELTQSPSSLSASVGDRTVTSGRASORINTYNTQHKRGPALKLIYAAASSLQGVPSRF 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      20 QMTQSPSSLSASVGDRTVITCRASQISINYNWYORKKAPKLIYAAASSLQGVPSRF 79
QY      61 SGSGVGTDTLTITSLQPEDFASYYCOESLSASYTFGQGTKEIKR 106
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      80 SGSGSGTDTLTITSLQPEDFATYYCOQSYNTPWTFGQGTKEIKR 125

RESULT 2
S40331
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40331
R:Klein, R.; Jaenichen, R.; Zachau, H. G.
Bur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40331
A:Status: Preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72441; NID:G441350; PIDN:CAA51109.1; PID:G441351
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin homology
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match      84.5%; Score 459; DB 2; Length 123;
```

Best Local Similarity 85.7%; Pred. No. 7.9e-34;  
Matches 90; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKRGKAPKLLITYAASSLQSGVPSRF 60  
Db 19 QMTQSPSSLSASVGDRTVITCRASQSISSYINWYQOKRKAPKLLITYAASSLQSGVPSRF 78

Qy 61 GSGGYGTDFTLTISLQPEDFASYYCOESLSASYTFGGGTVEIKR 105  
Db 79 GSGSGTDFLTLTISLQPEDFATYYCQGSYSTPTFGGTVEIKR 123

RESULT 3  
Ig kappa chain V region (monoclonal scrtational autoantibody strab SA-1A) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: B49047  
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.  
Eur. J. Immunol. 22, 2231-2236, 1992  
A:Title: Human monoclonal autoantibodies isolated from thymic B lymphocytes  
A:Reference number: A49047; MUID:92387224; PMID:1516616  
A:Accession: B49047  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-108 <VIC>  
A:Cross-references: UNIPROT:Q96SAG; UNIPROT:Q9UL77  
A:Experimental source: thymic B lymphocytes  
A:Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIPI:113209)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 458; DB 2; Length 108;  
Best Local Similarity 84.9%; Pred. No. 8.5e-34;  
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKRGKAPKLLITYAASSLQSGVPSRF 60  
Db 3 QMTQSPSSLSASVGDRTVITCRASQSISSYINWYQOKRKAPKLLITYAASSLQSGVPSRF 62

Qy 61 GSGGYGTDFTLTISLQPEDFASYYCOESLSASYTFGGGTVEIKR 106  
Db 63 GSGSGTDFLTLTISLQPEDFATYYCQGSYSTPTFGGTVEIKR 108

RESULT 4  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S47182  
R:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.  
submitted to the EMBL Data Library, June 1994  
A:Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient  
A:Reference number: S47181  
A:Accession: S47182  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-108 <MC1>  
A:Cross-references: EMBL:X79786; NID:G506422; PIDN:CAA56182.1; PID:G506423  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 456; DB 2; Length 108;  
Best Local Similarity 84.9%; Pred. No. 1.3e-33;  
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKRGKAPKLLITYAASSLQSGVPSRF 60  
Db 3 ELTQSPSSLSASVGDRTVITCRASQSISSYINWYQOKRKAPKLLITYAASSLQSGVPSRF 62

Qy 61 GSGGYGTDFTLTISLQPEDFASYYCOESLSASYTFGGGTVEIKR 106

Db 63 GSGSGTDFLTLTISLQPEDFATYYCQGSYSTPTFGGTVEIKR 108

RESULT 5  
Ig kappa chain - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S31998  
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
A:Reference number: S31977  
A:Accession: S31998  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-109 <POR>  
A:Cross-references: EMBL:Z15075; NID:G38501; PIDN:CAA78790.1; PID:G38502  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 452; DB 2; Length 109;  
Best Local Similarity 83.8%; Pred. No. 2.9e-33;  
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKRGKAPKLLITYAASSLQSGVPSRF 61  
Db 4 MTQSPSSLSASVGDRTVITCRASQSISSYINWYQOKRKAPKLLITYAASSLQSGVPSRF 63

Qy 62 GSGGYGTDFTLTISLQPEDFASYYCOESLSASYTFGGGTVEIKR 106  
Db 64 GSGGTDFTLTISLQPEDFATYYCQGSYSTPTFGGTVEIKR 108

RESULT 6  
Ig kappa chain - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S31979  
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
A:Reference number: S31977  
A:Accession: S31979  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-109 <POR>  
A:Cross-references: EMBL:Z15075; NID:G38489; PIDN:CAA78784.1; PID:G38490  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 452; DB 2; Length 109;  
Best Local Similarity 81.9%; Pred. No. 2.9e-33;  
Matches 86; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKRGKAPKLLITYAASSLQSGVPSRF 61  
Db 4 MTQSPSSLSASVGDRTVITCRASQSISSYINWYQOKRKAPKLLITYAASSLQSGVPSRF 63

Qy 62 GSGGYGTDFTLTISLQPEDFASYYCOESLSASYTFGGGTVEIKR 106  
Db 64 GSGGTDFTLTISLQPEDFATYYCQGSYSTPTFGGTVEIKR 108

RESULT 7  
Ig kappa chain - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C:Accession: S31980; S32000  
 R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
 A:Submitted to the EMBL Data Library, June 1992  
 C:Description: Lack of promiscuity in autocatalytic H and L chain combinations as  
 A:Reference number: S31977  
 A:Accession: S31980  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-109 <FOR>  
 A:Cross-references: EMBL:Z15076; NID:g38491; PIDN:CAA78785.1; PID:g38492; EMBL:Z15083; N  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 448; DB 2; Length 109;  
 Best Local Similarity 81.0%; Pred. No. 6.6e-33;  
 Matches 85; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Query 2 LTQSPSSLSASVGVDRVTISCRASQRIINTYLMWYOHKPKAPKLLIYAASLSQGVPSRFS 61  
 Db 4 MTQSPSSLSASVGVDRVTISCRASQNIKGYLMWYOHKPKAPKLLIYGTSTLSQGVPSRFS 63

Query 62 GSGYGTDTFTLTISLQFEDFASYYCOSLSASYTFGGGTKEIKR 106  
 Db 64 GSGGTDTFTLTISLQFEDFATYFCQSYSSPYTFGGGTKEIKR 108

RESULT 8  
 S44122  
 Ig kappa chain V region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
 C:Accession: S44122  
 R:Hawkins, R.E.; Zhu, D.; Owecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
 A:Submitted to the EMBL Data Library, March 1994  
 C:Description: Idiolytic vaccination against human B-cell lymphoma: rescue of variable r  
 A:Reference number: S44105  
 A:Accession: S44122  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-108 <HAW>  
 A:Cross-references: EMBL:Z31390; NID:g472976; PIDN:CAA83265.1; PID:g940533  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 446; DB 2; Length 108;  
 Best Local Similarity 83.0%; Pred. No. 9.8e-33;  
 Matches 88; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Query 1 ELTQSPSSLSASVGVDRVTISCRASQRIINTYLMWYOHKPKAPKLLIYAASLSQGVPSRFP 60  
 Db 3 QMTQSPSSLSASVGVDRVTISCRASQISISYLMWYOHKPKAPKLLIYASLSQGVPSRFP 62

Query 61 GSGYGTDTFTLTISLQFEDFASYYCOSLSASYTFGGGTKEIKR 106  
 Db 63 GSGGTDTFTLTISLQFEDFATYFCQSYSSPYTFGGGTKEIKR 108

RESULT 9  
 S32001  
 Ig kappa chain - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: S32001  
 R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
 A:Submitted to the EMBL Data Library, June 1992  
 C:Description: Lack of promiscuity in autocatalytic H and L chain combinations as  
 A:Reference number: S31977  
 A:Accession: S32001  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-109 <FOR>

A:Cross-references: EMBL:Z15082; NID:g38503; PIDN:CAA78791.1; PID:g38504  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 445; DB 2; Length 109;  
 Best Local Similarity 80.0%; Pred. No. 1.2e-32;  
 Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Query 2 LTQSPSSLSASVGVDRVTISCRASQRIINTYLMWYOHKPKAPKLLIYAASLSQGVPSRFS 61  
 Db 4 MTQSPSSLSASVGVDRVTISCRASQNIKGYLMWYOHKPKAPKLLIYGTSTLSQGVPSRFS 63

Query 62 GSGYGTDTFTLTISLQFEDFASYYCOSLSASYTFGGGTKEIKR 106  
 Db 64 GSGGTDTFTLTISLQFEDFATYFCQSYSSPYTFGGGTKEIKR 108

RESULT 10  
 S19674  
 Ig kappa chain V region (clone alpha-TE19) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
 C:Accession: S19674  
 R:Markus, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.  
 A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph  
 A:Reference number: S19663; MUID:92085276; PMID:1748994  
 A:Accession: S19674  
 A:Molecule type: mRNA  
 A:Residues: 1-108 <MAR>  
 A:Cross-references: EMBL:X61642; NID:g37860; PIDN:CAA43823.1; PID:g1335386  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 441; DB 2; Length 108;  
 Best Local Similarity 82.9%; Pred. No. 2.7e-32;  
 Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Query 2 LTQSPSSLSASVGVDRVTISCRASQRIINTYLMWYOHKPKAPKLLIYAASLSQGVPSRFS 61  
 Db 4 LTQSPSSLSASVGVDRVTITCRASQISISYLMWYOHKPKAPKLLIYAASLSQGVPSRFS 63

Query 62 GSGYGTDTFTLTISLQFEDFASYYCOSLSASYTFGGGTKEIKR 106  
 Db 64 GSGGTDTFTLTISLQFEDFATYFCQSYSSPYTFGGGTKEIKR 108

RESULT 11  
 S31981  
 Ig kappa chain - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C:Accession: S31981  
 R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
 A:Submitted to the EMBL Data Library, June 1992  
 C:Description: Lack of promiscuity in autocatalytic H and L chain combinations as  
 A:Reference number: S31977  
 A:Accession: S31981  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-109 <FOR>  
 A:Cross-references: EMBL:Z15077; NID:g38493; PIDN:CAA78786.1; PID:g38494  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 439; DB 2; Length 109;  
 Best Local Similarity 80.0%; Pred. No. 4.1e-32;  
 Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Query 2 LTQSPSSLSASVGVDRVTISCRASQRIINTYLMWYOHKPKAPKLLIYAASLSQGVPSRFS 61

Db 4 MTQSPSSLSASVGDRTVITCRASQDISRIYLMWYQKPKAKPLIYHGAATSLQSGVPSRFS 63  
Oy 62 GSGGCTDFTLTITSSLOPEDFASYYCOESLSASTYFGGCTKVEIKR 106  
64 GSGGCTDFTLTITSSLOPEDFATYTCQOSYSTPFTFGGCTKLEIKR 108

## RESULT 12

552793  
Ig kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 19-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 21-Jan-2000  
C:Accession: S52793  
R:Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995  
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-  
A:Reference number: S52789  
A:Accession: S52793  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-129 <ROC>  
A:Cross-references: EMBL:X85997; NID:G758600; PIDN:CAA5989.1; PID:G758601  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 439; DB 2; Length 129;  
Best Local Similarity 81.9%; Pred. No. 4.8e-32;  
Matches 86; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Oy 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPKAKPLIYAASSLQSGVPSRF 60  
Db 25 QMTQSPSSLSASVGDRTVITCRASQNTISYLMWYQKPKAKPLIYAASSLQSGVPSRF 84  
Oy 61 GSGGCTDFTLTITSSLOPEDFASYYCOESLSASTYFGGCTKVEIKR 105  
Db 85 VGSGGCTDFTLTITSSLOPEDFATYTCQOYSAPLTFGGCTKVEIKR 129

## RESULT 13

S36264  
Ig lambda chain V region (clone alpha-CE4-8A) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C:Accession: S36264  
R:Griffith, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36256; MUID:93178448; PMID:7679990  
A:Accession: S36264  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-107 <GRI>  
A:Cross-references: EMBL:Z18845; NID:G33426; PIDN:CAA79297.1; PID:G939919  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 438; DB 2; Length 107;  
Best Local Similarity 83.7%; Pred. No. 4.9e-32;  
Matches 87; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Oy 2 LTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPKAKPLIYAASSLQSGVPSRFS 61  
Db 4 LTQSPSSLSASVGDRTVITCRASQISISYLMWYQKPKAKPLIYAASSLQSGVPSRFS 63

Oy 62 GSGGCTDFTLTITSSLOPEDFASYYCOESLSASTYFGGCTKVEIKR 105  
Db 64 GSGGCTDFTLTITSSLOPEDFATYTCQOYSNPPLTFGGCTKVDIKR 107

## RESULT 14

S31977  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S31977  
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
A:Reference number: S31977  
A:Accession: S31977  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-108 <POR>  
A:Cross-references: UNIPROT:Q96SA9; EMBL:Z15073  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.5%; Score 437; DB 2; Length 108;  
Best Local Similarity 82.9%; Pred. No. 6.1e-32;  
Matches 87; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Oy 2 LTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPKAKPLIYAASSLQSGVPSRFS 61  
Db 4 MTQSPSSLSASVGDRTVITCRASQISAYLMWYQKPKAKPLIYAASSLQSGVPSRFS 63  
Oy 62 GSGGCTDFTLTITSSLOPEDFASYYCOESLSASTYFGGCTKVEIKR 106  
Db 64 GSGGCTDFTLTITSSLOPEDFATYTCQOSYPTVDFHGGCTKVEIKR 108

## RESULT 15

S31983  
Ig kappa chain - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S31983  
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
A:Reference number: S31977  
A:Accession: S31983  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-109 <POR>  
A:Cross-references: EMBL:Z15079; NID:G38497; PIDN:CAA78788.1; PID:G38498  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 436; DB 2; Length 109;  
Best Local Similarity 79.0%; Pred. No. 7.6e-32;  
Matches 83; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Oy 2 LTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPKAKPLIYAASSLQSGVPSRFS 61  
Db 4 MTQSPSSLSASVGDRTVITCRASQISAYLMWYQKPKAKPLIYAASSLQSGVPSRFS 63  
Oy 62 GSGGCTDFTLTITSSLOPEDFASYYCOESLSASTYFGGCTKVEIKR 106  
Db 64 GSGGCTDFTLTITSSLOPEDFATYTCQOSYSSPYTFGGCTKLEIER 108

Search completed: July 26, 2005, 09:27:50  
Job time : 14.6515 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 26, 2005, 08:52:21 ; Search time 66.6515 Seconds

(without alignments)  
814.391 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543

Sequence: 1 ELTQSPSSLSASVGDRTVIS.....QESLSASTGCGTKVKEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprotc:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	85.6	108	2 Q9UL77	Q9UL77 homo sapien
2	449.5	82.8	107	2 Q96SA9	Q96SA9 homo sapien
3	439.5	80.9	107	2 Q9UL81	Q9UL81 homo sapien
4	439	80.8	236	2 Q6GMX0	Q6GMX0 homo sapien
5	436	80.3	129	1 KVI1W_HUMAN	P04431 homo sapien
6	436	80.3	236	2 Q6GMX8	Q6GMX8 homo sapien
7	434	79.9	236	2 Q6GMW1	Q6GMW1 homo sapien
8	433	79.7	108	1 KVI1E_HUMAN	P01597 homo sapien
9	430	79.2	108	1 KVI1H_HUMAN	P01600 homo sapien
10	424	78.1	236	2 Q6PIH7	Q6PIH7 homo sapien
11	422	77.7	108	2 Q9UL79	Q9UL79 homo sapien
12	420	77.3	108	1 KVI1N_HUMAN	P01606 homo sapien
13	420	77.3	108	2 Q9UL70	Q9UL70 homo sapien
14	418	77.0	234	2 Q7Z473	Q7Z473 homo sapien
15	416	76.6	108	1 KVI1F_HUMAN	P01598 homo sapien
16	414	76.2	108	1 KVI1K_HUMAN	P01603 homo sapien
17	413	76.1	108	1 KVI1J_HUMAN	P04430 homo sapien
18	412	75.9	108	1 KVI1O_HUMAN	P01607 homo sapien
19	412	75.9	236	2 Q7Z3V4	Q7Z3V4 homo sapien
20	409	75.3	108	1 KVI1G_HUMAN	P01599 homo sapien
21	408	75.1	108	1 KVI1M_HUMAN	P01605 homo sapien
22	407	75.0	108	1 KVI1B_HUMAN	P01594 homo sapien
23	406	74.8	108	1 KVI1R_HUMAN	P01593 homo sapien
24	404	74.4	108	1 KVI1A_HUMAN	P01610 homo sapien
25	400	73.7	236	2 Q6PIH4	Q6PIH4 homo sapien
26	399.5	73.6	107	1 KVI1D_HUMAN	P01596 homo sapien
27	399	73.5	108	1 KVI1S_HUMAN	P01611 homo sapien
28	398	73.3	108	1 KVI1P_HUMAN	P01608 homo sapien
29	397	73.1	108	1 KVI1L_HUMAN	P01604 homo sapien
30	397	73.1	129	1 KVI1X_HUMAN	P04432 homo sapien
31	397	73.1	236	2 Q6GMX9	Q6GMX9 homo sapien

32	396	72.9	108	1 KVI1Y_HUMAN	P80362 homo sapien
33	396	72.9	236	2 Q6PIH5	Q6PIH5 homo sapien
34	394	72.6	244	2 Q65ZC8	Q65ZC8 homo sapien
35	391	72.0	108	1 KVI1Q_HUMAN	P01609 homo sapien
36	391	72.0	240	2 Q65ZC9	Q65ZC9 homo sapien
37	385.5	71.0	109	1 KVI1T_HUMAN	P01612 homo sapien
38	384	70.7	108	1 KVI1C_HUMAN	P01595 homo sapien
39	376	69.2	108	1 KVI1T_MOUSE	P01653 mus musculus
40	373	68.7	108	1 KVI5S_MOUSE	P01652 mus musculus
41	371	68.3	108	2 Q9UL83	Q9UL83 homo sapien
42	371	68.3	116	2 Q96PE6	Q96PE6 homo sapien
43	370.5	68.2	109	1 KVI3B_HUMAN	P01623 homo sapien
44	370	68.1	108	1 KVI5Q_MOUSE	P01650 mus musculus
45	368.5	67.9	109	1 KVI3B_HUMAN	P01620 homo sapien

#### ALIGNMENTS

RESULT 1									
ID	Q9UL77	PRELIMINARY;	PRT;	108 AA.					
AC	Q9UL77								
DT	01-MAY-2000 (TrEMBLrel. 13, Created)								
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)								
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)								
DE	Myosin-reactive immunoglobulin light chain variable region (Fragment).								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.								
OX	NCBI_Taxid=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=98271139; PubMed=9614934; DOI=10.1006/clin.1998.4531;								
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;								
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.;"								
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).								
DR	EMBL; AF035037; AAD56273.1; -.								
DR	PIR; B49047; B49047.								
DR	PIR; S34083; S34083.								
DR	HSSP; P01607; IBMW.								
DR	InterPro; IPR007110; Ig-like.								
DR	InterPro; IPR003596; Ig_v.								
DR	SMART; SM00406; IGv; 1.								
DR	PROSITE; PS50835; IG_LIKE; 1.								
FT	NON_TER	1	1						
FT	NON_TER	108	108						
SEQ	SEQUENCE	108 AA;	11738 MW;	C06681716C4D16F3 CRC64;					
	Query Match		85.6%;	Score 465;	DB 2;	Length 108;			
	Best Local Similarity		84.9%;	Pred. No. 2e-41;					
	Matches	90;	Conservative	9;	Mismatches	7;	Indels	0;	Gaps
									0;
Qy	1	ELTQSPSSLSASVGDRTVISCRASQRTINTYLNWQHKGKAPKLLIYAASLSGVSRRF	60						
	:::	:::							
Db	3	QMTQSPSSLSASVGDRTVITCRASQGISSTYLNWYQKPKGKAPNLLIYAASLSGVSRRF	62						
Qy	61	SGSGYGTDFLTITSSLPEDFPASVYCOESLSASTFGQTKVEIKR	106						
Db	63	SGSGSGTDFLTITSSLPEDFPATFYCOOSYSTSTWFGGTVEIKR	108						
RESULT 2									
ID	Q96SA9	PRELIMINARY;	PRT;	107 AA.					
AC	Q96SA9;								
DT	01-DEC-2001 (TrEMBLrel. 19, Created)								
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)								
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)								
DE	Anti-streptococcal/anti-myosin immunoglobulin kappa light chain								

DB	Variable region (Fragment)
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euteheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98375893; PubMed=9712075;
RA	Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT	"Molecular analysis of polyclonal monoclonal antibodies from
RT	rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT	antibody V region genes."/
RL	J. Immunol. 161:2020-2031(1998).
DR	EMBL: U96396; AAB68785.1; --.
DR	PIR: B49047; B49047.
DR	PIR: PH0867; PH0867.
DR	PIR: S16840; S16840.
DR	PIR: S31977; S31977.
DR	PIR: S34083; S34083.
DR	PIR: S34086; S34086.
DR	HSSP: P01607; 1BMW.
DR	InterPro: IPR007110; Ig-like.
DR	InterPro: IPR003596; Ig_v.
DR	SMART: SM00406; IGV; 1.
DR	PROSITE: PS50835; IG-LIKE; 1.
FT	NON_TER 1
FT	NON_TER 1
SO	SEQUENCE 107 AA; 11520 MW; 4BB4359C5B577F16 CRC64;
QY	Query Match 82.8%; Score 449.5; DB 2; Length 107;
Db	Best Local Similarity 84.9%; Pred. No. 8.7e-40;
	Matches 90; Conservative 8; Mismatches 7; Indels 1; Gaps 1;
QY	1 ELTSPSSLSVSGDRTVITSCRASGRITMYNTWYQHKRGKPKLLIYAASSLQSGVPSRF 60
Db	3 QMTSPSSLSVSGDRTVITSCRASGRITMYNTWYQHKRGKPKLLIYAASSLQSGVPSRF 62
QY	61 SGGSGYDFTLTLSLQFEDPASYCCQSLASVYFGGQTKVEIKR 106
Db	63 SGGSGYDFTLTLSLQFEDPASYCCQSLASVYFGGQTKVEIKR 107
RESULT 3	
ID	Q9UL81 PRELIMINARY; PRT; 107 AA.
AC	Q9UL81.
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euteheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA	Young D.C.;
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal
RT	fetus."/
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).
DR	EMBL: AF035033; AAD56269.1; --.
DR	HSSP: P01607; 1BMW.
DR	InterPro: IPR007110; Ig-like.
DR	InterPro: IPR003596; Ig_v.
DR	SMART: SM00406; IGV; 1.
DR	PROSITE: PS50835; IG-LIKE; 1.
FT	NON_TER 1
FT	NON_TER 1
SO	SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

	Query Match	80.9%	Score 439.5;	DB 2;	Length 107;	
	Best Local Similarity	82.1%	Pred. No. 1e-38;			
	Matches 87;	Conservative	8;	Mismatches 10;	Indels 1;	Gaps 1;
Oy	1 ELTQSPSSLASVGDRTYISGRASQRINTYLIMYOHRKPKAPKLLIYAASSLQSGVPSRF 60 :::      3 QMTQSPSSLASVGDRTYTITCRASQSISNTLMWYQKRPKRNPLLIYAASSLQSGVPSRF 62 :::					
Dd	61 SGGGVTDFLTITSLDPEDPASYCOESLSASTTFEGCTKVEIKR 106    ::  63 SGSSGSVDFTLTISGLQAEDFATYYCOOSYSA-LTFEPGTGVDIRR 107    ::					
RESULT 4						
ID	Q6GMXO	PRELIMINARY;	PRT;	236 AA.		
AC	Q6GMXO;					
DT	05-JUL-2004 (TREMBLrel. 27, Created)					
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)					
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)					
DS	Hypothetical protein.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Spleen;					
RA	MEBLINB=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;					
RA	Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,					
RA	Altschul S.F., Zeeberg B., Butow K.H., Schaefter C.F., Bhat N.K.,					
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,					
RA	Ditachenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,					
RA	Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,					
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,					
RA	Bohak S.A., McGowan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,					
RA	Villalob D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA	Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,					
RA	Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,					
RA	Bakerleguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,					
RA	Krzywinski M.I., Skelisa U., Smatius D.E., Schnerch A., Schein J.E.,					
RA	Jones S.J., Maiza M.A.;					
RT	"Generation and initial analysis of more than 15,000 full-length human					
RL	and mouse cDNA sequences."					
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Spleen;					
RA	Straubeberg R.;					
RL	Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.					
DR	EMBL; BC073775; AAAH73775.1; -					
DR	InterPro; IPR003599; Ig.					
DR	InterPro; IPR007110; Ig-like.					
DR	InterPro; IPR003597; Ig cl.					
DR	InterPro; IPR003006; Ig_MHC.					
DR	InterPro; IPR003596; Ig_V.					
DR	Pfam; PF07654; CL-Bet; 1.					
DR	Pfam; PF00047; Ig; 2.					
DR	SMART; SM00409; IG; 2.					
DR	SMART; SM00407; IGC1; 1.					
DR	SMART; SM00406; IGV; 1.					
DR	PROSITE; PSS0835; IG LIKE; 2.					
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.					
KW	Hypothetical protein.					
SQ	SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;					
Query Match	80.8%; Score 439;	DB 2;	Length 236;			
Best Local Similarity	81.1%;	Pred. No. 2.7e-36;				
Matches 86;	Conservative	8;	Mismatches 12;	Indels 0;	Gaps 0;	

QY 1 ELTOSPSLSASVGRVITISCRASORINTYLMWYOHKPKAKLLIYAASSLSQGVPSRF 60  
 DB 25 QMTOSPSLSASVGRVITISCRASORINTYLMWYOHKPKAKLLIYAASSLSQGVPSRF 84  
 QY 61 SSGSGGTDFLTITISLQPEDFASYYCOESLSASTYFGGCTVETIKR 106  
 DB 85 SSGSGGTDFLTITISLQPEDFATYYCOOSYINPLTFGGGTINVEIKR 130

## RESULT 5

KY1W HUMAN STANDARD; PRT; 129 AA.  
 ID KVAL HUMAN

AC P04431.13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Walker precursor.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 CC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85014148; PubMed=6091049;  
 RA Klobbeck H.G., Combricato G., Zachau H.G.;  
 RT "Immunoglobulin genes of the kappa light chain type from two human  
 RL Nucleic Acids Res. 12:6995-7006 (1984).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC DR EMBL; X00965; CAA25477.1; ALT\_TERM.  
 DR PIR; A01883; KIHUMK.  
 DR HSRP; P01607; IBMW.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; P:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 1 129  
 FT DOMAIN 23 45 Ig kappa chain V-I region Walker.  
 FT DOMAIN 46 56 Framework-1.  
 FT DOMAIN 57 71 Complementarity-determining-1.  
 FT DOMAIN 72 78 Framework-2.  
 FT DOMAIN 79 110 Complementarity-determining-2.  
 FT DOMAIN 111 129 Framework-3.  
 FT DOMAIN 120 129 Complementarity-determining-3.  
 FT DISULFID 45 110 Framework-4.  
 FT NON TER 129 129 By similarity.  
 SQ SEQUENCE 129 AA; 14069 MW; F941FA07DAFC2F9 CRC64;

Query Match 80.3%; Score 436; DB 1; Length 129;  
 Best Local Similarity 81.9%; Pred. No. 2.9e-38;  
 Matches 86; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITISCRASORINTYLMWYOHKPKAKLLIYAASSLSQGVPSRF 60  
 DB 25 QMTOSPSLSASVGRVITISCRASORINTYLMWYOHKPKAKLLIYAASSLSQGVPSRF 84  
 QY 61 SSGSGGTDFLTITISLQPEDFASYYCOESLSASTYFGGCTVETIKR 106  
 DB 85 SSGSGGTDFLTITISLQPEDFATYYCOOSYINPLTFGGGTINVEIKR 130

DB 85 SSGSGGTDFLTITISLQPEDSATYYCOOSYSTLTITFGGCTRLTIRK 129

## RESULT 6

OG6MX8 PRELIMINARY; PRT; 236 AA.  
 ID OG6MX8

AC OG6MX8  
 DT 05-JUN-2004 (TREMBLrel. 27, Created)  
 DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 CC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pailey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko J., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RL [2]  
 RN RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RL Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073764; AAH73764.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; Cl-sec; 1.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25707 MW; 4FC8B14B659EFC9 CRC64;

Query Match 80.3%; Score 436; DB 2; Length 236;  
 Best Local Similarity 80.2%; Pred. No. 5.7e-38;  
 Matches 85; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITISCRASORINTYLMWYOHKPKAKLLIYAASSLSQGVPSRF 60  
 DB 25 QMTOSPSLSASVGRVITISCRASORINTYLMWYOHKPKAKLLIYAASSLSQGVPSRF 84  
 QY 61 SSGSGGTDFLTITISLQPEDFASYYCOESLSASTYFGGCTVETIKR 106  
 DB 85 SSGSGGTDFLTITISLQPEDFATYYCOOSYINPLTFGGGTINVEIKR 130

```

RESULT 7
Q6GMW1 PRELIMINARY; PRT; 236 AA.
ID Q6GMW1
AC Q6GMW1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tashyuki S., Carinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL, BC073791, AAH73791.1; -.
DR InterPro; IPR003597; IG_1.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003597; IG_1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match 79.9%; Score 434; DB 2; Length 236;
Best Local Similarity 81.1%; Pred. No. 9.2e-38;
Matches 86; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSISASVGDRTVITSCRASQRIINTYINWYQHKGKAPKLLIYAASSLQGVPSRF 60
DB 25 QMTQSPSSISASVGDRTVITSCRASQRIINTYINWYQHKGKAPKLLIYAASSLQGVPSRF 84
QY 61 SGSGGTDFTLTISLSLOPEDFASYYCOESLSASTPFGGTVEIKR 106
DB 85 SGSGGTDFTLTISLSLOPEDFATYTCLODYNPMTFGGTVEIKR 130

RESULT 8
KYLE_HUMAN
ID KYLE_HUMAN STANDARD; PRT; 108 AA.

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AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P., Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain.";
RL Biochem. J. 123:945-958(1971).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
DR HSSP; P01607; 1BWV.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Complementarity-determining-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Framework-3.
FT DOMAIN 98 107 Complementarity-determining-3.
FT DISULFID 23 88 Framework-4.
FT NON TER 108 108 By similarity.
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 79.7%; Score 433; DB 1; Length 108;
Best Local Similarity 77.4%; Pred. No. 4.9e-38;
Matches 82; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTQSPSSISASVGDRTVITSCRASQRIINTYINWYQHKGKAPKLLIYAASSLQGVPSRF 60
DB 3 ZMTQSPSSISASVGDRTVITSCRASQRIINTYINWYQHKGKAPKLLIYAASSLQGVPSRF 62
QY 61 SGSGGTDFTLTISLSLOPEDFASYYCOESLSASTPFGGTVEIKR 106
DB 63 SGSGGTDFTLTISLSLOPEDFATYTCLODYNPMTFGGTVEIKR 108

RESULT 9
KYLE_HUMAN
ID KYLE_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-1- MISCELLANEOUS: This is a Bence-Jones protein.

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PIR; A01868; K1HUUH.  
DR PDB; 1F6L; X-ray; L=1-108.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR 3D-structure; Bence-Jones protein; direct protein sequencing;  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 34 Complementarity-determining-1.  
FT DOMAIN 35 49 Framework-2.  
FT DOMAIN 50 56 Complementarity-determining-2.  
FT DOMAIN 57 88 Framework-3.  
FT DOMAIN 89 97 Complementarity-determining-3.  
FT DOMAIN 98 107 Framework-4.  
FT DISULFID 23 88 By similarity.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;  
Query Match 79.2%; Score 430; DB 1; Length 108;  
Best Local Similarity 78.3%; Pred. No. 1e-37; Mismatches 10; Indels 0; Gaps 0;  
Matches 83; Conservative 13; Mismatches 10; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLSQGVPSRF 60  
DB 3 QLTQSPSSLSASVGDRTVITTCRASQGISISYLMWYQKRGKAPQVLIYAASSLSQGVPSRF 62  
QY 61 SGSGVGTDFLTLLISLQFEDFASYYCOESLSASYTFGGGTVEIKR 106  
DB 63 SGSGSGTDFLTLLISLQFEDFATYYCCQNYITPTSGGTVEIKR 108  
RESULT 10  
Q6PIH7 PRELIMINARY; PRT; 236 AA.  
ID Q6PIH7  
AC Q6PIH7  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Sculter G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
RA Datsenko L., Martushina K., Farmer A.A., Rubin G.W., Hong L.,  
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Sanchez A.,  
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimshaw J., Schmutz J., Myers R.M., Buterfield Y.S.,  
RA Krzywicki M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Maita M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]

RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC034141; AAH34141.1; -.  
DR HSSP; P01607; IAR2.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;  
Query Match 78.1%; Score 424; DB 2; Length 236;  
Best Local Similarity 80.2%; Pred. No. 1.1e-36; Mismatches 12; Indels 0; Gaps 0;  
Matches 85; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLSQGVPSRF 60  
DB 25 QLTQSPSSLSASVGDRTVITTCRASQGISISYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 84  
QY 61 SGSGVGTDFLTLLISLQFEDFASYYCOESLSASYTFGGGTVEIKR 106  
DB 65 SGSGSGTDFLTLLISLQFEDFATYYCCQNSPPTFGGTVEIKR 130  
RESULT 11  
Q9UL79 PRELIMINARY; PRT; 108 AA.  
ID Q9UL79  
AC Q9UL79  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE "Myosin-reactive immunoglobulin light chain variable region (Fragment)."  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;  
RA Wu X., Liu B., Van der Werf P.L., Kalls N.N., Berny S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
DR EMBL; AF035035; AAD56271.1; -.  
DR PIR; S23638; S23638.  
DR PIR; S30521; S30521.  
DR PIR; S34090; S34090.  
DR HSSP; P01607; IBMW.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON TER 1 1  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FBA8 CRC64;  
Query Match 77.7%; Score 422; DB 2; Length 108;  
Best Local Similarity 80.0%; Pred. No. 7.2e-37; Mismatches 14; Indels 0; Gaps 0;  
Matches 84; Conservative 7; Mismatches 14; Indels 0; Gaps 0;  
QY 2 LTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLSQGVPSRF 61  
DB 1 LTQSPSSLSASVGDRTVITTCRASQGISISYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 84

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Db 4 MTQSPSLISASTGDRVTISCRMSQGISSTYLAWYQKPGKAPBLLIYAASLQSGVPSRFS 63
Qy 62 GSGGYDTFTLTISLQFEDFASVYCOESLSASVYTFGCGTKVEIKR 106
Db 64 GSGSGTDTFTLTISLQSGSEDFATVYCOQYVSPPFTFGGCTKVEIKR 108

RESULT 12
ID KVIN HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenström's
CC macroglobulin.
CC PIR: A01872; K1H10U.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KV Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283DA4A24105827E CRC64;

Query Match 77.3%; Score 420; DB 1; Length 108;
Best Local Similarity 68.9%; Pred. No. 1.2e-36;
Matches 73; Conservative 22; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ELTQSPSLASVGDRTVISCRAQRINTYLNWYQHKPGKAPKLLIYAASLQSGVPSRF 60
Db 3 QMTQSPSLASVGDRTVISCRAQRINTYLNWYQHKPGKAPKLLIYAASLQSGVPSRF 62

Qy 61 GSGGYDTFTLTISLQFEDFASVYCOESLSASVYTFGCGTKVEIKR 106
Db 63 GSGSGTDTFTLTISLQSGSEDFATVYCOQYVSPPFTFGGCTKVEIKR 108

RESULT 13
ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kall N.N., Berney S.M.;
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; P08633; P0863.
DR HSSP; P01607; 1BMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 77.3%; Score 420; DB 2; Length 108;
Best Local Similarity 79.2%; Pred. No. 1.2e-36;
Matches 84; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ELTQSPSLASVGDRTVISCRAQRINTYLNWYQHKPGKAPKLLIYAASLQSGVPSRF 60
Db 3 QMTQSPSLASVGDRTVISCRAQRINTYLNWYQHKPGKAPKLLIYAASLQSGVPSRF 62

Qy 61 GSGGYDTFTLTISLQFEDFASVYCOESLSASVYTFGCGTKVEIKR 106
Db 63 GSGSGTDTFTLTISLQSGSEDFATVYCOQYVSPPFTFGGCTKVEIKR 108

RESULT 14
ID Q72473 PRELIMINARY; PRT; 234 AA.
AC Q72473;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditschenko L., Marutina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
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RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC056256; AAH56256.1; -.  
DR HSSP; P01834; 1HEZ.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003597; IG\_C1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-seel; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;  
  
Query Match 77.0%; Score 418; DB 2; Length 234;  
Best Local Similarity 77.1%; Pred. No. 4,5e-36;  
Matches 81; Conservative 10; Mismatches 14; Indels 0; Gaps 0;  
  
QY 2 LTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPKAPKLIYAASSLSQGVPSRFS 61  
DB 24 MTQSPSSFSASTGDRVITTCRASQSIGSLAWYQOKPKAPOLLIIYAASLTLSQGVPSRFS 83  
  
QY 62 GSGGYGDTFTLTITSSLSQFEDFASVYCOESLSASTFGQGTVEIKR 106  
DB 84 GSGGYGDTFTLTITSSLSQFEDFASVYCOQYTYPTFGQGTVEIKR 128  
  
RESULT 15  
KVIF HUMAN  
ID \_KVIF\_HUMAN STANDARD; PRT; 108 AA.  
AC P01598;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-1 region EU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71064023; PubMed=5489770;  
RA Gall W.E.; Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
RT acid sequence of the light chain.";  
RL Biochemistry 9:3188-3196(1970).  
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein.  
DR HSSP; P01607; 1BWM.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region.  
FT DOMAIN 1 23 Framework-1;  
FT DOMAIN 24 34 Complementarity-determining-1.  
FT DOMAIN 35 49 Framework-2.  
FT DOMAIN 50 56 Complementarity-determining-2.

FT DOMAIN 57 88 Framework-3.  
FT DOMAIN 89 97 Complementarity-determining-3.  
FT DOMAIN 98 107 Framework-4.  
FT DISULFID 23 88  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2P4D88823 CRC64;  
  
Query Match 76.6%; Score 416; DB 1; Length 108;  
Best Local Similarity 77.1%; Pred. No. 3.1e-36;  
Matches 81; Conservative 12; Mismatches 12; Indels 0; Gaps 0;  
  
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPKAPKLIYAASSLSQGVPSRFS 60  
DB 3 QMTQSPSTLSASVGDRTVITTCRASQINTYLMWYQOKPKAPKLIYAASSLSQGVPSRFS 62  
  
QY 61 GSGGYGDTFTLTITSSLSQFEDFASVYCOESLSASTFGQGTVEIKR 105  
DB 63 GSGGYGDTFTLTITSSLSQFEDFASVYCOQYNSDKMFGQGTVEIKR 107  
  
Search completed: July 26, 2005, 09:26:19  
Job time : 66.6515 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 08:50:20 ; Search time 79.3394 Seconds  
(without alignments)  
516.724 Million cell updates/sec

Title: US-10-027-725A-10

Sequence: 1 ELTQSPSSLSASVGDRTVTS.....QESLSASTYFGGTRKVEIKR 106

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	98.2	106	5	ABG30448 Human IGE
2	475	87.5	107	2	AAR54260 Anti-HIV
3	475	87.5	107	2	AAW01283 VL region
4	475	87.5	107	3	AAW98244 Anti-gp12
5	475	87.5	107	3	AAV95135 Anti-gp12
6	474	87.3	107	3	AAV93667 Human ant
7	474	87.3	107	6	ABO27474 Anti-Rh(D
8	472	86.9	107	4	AAV93663 Human ant
9	472	86.9	107	4	AAV93664 Human ant
10	472	86.9	107	4	AAV93590 Human ant
11	472	86.9	107	6	ABO27471 Anti-Rh(D
12	472	86.9	107	6	ABO27397 Anti-Rh(D
13	472	86.9	107	6	ABO27470 Anti-Rh(D
14	471	86.7	107	4	AAV93644 Human ant
15	471	86.7	107	6	ABO27451 Anti-Rh(D
16	468	86.2	107	4	AAV93593 Human ant
17	468	86.2	107	6	ABO27400 Anti-Rh(D
18	468	86.2	244	8	ADH34565 scFv SC02
19	468	86.2	244	8	ADR23318 Human CD7
20	468	86.2	244	8	ADR23330 Human CD7
21	468	86.2	244	8	ADR23332 Human CD7
22	468	86.2	245	8	ADR23320 Human CD7
23	468	86.2	249	8	ADR23322 Human CD7
24	468	86.2	249	8	ADR23326 Human CD7
25	467	86.0	107	2	AAR54261 Anti-HIV

26	467	86.0	107	2	AAW01284 VL region
27	467	86.0	107	3	AAV98245 Anti-gp12
28	467	86.0	107	3	AAV95136 Anti-gp12
29	467	86.0	114	2	AAW13922 Light cha
30	465	85.6	111	4	AAV63656 Amino aci
31	465	85.6	111	6	ABJ38615 Hepatitis
32	465	85.6	132	2	AAW22842 Human ant
33	465	85.6	240	6	ABJ38595 Hepatitis
34	465	85.6	299	4	AAV63660 Amino aci
35	464.5	85.5	108	4	AAV93589 Human ant
36	464.5	85.5	108	4	AAV93600 Human ant
37	464.5	85.5	108	6	ABO27407 Anti-Rh(D
38	464.5	85.5	108	6	ABO27396 Anti-Rh(D
39	464	85.5	107	4	AAV93594 Human ant
40	464	85.5	107	6	ABO27401 Anti-Rh(D
41	464	85.5	108	6	ABP96009 HSA antib
42	464	85.5	108	8	ADL92386 Anti-HSA
43	464	85.5	108	8	ADQ14601 Single-do
44	464	85.5	108	8	ADQ77191 Dummy VK
45	464	85.5	108	8	ADQ77181 VK dummy

## ALIGNMENTS

RESULT 1	
ABG30448	ABG30448 standard; protein; 106 AA.
XX	
AC	ABG30448;
XX	
DT	21-OCT-2002 (first entry)
XX	
DE	Human IGE Fab clone 94 light chain protein.
KW	Human; fab; anti-allergic; vaccine; grass pollen; phi p 2;
KM	liniothy grass pollen allergen; passive immunotherapy.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	/note= "FRI region"
FT	Region
FT	/note= "CDR1 region"
FT	Region
FT	/note= "FR2 region"
FT	Region
FT	/note= "CDR2 protein"
FT	Region
FT	/note= "FR3 region"
FT	Region
FT	/note= "CDR2 region"
FT	Region
FT	/note= "FR4 region"
XX	
FN	WO200253595-A1.
XX	
PD	11-JUL-2002.
XX	
PF	27-DEC-2001; 2001WO-SE002908.
XX	
FR	29-DEC-2000; 2000SE-00004892.
XX	
PA	(PHNA) PHARMACIA DIAGNOSTICS AB.
XX	
PI	Flicker S, Steinberger P, Kraft D, Valenta R;
XX	
DR	WPI: 2002-583604/62.
DR	N-P8DB; ABK89640.
PT	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT	variable region of group 2 allergen specific-human IGE Fabs, useful for

PT diagnosing or passive immunotherapy of type I allergy, for environmental  
PT allergen detection.  
XX  
PS Disclosure; Page 39; 45pp; English.  
XX  
CC This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE fabs and methods for their use. The proteins  
CC of the invention may have anti-allergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE  
CC antibodies to Pnt p 2 (a major Timothy grass pollen allergen). The group  
CC 2 allergen-specific fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergic patients  
CC IgE antibodies to Pnt p 2. The present sequence represents the human IgG  
CC fab, clone 94 light chain protein of the invention  
XX  
SQ Sequence 106 AA;  
XX  
Query Match 98.2%; Score 533; DB 5; Length 106;  
Best Local Similarity 99.1%; Pred. No. 4.6e-33;  
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 1 ELTQSPSLASVQDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASLSQGVPSRF 60  
Db 1 ELTQSPSLASVQDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASLSQGVPSRF 60  
XX  
QY 61 SGSGYGTDFLTITSSLOPEDFASYYCOESLSASTYFGCGTKVEIKR 106  
Db 61 SGSGYGTDFLTITSSLOPEDFASYYCOESLSASTYFGCGTKVEIKR 106  
XX  
RESULT 2  
AAR54260  
ID AAR54260 standard; protein; 107 AA.  
XX  
AC AAR54260;  
XX  
DT 25-MAR-2003 (revised)  
DT 10-NOV-1994 (first entry)  
XX  
DE Anti-HIV gp120 immunoglobulin light chain variable region b22.  
XX  
KW Human immunodeficiency virus; HIV; glycoprotein gp120; epitope;  
KW neutralisation; monoclonal antibody; kappa light chain; variable region;  
KW framework; complementarity determining region.  
XX  
OS Homo sapiens.  
XX  
FH Key location/Qualifiers  
FT 1..21  
FT /label= FR1  
FT 22..33  
FT /label= CDR1  
FT 34..48  
FT /label= FR2  
FT 49..55  
FT /label= CDR2  
FT 56..87  
FT /label= FR3  
FT 88..95  
FT /label= CDR3  
FT 96..107  
FT /label= FR4  
XX  
MO9407922-A1.  
XX  
PD 14-APR-1994.  
XX

PF 30-SEP-1993; 93WO-US009328.  
XX  
PR 30-SEP-1992; 92US-00954148.  
XX  
PA (SCRI) SCRIPPS RES INST.  
XX  
PI Burton DR, Barbas CF, Lerner RA;  
XX  
DR WPI; 1994-135516/16.  
XX  
PT New human monoclonal antibodies neutralising HIV - react with gp120 or  
PT gp1 and nucleic acid encoding them, useful for in vivo or in vitro  
PT diagnosis and for passive immuno-therapy.  
XX  
XX Claim 5; Page 189; 248pp; English.  
XX  
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification  
CC using primers specific for heavy and light chain variable regions. The  
CC amplification products were inserted into a dicistronic vector to produce  
CC a library of fragments. E.coli XL1 Blue cells were transformed with the  
CC library. Filamentous phage were produced which expressed the MAb regions  
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of  
CC immunoreactive clones. The light chain VK region sequence AAR54260  
XX neutralises HIV gp120. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 107 AA;  
XX  
Query Match 87.5%; Score 475; DB 2; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.1e-28;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
XX  
QY 1 ELTQSPSLASVQDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASLSQGVPSRF 60  
Db 1 ELTQSPSLASVQDRTVITSCRASQSISSYLMWYQKRGKAPKLLIYAASLSQGVPSRF 60  
XX  
QY 61 SGSGYGTDFLTITSSLOPEDFASYYCOESLSASTYFGCGTKVEIKR 106  
Db 61 SGSGYGTDFLTITSSLOPEDFATYYCOOSYSTPTTFQGTKEIKR 106  
XX  
RESULT 3  
AAW01283  
ID AAW01283 standard; protein; 107 AA.  
XX  
AC AAW01283;  
XX  
DT 29-JAN-1997 (first entry)  
XX  
DE VL region of HIV neutralising MAb, clone b22 and B35.  
XX  
KW Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;  
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;  
KW virus infectivity assay; precursor gp160; immunocompetence; human;  
KW anti-HIV antibody; detection; HIV infection.  
XX  
OS Homo sapiens.  
XX  
FH Key location/Qualifiers  
FT 1..21  
FT /label= FR1  
FT 22..32  
FT /label= CDR1  
FT 33..47  
FT /label= FR2  
FT 48..54  
FT /label= CDR2  
FT 55..86  
FT /label= FR3  
FT 87..95  
FT /label= CDR3  
FT 96..107  
FT /label= FR4  
XX  
Region  
XX

PN MO9602273-A1.  
 XX 01-FEB-1996.  
 PD 11-JUL-1995; 95WO-US008743.  
 XX 18-JUL-1994; 94US-00276852.  
 PR (SCRI ) SCRIPPS RES INST.  
 XX Burton DR, Barbas CF, Lerner RA;  
 DR WPI, 1996-179601/18.  
 XX Monoclonal antibody binding to VI/V2 loop of HIV gp120 - used in passive  
 PT immuno-therapy and detection of HIV infection.  
 PS Example; Fig 11; 366pp; English.  
 XX The sequences given in AAM01261-92 represent the light chain variable  
 CC regions (VL) of a series of monoclonal antibodies (MAb's) which are  
 CC immunoreactive with HIV glycoprotein gp120 and are capable of  
 CC neutralising HIV. This sequence represents the sequence of the JK2 gene  
 CC clones, b22 and B35. A MAb containing this VL sequence has the capacity  
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay by  
 CC 50 % at a concentration of less than 700 ng of antibody/ml, and binds  
 CC mature gp120 preferentially over the precursor gp160. The MAb may be used  
 CC for determining immunocompetence of a human anti-HIV antibody and in the  
 CC detection of HIV infection  
 CC  
 SQ Sequence 107 AA;  
 QY Query Match 87.5%; Score 475; DB 2; Length 107;  
 Best Local Similarity 87.7%; Pred. No. 1.1e-28;  
 Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 Db 1 ELTOSPSLSASVGRVTITSCRASORINTYLMWYQHKRKPRLIYAASSLSQGVPSRF 60  
 1 ELTOSPSLSASVGRVTITSCRASOSISSYLMWYQHKRKPRLIYAASSLSQGVPSRF 60  
 QY 61 SSGSGVTDFTLTISLQPEDFASYYCOESLSASYTFGGGTVEIKR 106  
 61 SSGSGVTDFTLTISLQPEDFATYCCQOSYTPYTFGGGTVEIKR 106  
 Db  
 RESULT 4  
 ID AAY98244 standard; protein; 107 AA.  
 XX AAY98244;  
 AC AAY98244;  
 DT 04-JUL-2000 (first entry)  
 DE Anti-gp120 antibody light chain variable region from clone b22.  
 XX  
 KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;  
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;  
 KW passive immunotherapy; reduce severity; HIV-induced disease;  
 KW immunocompetence; active immunisation.  
 XX  
 OS Homo sapiens.  
 XX AU9948754-A.  
 PN 17-FEB-2000.  
 PD 16-SEP-1999; 99AU-00048754.  
 XX 16-SEP-1999; 99AU-00048754.  
 PR (SCRI ) SCRIPPS RES INST.  
 XX Burton DR, Barbas CF, Lerner RA;  
 XX PI

XX WPI, 2000-246867/22.  
 DR Human neutralizing monoclonal antibodies to human immunodeficiency virus  
 PT (HIV) used for providing passive immunotherapy to HIV are specific for  
 PT glycoprotein-120.  
 XX Example 9; Fig 11; 374pp; English.  
 XX This sequence represents a fragment of the antibodies of the invention.  
 CC The invention relates to the production of an anti-HIV (human  
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable  
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity  
 CC assay by 50% at a concentration of less than 70 ng/ml. The method for the  
 CC production of the antibody comprises: (a) providing a first  
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence  
 CC (which does not comprise the sequence represented by AAY98206) and a  
 CC second polynucleotide encoding a light chain immunoglobulin amino acid  
 CC sequence; (b) inserting the first and second polynucleotide sequences  
 CC into a host cell; (c) maintaining the host cell in conditions which allow  
 CC the amino acid sequences encoded by the polynucleotides to be expressed  
 CC in the host cell; and (d) isolating the antibody comprising the heavy and  
 CC light chain immunoglobulin amino acid sequences from the host cell. The  
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive  
 CC immunotherapy to HIV in a human. They can be administered to high-risk  
 CC patients to reduce the likelihood and/or severity of HIV-induced disease  
 CC and to patients who are already HIV-infected. The antibodies are used for  
 CC neutralising field isolates which provides information about the  
 CC immunocompetence of an immune response in HIV patients, for detecting HIV  
 CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for  
 CC producing anti-idiotypic antibodies which can be used for active  
 CC immunisation and to screen human monoclonal antibodies to identify those  
 CC with the same binding specificity and to monitor the course of HIV  
 CC disease therapy by measuring the changes in concentration of HIV present  
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120  
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and  
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease  
 CC reduce the problems of significant host immune response to the antibodies  
 CC associated with monoclonal antibodies of xenogeneic or chimeric  
 CC derivation  
 CC  
 SQ Sequence 107 AA;  
 QY Query Match 87.5%; Score 475; DB 3; Length 107;  
 Best Local Similarity 87.7%; Pred. No. 1.1e-28;  
 Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 Db 1 ELTOSPSLSASVGRVTITSCRASORINTYLMWYQHKRKPRLIYAASSLSQGVPSRF 60  
 1 ELTOSPSLSASVGRVTITSCRASOSISSYLMWYQHKRKPRLIYAASSLSQGVPSRF 60  
 QY 61 SSGSGVTDFTLTISLQPEDFASYYCOESLSASYTFGGGTVEIKR 106  
 61 SSGSGVTDFTLTISLQPEDFATYCCQOSYTPYTFGGGTVEIKR 106  
 Db  
 RESULT 5  
 ID AAY95135 standard; protein; 107 AA.  
 XX AAY95135;  
 AC AAY95135;  
 DT 30-JUN-2000 (first entry)  
 DE Anti-gp120 antibody light chain variable region from clone b22.  
 XX  
 KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;  
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;  
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.  
 XX  
 OS Homo sapiens.  
 XX AU9948756-A.  
 PN

```
XX 17-FEB-2000.
PD
XX
XX 16-SEP-1999; 99AU-00048756.
PE
XX 16-SEP-1999; 99AU-00048756.
PR
XX (SCRI ) SCRIPPS RES INST.
PA
XX Burton DR, Barbac CF, Lerner RA;
PI
XX WPI; 2000-293393/26.
PT
XX Novel human monoclonal antibodies which immunoreact with and neutralize
PT human immunodeficiency virus useful for treating HIV infections.
PS
XX Example 9; Fig 11; 366pp; English.
XX
XX The present sequence represents a fragment of an anti-human
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
CC in vitro virus infectivity assay by 50%, at a concentration of less than
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
CC immunotherapy of HIV induced disease. They are useful as neutralising
CC field isolates and provide useful information regarding the
CC immunocompetence of an immune response in HIV infected patients. The
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
CC which can be used to screen human monoclonal antibodies to identify
CC whether the antibody has the same binding specificity as the antibodies
CC of the invention. The neutralising antibodies define new epitopes on the
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
CC immunotherapeutic human monoclonal antibodies. A major advantages of the
CC monoclonal antibodies derives from the fact that they are encoded by a
CC human polynucleotide sequence. Thus in vivo use of the monoclonal
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
CC reduces the problems of significant host immune response to the passively
CC administered antibodies which is a problem commonly encountered when
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
CC An additional major advantage of the monoclonal antibodies described
CC derives from the fact that they immunoreact with a unique determinant
CC present on mature HIV glycoprotein gp120. This class of antibodies is
CC particularly effective at neutralising field isolates of HIV
CC
XX
SQ Sequence 107 AA;
Query March 87.5%; Score 475; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.1e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAKPKLLIYAASSLSQGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITTCRASQISISYLNWYQKRGKAPKLLIYAASSLSQGVPSRF 60
QY 61 SSGSGYGTDFLTITISLQFEDFASYYCOESLSASTTFGCGTKVEIKR 106
DB 61 SSGSGGTDFLTITISLQPEDFATYYCOOSYSTPTFFCGTKLEIKR 106
RESULT 6
AAG93667
ID AAG93667 standard; protein; 107 AA.
XX
XX AAG93667;
XX
XX 14-SEP-2001 (first entry)
XX
XX Human anti-Rh(D) antibody clone SH54 protein sequence.
DE
XX Human anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
```

```
OS Homo sapiens.
XX
XX US6255455-B1.
PN
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 99US-00240274.
PF
XX 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
XX
XX (VPE-) UNIV PENNSYLVANIA.
PA
XX Siegel DL;
PI
XX WPI; 2001-388931/41.
DR
XX N-PSDB; AAH68724.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Claim 1; Col 70; 162pp; English.
PS
XX
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68815 to AAH68726 represent the Rh phenotype sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
XX
SQ Sequence 107 AA;
Query March 87.3%; Score 474; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-28;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAKPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSMSASVGDRTVITTCRASQSIGTYLNWYQKRGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGYGTDFLTITISLQFEDFASYYCOESLSASTTFGCGTKVEIKR 106
DB 62 SSGSGGTDFLTITISLQPEDFATYYCOOSYSTPTFFCGTKVEIKR 107
RESULT 7
ABO27474
ID ABO27474 standard; protein; 107 AA.
XX
XX ABO27474;
XX
XX 12-SEP-2003 (first entry)
XX
XX Anti-Rh(D) light chain SH54.
DE
XX Human; RH(D) binding protein; blood typing; blood product; antibody;
KW magnetically activated cell sorting.
XX
XX Homo sapiens.
OS
XX US2003040605-A1.
PN
XX 27-FEB-2003.
XX
XX 04-MAY-2001; 2001US-00848798.
XX
```

PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-0088404S.  
 PR 10-APR-1998; 98US-0081380P.  
 PR 29-JAN-1999; 99US-00240274.  
 XX (TYPE-) UNIV PENNSYLVANIA.  
 PI Siegel DL;  
 XX WPI; 2003-512273/48.  
 DR N-PSDB; ACD45388.  
 XX New human Rh(D) -binding protein useful for various diagnostic and  
 PT therapeutic applications, including typing of blood or blood products.  
 XX Claim 4; Page 53; 187pp; English.  
 CC The invention relates to an isolated Rh(D) binding protein. The protein  
 CC can be used for magnetically activated cell sorting. The protein is  
 CC useful in various diagnostic and therapeutic applications in humans,  
 CC including typing of blood or blood products. The present sequence  
 CC represents the amino acid sequence of a human anti-Rh(D) chain  
 XX  
 SQ Sequence 107 AA;  
 Query Match 87.3%; Score 474; DB 6; Length 107;  
 Best Local Similarity 87.7%; Pred. No. 1.3e-28;  
 Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLASVGDRTVTCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLQSGVPSRF 60  
 DB 2 ELTQSPSSMSASVGDRTVTCRASQSIGTYLMWYQHKRGKAPKLLIYAASSLQSGVPSRF 61  
 QY 61 SSGSGYGTDFLTITISLQPEDFASYYCOESLSASYTFGQGTVEIKR 106  
 DB 62 SSGSGGTDFLTITISLQPEDFATYTCQOSYSTPMTFGQGTVEIKR 107  
 RESULT 8  
 AAG93663  
 ID AAG93663 standard; protein; 107 AA.  
 XX  
 AC AAG93663;  
 XX 14-SEP-2001 (first entry)  
 DT  
 XX Human anti-Rh(D) antibody clone SH49 protein sequence.  
 DE  
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.  
 XX  
 OS Homo sapiens.  
 OS  
 PN US6255455-B1.  
 XX  
 PD 03-JUL-2001.  
 XX  
 PE 29-JAN-1999; 99US-00240274.  
 XX  
 PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-0088404S.  
 PR 10-APR-1998; 98US-0081380P.  
 XX (TYPE-) UNIV PENNSYLVANIA.  
 PA  
 PI Siegel DL;  
 XX WPI; 2001-388931/41.  
 DR N-PSDB; AAH68720.  
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine.

XX  
 PS Claim 1; Col 69; 162pp; English.  
 CC The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 107 AA;  
 Query Match 86.9%; Score 472; DB 4; Length 107;  
 Best Local Similarity 86.8%; Pred. No. 1.9e-28;  
 Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLASVGDRTVTCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLQSGVPSRF 60  
 DB 2 ELTQSPSSLSASVGDRTVTCRASQSISSYLMWYQHKRGKAPKLLIYAASSLQSGVPSRF 61  
 QY 61 SSGSGYGTDFLTITISLQPEDFASYYCOESLSASYTFGQGTVEIKR 106  
 DB 62 SSGSGGTDFLTITISLQPEDFATYTCQOSYSTPMTFGQGTVEIKR 107  
 RESULT 9  
 AAG93664  
 ID AAG93664 standard; protein; 107 AA.  
 XX  
 AC AAG93664;  
 XX 14-SEP-2001 (first entry)  
 DT  
 XX Human anti-Rh(D) antibody clone SH50 protein sequence.  
 DE  
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.  
 XX  
 OS Homo sapiens.  
 OS  
 PN US6255455-B1.  
 XX  
 PD 03-JUL-2001.  
 XX  
 PE 29-JAN-1999; 99US-00240274.  
 XX  
 PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-0088404S.  
 PR 10-APR-1998; 98US-0081380P.  
 XX (TYPE-) UNIV PENNSYLVANIA.  
 PA  
 PI Siegel DL;  
 XX WPI; 2001-388931/41.  
 DR N-PSDB; AAH68721.  
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine.  
 XX  
 PS Claim 1; Col 69; 162pp; English.  
 CC The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies

CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAH6815 to AAH68726 represent the nucleotide sequence which encode  
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
CC chain CDR3 amino acid sequences which are given in the exemplification of  
CC the present invention  
XX  
SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;  
Best Local Similarity 86.8%; Pred. No. 1.9e-28;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKPKAKPKLLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYINWYQKPKAKPKLLIYAASSLSQGVPSRF 61  
QY 61 SGGSGYGFDTLTITSSLOFEDFASYYCOESLSASTYFGGKTVEIKR 106  
DB 62 SGGSGYGFDTLTITSSLOFEDFATYYCOQSYSTPMTFGGKTVEIKR 107

RESULT 10  
AAG93590  
ID AAG93590 standard; protein; 107 AA.  
XX  
AC AAG93590;  
XX  
DT 14-SEP-2001 (first entry)  
XX  
DE Human anti-Rh(D) chain 102 protein sequence.  
XX  
KW Human, anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
KM red blood cell; Rh phenotype; diagnosis; therapeutic.  
XX  
OS Homo sapiens.  
XX  
PN US6255455-B1.  
XX  
PD 03-JUL-2001.  
XX  
PF 29-JAN-1999; 99US-00240274.  
XX  
PR 11-OCT-1996; 96US-0028550P.  
PR 27-JUN-1997; 97US-00884045.  
PR 10-APR-1998; 98US-0081380P.  
PR 10-APR-1998; 98US-0081380P.  
XX  
PA (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Siegel DL;  
XX  
DR WPI; 2001-388931/41.  
DR N-PSDB; AAH68647.  
XX  
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine.  
PS  
SQ Claim 1; Col 43; 162pp; English.

CC The present invention describes an isolated Rh(D) binding protein,  
CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
CC immunostimulant activity, and can be used as an immune system stimulant.  
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAH6815 to AAH68726 represent the nucleotide sequence which encode  
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
CC chain CDR3 amino acid sequences which are given in the exemplification of  
CC the present invention  
XX  
SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.9e-28;  
Matches 92; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKPKAKPKLLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYINWYQKPKAKPKLLIYAASSLSQGVPSRF 61  
QY 61 SGGSGYGFDTLTITSSLOFEDFASYYCOESLSASTYFGGKTVEIKR 106  
DB 62 SGGSGYGFDTLTITSSLOFEDFATYYCOQSYSTPMTFGGKTVEIKR 107

RESULT 11  
ABO27471  
ID ABO27471 standard; protein; 107 AA.  
XX  
AC ABO27471;  
XX  
DT 12-SEP-2003 (first entry)  
XX  
DE Anti-Rh(D) light chain SH50.  
XX  
KW Human, RH(D) binding protein; blood typing; blood product; antibody;  
KM magnetically activated cell sorting.  
XX  
OS Homo sapiens.  
XX  
PN US2003040605-A1.  
XX  
PD 27-FEB-2003.  
XX  
PF 04-MAY-2001; 2001US-00848798.  
XX  
PR 11-OCT-1996; 96US-0028550P.  
PR 27-JUN-1997; 97US-00884045.  
PR 10-APR-1998; 98US-0081380P.  
PR 29-JAN-1999; 99US-00240274.  
XX  
PA (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Siegel DL;  
XX  
DR WPI; 2003-512273/48.  
DR N-PSDB; ACD45385.  
XX  
PT New human Rh(D)-binding protein useful for various diagnostic and  
PT therapeutic applications, including typing of blood or blood products.  
PS  
SQ Claim 4; Page 52; 187pp; English.

CC The invention relates to an isolated Rh(D) binding protein. The protein  
CC can be used for magnetically activated cell sorting. The protein is  
CC useful in various diagnostic and therapeutic applications in humans,  
CC including typing of blood or blood products. The present sequence  
CC represents the amino acid sequence of a human anti-Rh(D) chain  
XX  
SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;  
Best Local Similarity 86.8%; Pred. No. 1.9e-28;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKPKAKPKLLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYINWYQKPKAKPKLLIYAASSLSQGVPSRF 61  
QY 61 SGGSGYGFDTLTITSSLOFEDFASYYCOESLSASTYFGGKTVEIKR 106  
DB 62 SGGSGYGFDTLTITSSLOFEDFATYYCOQSYSTPMTFGGKTVEIKR 107

RESULT 12  
 ABO27397 standard; protein, 107 AA.  
 XX  
 AC ABO27397;  
 XX  
 DT 12-SEP-2003 (first entry)  
 XX  
 DE Anti-Rh(D) chain 102.  
 XX  
 KM Human, RH(D) binding protein; blood typing; blood product; antibody;  
 XX magnetically activated cell sorting.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003040605-A1.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 04-MAY-2001; 2001US-00848798.  
 XX  
 PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 PR 29-JAN-1999; 99US-00240274.  
 XX  
 PA (TYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Siegel DL;  
 XX  
 DR WPI; 2003-512273/48.  
 DR N-PSDB; ACD45311.  
 XX  
 PT New human Rh(D)-binding protein useful for various diagnostic and  
 PT therapeutic applications, including typing of blood or blood products.  
 XX  
 PS Claim 4; Page 26; 187pp; English.  
 XX  
 CC The invention relates to an isolated Rh(D) binding protein. The protein  
 CC can be used for magnetically activated cell sorting. The protein is  
 CC useful in various diagnostic and therapeutic applications in humans,  
 CC including typing of blood or blood products. The present sequence  
 CC represents the amino acid sequence of a human anti-Rh(D) chain  
 XX  
 SQ Sequence 107 AA;  
 Query Match 86.9%; Score 472; DB 6; Length 107;  
 Best Local Similarity 87.7%; Pred. No. 1.9e-28;  
 Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTVTCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSGVSRRF 60  
 DB 2 ELTQSPSSLSASVGDRTVTCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSGVSRRF 61  
 QY 61 SSGSGYGDFTLTISLQPEDFASYYCOESLSASYTFGQGTVEIKR 106  
 DB 62 SSGSGYGDFTLTISLQPEDFATYYCOQSYSTMTFQGKIVEIKR 107  
 RESULT 13  
 ABO27470 standard; protein, 107 AA.  
 XX  
 AC ABO27470;  
 XX  
 DT 12-SEP-2003 (first entry)  
 XX  
 DE Anti-Rh(D) light chain SH49.  
 XX  
 KM Human, RH(D) binding protein; blood typing; blood product; antibody;  
 KM magnetically activated cell sorting.  
 XX  
 OS Homo sapiens.

XX  
 PN US2003040605-A1.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 04-MAY-2001; 2001US-00848798.  
 XX  
 PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 PR 29-JAN-1999; 99US-00240274.  
 XX  
 PA (TYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Siegel DL;  
 XX  
 DR WPI; 2003-512273/48.  
 DR N-PSDB; ACD45384.  
 XX  
 PT New human Rh(D)-binding protein useful for various diagnostic and  
 PT therapeutic applications, including typing of blood or blood products.  
 XX  
 PS Claim 4; Page 52; 187pp; English.  
 XX  
 CC The invention relates to an isolated Rh(D) binding protein. The protein  
 CC can be used for magnetically activated cell sorting. The protein is  
 CC useful in various diagnostic and therapeutic applications in humans,  
 CC including typing of blood or blood products. The present sequence  
 CC represents the amino acid sequence of a human anti-Rh(D) chain  
 XX  
 SQ Sequence 107 AA;  
 Query Match 86.9%; Score 472; DB 6; Length 107;  
 Best Local Similarity 86.8%; Pred. No. 1.9e-28;  
 Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTVTCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSGVSRRF 60  
 DB 2 ELTQSPSSLSASVGDRTVTCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSGVSRRF 61  
 QY 61 SSGSGYGDFTLTISLQPEDFASYYCOESLSASYTFGQGTVEIKR 106  
 DB 62 SSGSGYGDFTLTISLQPEDFATYYCOQSYSTMTFQGKIVEIKR 107  
 RESULT 14  
 AAG93644 standard; protein, 107 AA.  
 XX  
 AC AAG93644;  
 XX  
 DT 14-SEP-2001 (first entry)  
 XX  
 DE Human anti-Rh(D) antibody clone SH13 protein sequence.  
 XX  
 KM Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6255455-B1.  
 XX  
 PD 03-JUL-2001.  
 XX  
 PF 29-JAN-1999; 99US-00240274.  
 XX  
 PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 XX  
 PA (TYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Siegel DL;

XX WPI; 2001-388931/41.  
DR N-PSDB; AAH68701.  
XX  
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
diagnostics requiring a human instead of an animal antibody and in  
therapeutic medicine.  
XX  
PS Claim 1; Col 68; 162pp; English.  
XX  
CC The present invention describes an isolated Rh(D) binding protein,  
CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AA69358 to AA69369. (I) has  
CC immunostimulant activity, and can be used as an immune system stimulant.  
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAH6815 to AAH68726 represent the nucleotide sequence which encode  
CC AA69358 to AA69369. AA69369 to AA69367 represent anti-Rh(D) heavy  
CC chain CDR3 amino acid sequences which are given in the exemplification of  
CC the present invention  
XX  
SQ Sequence 107 AA;

Query Match 86.7%; Score 471; DB 4; Length 107;  
Best Local Similarity 86.8%; Pred. No. 2.3e-28;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTYISCRASORINTYINWYOHKPKAKPLIYAASSLQSGVPSRF 60  
Db 2 ELTQSPSLASVGDRTYITCRASQSISSYINWYQKPKAKPLIYAASSLRGVSRRF 61  
QY 61 SSGSGYTDFTLTITISLQFEDPASYCOESLSASTFQGTKEIKR 106  
62 SSGSGYTDFTLTITISLQFEDPASYCOESLSASTFQGTKEIKR 107  
Db

## RESULT 15

ABO27451  
ID ABO27451 standard; protein; 107 AA.

XX AC ABO27451;

XX DT 12-SEP-2003 (first entry)

XX DE Anti-Rh(D) light chain SH3.

XX Human: RH(D) binding protein; blood typing; blood product; antibody;  
KW magnetically activated cell sorting.  
XX  
OS Homo sapiens.

XX PN US2003040605-A1.

XX PD 27-FEB-2003.

XX PF 04-MAY-2001; 2001US-00848798.

XX PR 11-OCT-1996; 96US-0028550P.

XX PR 27-JUN-1997; 97US-0088404S.

XX PR 10-APR-1998; 98US-0081380P.

XX PR 29-JAN-1999; 99US-00240274.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Siegel DL;

XX WPI; 2003-512273/48.

XX DR N-PSDB; ACD45365.

XX New human Rh(D) binding protein useful for various diagnostic and  
PT therapeutic applications, including typing of blood or blood products.  
XX

PS Claim 4; Page 50; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein  
CC can be used for magnetically activated cell sorting. The protein is  
CC useful in various diagnostic and therapeutic applications in humans,  
CC including typing of blood or blood products. The present sequence  
CC represents the amino acid sequence of a human anti-Rh(D) chain  
XX

SQ Sequence 107 AA;

Query Match 86.7%; Score 471; DB 6; Length 107;  
Best Local Similarity 86.8%; Pred. No. 2.3e-28;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTYISCRASORINTYINWYOHKPKAKPLIYAASSLQSGVPSRF 60  
Db 2 ELTQSPSLASVGDRTYITCRASQSISSYINWYQKPKAKPLIYAASSLRGVSRRF 61  
QY 61 SSGSGYTDFTLTITISLQFEDPASYCOESLSASTFQGTKEIKR 106  
62 SSGSGYTDFTLTITISLQFEDPASYCOESLSASTFQGTKEIKR 107  
Db

Search completed: July 26, 2005, 09:19:20  
Job time : 80.3394 secs



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OM protein - protein search, using SW model

Run on: July 26, 2005, 09:26:32 ; Search time 67.4545 Seconds

(without alignments)  
611.274 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543  
Sequence: 1 ELTQSPSSLSASVGDRTVTS.....QESLSASTYFGGKTVEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA:\*

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11: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	100.0	106	US-10-027-725A-10	Sequence 10, Appl
2	475	87.5	107	US-10-016-986-104	Sequence 104, App
3	474	87.3	107	US-09-848-798-119	Sequence 179, Appl
4	472	86.9	107	US-09-848-798-33	Sequence 33, Appl
5	472	86.9	107	US-09-848-798-175	Sequence 175, App
6	472	86.9	107	US-09-848-798-116	Sequence 116, App
7	471	86.7	107	US-09-848-798-136	Sequence 136, App
8	468	86.2	107	US-09-848-798-36	Sequence 36, Appl
9	468	86.2	107	US-10-783-311-198	Sequence 198, Appl
10	467	86.0	107	US-10-016-986-105	Sequence 105, App
11	465	85.6	111	US-10-203-754A-57	Sequence 57, Appl

12	464.5	85.5	108	10	US-09-848-798-32	Sequence 32, Appl
13	464.5	85.5	108	10	US-09-848-798-43	Sequence 43, Appl
14	464	85.5	107	10	US-09-848-798-37	Sequence 37, Appl
15	464	85.5	107	16	US-10-409-814A-4	Sequence 4, Appl
16	464	85.5	240	9	US-09-192-854-2	Sequence 2, Appl
17	464	85.5	240	9	US-09-968-561A-2	Sequence 2, Appl
18	464	85.5	240	11	US-09-968-744A-2	Sequence 2, Appl
19	464	85.5	240	11	US-09-968-561A-2	Sequence 2, Appl
20	464	85.5	240	16	US-10-744-774-1	Sequence 1, Appl
21	463	85.3	107	10	US-09-791-153A-67	Sequence 67, Appl
22	463	85.3	108	17	US-10-726-332-214	Sequence 214, App
23	463	85.3	108	17	US-10-805-177-64	Sequence 64, Appl
24	462	85.1	106	14	US-10-027-725A-12	Sequence 12, Appl
25	462	85.1	107	10	US-09-848-798-39	Sequence 39, Appl
26	462	85.1	107	10	US-09-848-798-39	Sequence 39, Appl
27	462	85.1	108	16	US-10-744-774-15	Sequence 15, Appl
28	462	85.1	108	17	US-10-805-177-20	Sequence 20, Appl
29	461	84.9	107	10	US-09-848-798-158	Sequence 158, Appl
30	461	84.9	108	17	US-10-726-332-18	Sequence 18, Appl
31	460.5	84.8	108	10	US-09-848-798-167	Sequence 167, App
32	460	84.7	106	14	US-10-027-725A-11	Sequence 11, Appl
33	460	84.7	106	16	US-10-466-242-38	Sequence 38, Appl
34	460	84.7	106	16	US-10-466-242-56	Sequence 56, Appl
35	460	84.7	108	17	US-10-726-332-28	Sequence 28, Appl
36	459.5	84.6	108	10	US-09-848-798-163	Sequence 163, App
37	459	84.5	108	17	US-10-726-332-209	Sequence 209, App
38	459	84.5	111	18	US-10-916-840-100	Sequence 100, App
39	458	84.3	107	10	US-09-848-798-35	Sequence 35, Appl
40	458	84.3	107	10	US-09-848-798-173	Sequence 173, Appl
41	458	84.3	108	17	US-10-477-830-90	Sequence 90, Appl
42	458	84.3	111	14	US-10-203-754A-56	Sequence 56, Appl
43	457	84.2	104	14	US-10-016-986-106	Sequence 106, App
44	457	84.2	107	10	US-09-848-798-40	Sequence 40, Appl
45	457	84.2	214	14	US-10-153-382-19	Sequence 19, Appl

#### ALIGNMENTS

RESULT 1  
US-10-027-725A-10  
; Sequence 10, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IGF-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-10

Query Match 100.0%; Score 543; DB 14; Length 106;  
Best Local Similarity 100.0%; Pred. No. 3.4e-42;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ELTQSPSSLSASVGDRTVTS	CRASGRINTYINMYQHKFGKAPKLLIYAASISQGVPRF	60
DB	1	ELTQSPSSLSASVGDRTVTS	CRASGRINTYINMYQHKFGKAPKLLIYAASISQGVPRF	60
QY	61	SSSGYDFTLLTSSLOFEDFASYYCOESLSASTYFGGKTVEIKR	106	
DB	61	SSSGYDFTLLTSSLOFEDFASYYCOESLSASTYFGGKTVEIKR	106	

RESULT 2

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US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Letner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-104

Query Match      87.5%; Score 475; DB 14; Length 107;
Best Local Similarity 87.7%; Pred. No. 5.8e-36;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITICRASQRIINTYINWYQHKPKKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITICRASQSISSYINWYQKPKKAPKLLIYAASSLSQGVPSRF 60

Qy 61 SSGSGVDFTLTISLTQPEDFASYYCOESLSASYTFQGGTKEIKR 106
Db 61 SSGSGVDFTLTISLTQPEDFATYYCOQSYSTPPTFGGKLEIKR 106

RESULT 3
US-09-848-798-179
; Sequence 179, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match      87.3%; Score 474; DB 10; Length 107;
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Best Local Similarity 87.7%; Pred. No. 7.2e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITICRASQRIINTYINWYQHKPKKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITICRASQSISSYINWYQKPKKAPKLLIYAASSLSQGVPSRF 61

Qy 61 SSGSGVDFTLTISLTQPEDFASYYCOESLSASYTFQGGTKEIKR 106
Db 62 SSGSGVDFTLTISLTQPEDFATYYCOQSYSTPPTFGGKLEIKR 107

RESULT 4
US-09-848-798-33
; Sequence 33, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-33

Query Match      86.9%; Score 472; DB 10; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.1e-35;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITICRASQRIINTYINWYQHKPKKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITICRASQSISSYINWYQKPKKAPKLLIYAASSLSQGVPSRF 61

Qy 61 SSGSGVDFTLTISLTQPEDFASYYCOESLSASYTFQGGTKEIKR 106
Db 62 SSGSGVDFTLTISLTQPEDFATYYCOQSYSTPPTFGGKLEIKR 107

RESULT 5
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
```

```

; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
; SEQ ID NO 198
; LENGTH: 116

```

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Light chain amino acid sequence  
US-10-783-311-198

Query Match 86.2%; Score 468; DB 17; Length 116;  
Best Local Similarity 85.8%; Pred. No. 2.8e-35;  
Matches 91; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTSPSSLSASVGDRTVITSCRASORINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60  
DB 4 QMTSPSSLSASVGDRTVITCRASQSISSYLNWYQKRGKAPKLLIYAASSLSQGVPSRF 63

QY 61 SSGSGYDFTLTISLQPEDFASYYCQESLSASYTFGGGTKEIKR 106  
DB 64 SSGSGYDFTLTISLQPEDFATYYCQGSYSTRWTFGGGTKEIKR 109

RESULT 10  
US-10-016-986-105  
Sequence 105, Application US/10016986  
Publication No. US20030187247A1  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
FILE REFERENCE: 313.2CON1  
CURRENT APPLICATION NUMBER: US/10/016, 986  
CURRENT FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: US 09/149, 898  
PRIOR FILING DATE: 1998-09-08  
PRIOR APPLICATION NUMBER: US 08/899, 575  
PRIOR FILING DATE: 1997-07-24  
PRIOR APPLICATION NUMBER: US 08/276, 852  
PRIOR FILING DATE: 1994-07-18  
PRIOR APPLICATION NUMBER: US 08/178, 302  
PRIOR FILING DATE: 1994-01-06  
PRIOR APPLICATION NUMBER: PCT/US93/09328  
PRIOR FILING DATE: 1993-09-30  
PRIOR APPLICATION NUMBER: US 07/954, 148  
PRIOR FILING DATE: 1992-09-30  
NUMBER OF SEQ ID NOS: 176  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 105  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized  
US-10-016-986-105

Query Match 86.0%; Score 467; DB 14; Length 107;  
Best Local Similarity 86.8%; Pred. No. 3.1e-35;  
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTSPSSLSASVGDRTVITSCRASORINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60  
DB 1 ELTSPSSLSASVGDRTVITCRASQSISSYLNWYQKRGKAPKLLIYAASSLSQGVPSRF 60

QY 61 SSGSGYDFTLTISLQPEDFASYYCQESLSASYTFGGGTKEIKR 106  
DB 61 SSGSGYDFTLTISLQPEDFATYYCQGSYSTRWTFGGGTKEIKR 106

RESULT 11  
US-10-203-754A-57  
Sequence 57, Application US/10203754A  
Publication No. US2003015732A1  
GENERAL INFORMATION:  
APPLICANT: ITAMI, Seima

APPLICANT: SEXI, Makoto  
APPLICANT: MATSURA, Yoshiharu  
APPLICANT: SHIBUI, Tatsuro  
APPLICANT: YOSHIMOTO, Yoshinisa  
APPLICANT: MIYAMURA, Tatsuo  
TITLE OF INVENTION: Therapeutic Agent for Hepatitis C  
FILE REFERENCE: P22257  
CURRENT APPLICATION NUMBER: US/10/203, 754A  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: PCT/JP01/00967  
PRIOR FILING DATE: 2001-02-13  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 57  
LENGTH: 111  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-203-754A-57

Query Match 85.6%; Score 465; DB 14; Length 111;  
Best Local Similarity 84.8%; Pred. No. 5e-35;  
Matches 89; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITSCRASORINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 61  
DB 4 MTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKRGKAPKLLIYAASSLSQGVPSRF 63

QY 62 SSGYDFTLTISLQPEDFASYYCQESLSASYTFGGGTKEIKR 106  
DB 64 SSGYDFTLTISLQPEDFATYYCQGSYSTRWTFGGGTKEIKR 108

RESULT 12  
US-09-848-798-32  
Sequence 32, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/848, 798  
CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240, 274  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028, 550  
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 32  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain I01  
US-09-848-798-32

Query Match 85.5%; Score 464.5; DB 10; Length 108;  
Best Local Similarity 86.9%; Pred. No. 5.4e-35;  
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTSPSSLSASVGDRTVITSCRASORINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60  
DB 2 ELTSPSSLSASVGDRTVITCRASQSISSYLNWYQKRGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SSGSGYDFTLTISLQPEDFASYYCQESLSA-SYTFGGGTKEIKR 106  
DB 62 SSGSGYDFTLTISLQPEDFATYYCQGSYSTRWTFGGGTKEIKR 108

RESULT 13  
US-09-848-798-43  
Sequence 43, Application US/09848798

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; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 112
US-09-848-798-43
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Query Match      85.5%; Score 464.5; DB 10; Length 108;
Best Local Similarity 86.9%; Pred. No. 5.4e-35;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;
```

```
QY      1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMYQHKPKAKPKLLIYAASSLSQGVPSRF 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQOKPKAKPKLLIYAASSLSQGVPSRF 61
```

```
QY      61 SSGSGGTDFLTITLISLQPEDFASYYCOESLSA-SYTFGQGTVEIKR 106
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      62 SSGSGGTDFLTITLISLQPEDFATYYCOOSYSTPTTFGQGTVEIKR 108
```

```
RESULT 14
US-09-848-798-37
; Sequence 37, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 106
US-09-848-798-37
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Query Match      85.5%; Score 464; DB 10; Length 107;
Best Local Similarity 85.8%; Pred. No. 5.9e-35;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
```

```
QY      1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMYQHKPKAKPKLLIYAASSLSQGVPSRF 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQOKPKAKPKLLIYAASSLSQGVPSRF 61
```

```
QY      61 SSGSGGTDFLTITLISLQPEDFASYYCOESLSASYYTFGQGTVEIKR 106
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      62 SSGSGGTDFLTITLISLQPEDFATYYCOOSYSTPTTFGQGTVEIKR 107
```

```
RESULT 15
US-10-409-814A-4
; Sequence 4, Application US/10409814A
; Publication No. US20040202995A1
; GENERAL INFORMATION:
; APPLICANT: de Wildt, Rudolf
; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND SCREENING METHODS
; FILE REFERENCE: 8039/2032
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/10/409,814A
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-409-814A-4
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Query Match      85.5%; Score 464; DB 16; Length 108;
Best Local Similarity 85.8%; Pred. No. 6e-35;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
```

```
QY      1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMYQHKPKAKPKLLIYAASSLSQGVPSRF 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      3 QMTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQOKPKAKPKLLIYAASSLSQGVPSRF 62
```

```
QY      61 SSGSGGTDFLTITLISLQPEDFASYYCOESLSASYYTFGQGTVEIKR 106
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      63 SSGSGGTDFLTITLISLQPEDFATYYCOOSYSTPTTFGQGTVEIKR 108
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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:09:56 ; Search time 21.5909 Seconds  
(without alignments)  
394.147 Million cell updates/sec

Title: US-10-027-725A-9  
Sequence: 1 LKSPGKLVKSGQLSLTCTV.....RSDGYTLDMGQGLTVSS 114

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Searched: 513545 seqs, 74649064 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PTCUS.COMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	521	84.9	473	3	US-09-049-672A-4
2	508	82.7	172	4	US-09-472-087-7
3	508	82.7	172	4	US-09-472-087-86
4	502.5	81.8	119	3	US-09-025-769B-39
5	502.5	81.8	119	3	US-09-025-769B-65
6	502.5	81.8	119	4	US-09-490-070A-39
7	502.5	81.8	119	4	US-09-490-070A-65
8	502.5	81.8	119	4	US-09-490-153-39
9	502.5	81.8	119	4	US-09-490-153-65
10	502.5	81.8	119	4	US-09-490-324-39
11	502.5	81.8	119	4	US-09-490-324-65
12	496	80.8	122	1	US-08-360-125-11
13	496	80.8	122	1	US-08-450-578-11
14	496	80.8	122	2	US-09-017-628-11
15	496	80.8	122	2	US-09-014-880-11
16	496	80.8	122	4	US-08-450-363-11
17	496	80.8	122	4	US-09-467-903-11
18	492.5	80.2	117	4	US-09-720-493-2
19	492	80.1	487	4	US-09-800-729-145
20	491	80.0	118	3	US-09-025-769B-25
21	491	80.0	118	4	US-09-490-070A-25
22	491	80.0	118	4	US-09-490-153-25
23	491	80.0	118	4	US-09-490-324-25
24	491	80.0	120	4	US-09-424-840B-20
25	487.5	79.4	119	1	US-08-360-125-5
26	487.5	79.4	119	2	US-08-450-578-5
27	487.5	79.4	119	2	US-09-017-628-5

28	487.5	79.4	119	2	US-09-014-880-5	Sequence 5, Appli
29	487.5	79.4	119	4	US-08-450-363-5	Sequence 5, Appli
30	487.5	79.4	119	4	US-09-467-903-5	Sequence 5, Appli
31	472	76.9	244	3	US-08-918-148-79	Sequence 79, Appli
32	472	76.9	244	4	US-09-138-091A-77	Sequence 77, Appli
33	467	76.1	118	3	US-08-545-809A-116	Sequence 116, App
34	466.5	76.0	142	2	US-08-480-774A-2	Sequence 2, Appli
35	460.5	75.0	119	2	US-08-652-816A-10	Sequence 10, Appli
36	460.5	75.0	155	4	US-09-471-276-888	Sequence 888, App
37	460	74.9	278	3	US-09-260-527-3	Sequence 3, Appli
38	457	74.4	118	3	US-08-545-809A-142	Sequence 142, App
39	457	74.4	118	4	US-09-343-698-6	Sequence 6, Appli
40	457	74.4	118	4	US-08-325-985-6	Sequence 6, Appli
41	455.5	74.2	117	4	US-09-232-290-47	Sequence 47, App
42	455	74.1	139	4	US-09-471-276-837	Sequence 837, App
43	450.5	73.4	219	3	US-09-460-384-37	Sequence 37, Appli
44	450	73.3	832	3	US-08-630-820-7	Sequence 7, Appli
45	450	73.3	832	4	US-09-273-453-7	Sequence 7, Appli

## ALIGNMENTS

RESULT 1  
US-09-049-672A-4  
Sequence 4, Application US/09049672A  
Patent No. 6135941  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Young, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baugun, Mariah R.  
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESS: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,672A  
FILING DATE: HERewith  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PANCUT01

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; CLONE: 1513264
US-09-049-672A-4
Query Match      84.9%; Score 521; DB 3; Length 473;
Best Local Similarity 83.2%; Pred. No. 2.6e-44;
Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

Oy 2  ESGGLVPSQTLSTCTVSGSGSIRSGGYWMSWIRPQPKGLEWIGYIHSGNTYNNPSL 61
Db 25  ESGGLVPSQTLSTCTVSGSGSIRSGGYWMSWIRPQPKGLEWIGYIHSGNTYNNPSL 84

Oy 62  KSRVTMSVDTSKNHSRLSSVTADTAATVYVCARSDG--YTLDMNGGGLTVTVSS 114
Db 85  KSRVTISVDTSKNPSLKLSSVTADTAATVYVCARDVGLRGANGMDVWGGLTVTVSS 143

RESULT 2
US-09-472-087-7
Sequence 7, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, ELLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PP1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      82.7%; Score 508; DB 4; Length 172;
Best Local Similarity 85.1%; Pred. No. 1.6e-43;
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Oy 3  SGPGLVPSQTLSTCTVSGSGSIRSGGYWMSWIRPQPKGLEWIGYIHSGNTYNNPSL 62
Db 1  SGPGLVPSQTLSTCTVSGSGSIRSGGYWMSWIRPQPKGLEWIGYIHSGNTYNNPSL 60

Oy 63  SRVTMSVDTSKNHSRLSSVTADTAATVYVCARSDG--YTLDMNGGGLTVTVSS 114
Db 61  SRVTISVDTSKNPSLKLSSVTADTAATVYVCARDVGLRGANGMDVWGGLTVTVSS 114

RESULT 3
US-09-472-087-86
Sequence 86, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, ELLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PP1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
```

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; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-86

Query Match      82.7%; Score 508; DB 4; Length 172;
Best Local Similarity 85.1%; Pred. No. 1.6e-43;
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Oy 3  SGPGLVPSQTLSTCTVSGSGSIRSGGYWMSWIRPQPKGLEWIGYIHSGNTYNNPSL 62
Db 1  SGPGLVPSQTLSTCTVSGSGSIRSGGYWMSWIRPQPKGLEWIGYIHSGNTYNNPSL 60

Oy 63  SRVTMSVDTSKNHSRLSSVTADTAATVYVCARSDG--YTLDMNGGGLTVTVSS 114
Db 61  SRVTISVDTSKNPSLKLSSVTADTAATVYVCARDVGLRGANGMDVWGGLTVTVSS 114

RESULT 4
US-09-025-769B-39
Sequence 39, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vlc
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Pluckethum, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
FAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-39

Query Match      81.8%; Score 502.5; DB 3; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.7e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

Oy 2  ESGGLVPSQTLSTCTVSGSGSIRSGGYWMSWIRPQPKGLEWIGYIHSGNTYNNPSL 61
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Db 6 ESGGLVPSSETLSITCTVSGSIS--YWSWIRQPGKGLWIGIYSGSTNYPNL 63  
 Oy 62 KSRVTMSVDTSKNHPSLRLSSVTADTAIVYCAR--SDG-YTLDNWGGGTLVTYSS 114  
 Db 64 KSRVTISVDTSKNPSLRLSSVTADTAIVYCARWGSGGFYAMDYWGGLVTYSS 119

RESULT 5

US-09-025-769B-65  
 ; Sequence 65, Application US/09025769B  
 ; Patent No. 6300064  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Knappik, Achim  
 ; APPLICANT: Knappik, Achim  
 ; APPLICANT: Pack, Peter  
 ; APPLICANT: Ilag, Vic  
 ; APPLICANT: Ge, Liming  
 ; APPLICANT: Moroney, Simon  
 ; APPLICANT: Plueckthun, Andreas  
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 ; NUMBER OF SEQUENCES: 373  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA: US/09/025, 769B  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-FEB-1998  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: James F. Haley, Jr., Esq.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: MORPHO/5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)596-9000  
 TELEFAX: (212)596-9080  
 INFORMATION FOR SEQ ID NO: 65:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 119 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-025-769B-65

Query Match

Best Local Similarity 81.8%; Score 502.5; DB 3; Length 119;  
 Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

Oy 2 ESGGLVPSQTLISITCTVSGSISIRSGYWSWIRQPGKGLWIGIYHSGNTYYPNL 61  
 Db 6 ESGGLVPSSETLSITCTVSGSIS--YWSWIRQPGKGLWIGIYSGSTNYPNL 63  
 Oy 62 KSRVTMSVDTSKNHPSLRLSSVTADTAIVYCAR--SDG-YTLDNWGGGTLVTYSS 114  
 Db 64 KSRVTISVDTSKNPSLRLSSVTADTAIVYCARWGSGGFYAMDYWGGLVTYSS 119

RESULT 6

US-09-490-070A-39  
 ; Sequence 39, Application US/09490070A  
 ; Patent No. 6696248  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Knappik, Achim

Pack, Peter  
 Ilag, Vic  
 Ge, Liming  
 Moroney, Simon  
 Plueckthun, Andreas  
 TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
 White & McAuliffe  
 STREET: 1666 K Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA: US/09/490, 070A  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 24-Jan-2000  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Colin G. Sandercock, Esq.  
 REGISTRATION NUMBER: 31,298  
 REFERENCE/DOCKET NUMBER: 37629-0005  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 912-2000  
 TELEFAX: (202) 912-2020  
 INFORMATION FOR SEQ ID NO: 39:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 119 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <Unknown>  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
 US-09-490-070A-39

Query Match

Best Local Similarity 81.8%; Score 502.5; DB 4; Length 119;  
 Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

Oy 2 ESGGLVPSQTLISITCTVSGSISIRSGYWSWIRQPGKGLWIGIYHSGNTYYPNL 61  
 Db 6 ESGGLVPSSETLSITCTVSGSIS--YWSWIRQPGKGLWIGIYSGSTNYPNL 63  
 Oy 62 KSRVTMSVDTSKNHPSLRLSSVTADTAIVYCAR--SDG-YTLDNWGGGTLVTYSS 114  
 Db 64 KSRVTISVDTSKNPSLRLSSVTADTAIVYCARWGSGGFYAMDYWGGLVTYSS 119

RESULT 7

US-09-490-070A-65  
 ; Sequence 65, Application US/09490070A  
 ; Patent No. 6696248  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Knappik, Achim  
 ; APPLICANT: Knappik, Achim  
 ; APPLICANT: Pack, Peter  
 ; APPLICANT: Ilag, Vic  
 ; APPLICANT: Ge, Liming  
 ; APPLICANT: Moroney, Simon  
 ; APPLICANT: Plueckthun, Andreas  
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 ; NUMBER OF SEQUENCES: 373  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
 ; White & McAuliffe  
 ; STREET: 1666 K Street, N.W., Suite 300

CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-070A-65  
Query Match 81.8%; Score 502.5; DB 4; Length 119;  
Best Local Similarity 85.3%; Pred. No. 3,7e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;  
Qy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGGYWWSWIRPPGKGLWIGYIYHSGNTYNPSTL 61  
Db 6 ESGGGLVPSSTLSTCTVSGSGSIS--YWSWIRQPPGKGLWIGYIYHSGNTYNPSTL 63  
Qy 62 KSRVTMSVDTSKKNFSLRLSSVTADTAAYVYCAR--SDG-YTLDMWGQGLTVTVSS 114  
Db 64 KSRVTISVDTSKKNFSLRLSSVTADTAAYVYCARWGSDGFYAMDYWGQGLTVTVSS 119  
RESULT 8  
US-09-490-153-39  
Sequence 39, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-153-39  
Query Match 81.8%; Score 502.5; DB 4; Length 119;  
Best Local Similarity 85.3%; Pred. No. 3,7e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;  
Qy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGGYWWSWIRPPGKGLWIGYIYHSGNTYNPSTL 61  
Db 6 ESGGGLVPSSTLSTCTVSGSGSIS--YWSWIRQPPGKGLWIGYIYHSGNTYNPSTL 63  
Qy 62 KSRVTMSVDTSKKNFSLRLSSVTADTAAYVYCAR--SDG-YTLDMWGQGLTVTVSS 114  
Db 64 KSRVTISVDTSKKNFSLRLSSVTADTAAYVYCARWGSDGFYAMDYWGQGLTVTVSS 119  
RESULT 9  
US-09-490-153-65  
Sequence 65, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000

TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-153-65

Query Match 81.8%; Score 502.5; DB 4; Length 119;  
Best Local Similarity 85.3%; Pred. No. 3.7e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMTROPKGLIEMIGYIHSGNTYNSL 61  
DB 6 ESGPGLVPSSTLSITCTVSGGSIIS--YWSWIRQPKGLEWIGYIYSGSTNYNSL 63  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCAR--SDG-YTLDNMGQGLVTVSS 114  
DB 64 KSRVTISVDTSKNPFSLRLSSVTADTAIVYCARWGSDGFYAMDYWGQGLVTVSS 119

## RESULT 10

US-09-490-324-39  
Sequence 39, Application US/09490324  
Patent No. 6828422

## GENERAL INFORMATION:

APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESSES:  
ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324  
FILING DATE: 24-Jan-2000

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995

## ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090

## INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-324-39

Query Match 81.8%; Score 502.5; DB 4; Length 119;  
Best Local Similarity 85.3%; Pred. No. 3.7e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMTROPKGLIEMIGYIHSGNTYNSL 61  
DB 6 ESGPGLVPSSTLSITCTVSGGSIIS--YWSWIRQPKGLEWIGYIYSGSTNYNSL 63  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCAR--SDG-YTLDNMGQGLVTVSS 114  
DB 64 KSRVTISVDTSKNPFSLRLSSVTADTAIVYCARWGSDGFYAMDYWGQGLVTVSS 119

## RESULT 11

US-09-490-324-65  
Sequence 65, Application US/09490324  
Patent No. 6828422

## GENERAL INFORMATION:

APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESSES:  
ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324  
FILING DATE: 24-Jan-2000

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995

## ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090

## INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-324-65

Query Match 81.8%; Score 502.5; DB 4; Length 119;  
Best Local Similarity 85.3%; Pred. No. 3.7e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMTROPKGLIEMIGYIHSGNTYNSL 61  
DB 6 ESGPGLVPSSTLSITCTVSGGSIIS--YWSWIRQPKGLEWIGYIYSGSTNYNSL 63  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCAR--SDG-YTLDNMGQGLVTVSS 114  
DB 64 KSRVTISVDTSKNPFSLRLSSVTADTAIVYCARWGSDGFYAMDYWGQGLVTVSS 119

RESULT 12  
US-08-360-125-11  
Sequence 11, Application US/08360125  
Patent No. 5767246  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5767246Ihiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Menderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:

NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-11  
Query Match 80.8%; Score 496; DB 1; Length 122;  
Best Local Similarity 81.2%; Pred. No. 1,7e-42;  
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;  
Qy 2 ESGPGLVPSQTSLTCTVSGSGSIRSGYYWMIROPFGKLEWIGYIYHSGNTYNPSSL 61  
Db 6 ESGPGLVPSSETLSLTCTVSGSGSISSSYYWGIROPFGKLEWIGSIIYSGSTYNPSSL 65  
Qy 62 KSRVTMSVDTSKNHFSLRISSTVTAADTAVYYCARSD---GYTLDNNGGCTLVTVSS 114  
Db 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARSGYGYGMDVWGQGTIVTVSS 122  
RESULT 13  
US-08-450-578-11  
Sequence 11, Application US/08450578  
Patent No. 5837845  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845Ihiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Menderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850

```

FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT FILING DATE: 1998-02-02
EARLIER APPLICATION NUMBER: 08/360,125
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 122
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-11

Query Match      80.8%; Score 496; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 1,7e-42;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

Cy       2   ESQGLVKEPQTSLTCTVGSGSIRGCGYWSWTRORPGGLEWIGIYHSGNTYNPSL 61
Db        6   EESGGLVKPESTLTCTTVSGGSISSSYYGWTRPPKGLEWIGSIYSGSYNPSL 65
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Cy       62   KSRVTYSVDTSKCNFSLRLSSVTADAVYVCARSD----GYLDNNQGQTLVVSS 114
Db        66   KSRVTITVDTSKNQFLSKLSVTADAVYVCARGSYGGYYTGMDWGQGTIVVSS 122
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 15
Sequence 11, Application US/09014880
Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiho HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids

```

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;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      ORIGINAL SOURCE:
;      CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-11

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Query Match      80.8%; Score 496; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 1.7e-42;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

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```

QY      2  ESGGGLVKKPSQTLTCTVSGGSIKSGGYWISWIRQPPGKLEWIGYIYHSGNTYINPSL 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      6  ESGGGLVKKPSQTLTCTVSGGSIKSSSYWGWIRQPPGKLEWIGSIYSGSTYINPSL 65

QY      62  KSRVTMSVDTSKNHSRLSSVTADPTAVYYCARSD---GYTLDNMGQGTLYTVSS 114
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      66  KSRVTISVDISKQPSLKLSSVTADPTAVYYCARSGYGGYYGMDVMGQGTLYTVSS 122

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Search completed: July 26, 2005, 09:30:00  
 Job time : 22.5909 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 09:07:26 ; Search time 14.6818 Seconds  
(without alignments)  
747.095 Million cell updates/sec

Title: US-10-027-725a-9

Perfect score: 614  
Sequence: 1 LESGPGVLPKPSQTLSTCTV.....RSDGYTLDNWGQGLTVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR 79: \*  
2: PIR1: \*  
3: PIR2: \*  
4: PIR3: \*  
5: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	501.5	81.7	135 2 S78051	Ig heavy chain pre
2	497.5	81.0	147 2 S13519	Ig heavy chain v r
3	492.5	80.2	140 2 I37782	Ig variable region
4	490	79.8	130 2 S30534	Ig heavy chain v r
5	488.5	79.6	116 2 S37456	Ig mu chain - huma
6	487.5	79.4	130 2 S31690	Ig heavy chain v r
7	480.5	78.3	121 2 S44113	Ig heavy chain v r
8	479.5	78.1	155 2 S31511	Ig heavy chain - h
9	477.5	77.8	146 2 S09710	Ig heavy chain v r
10	477.5	77.8	155 2 S31512	Ig heavy chain - h
11	473.5	77.1	146 2 S09711	Ig heavy chain v r
12	472.5	77.0	127 2 S19668	Ig heavy chain v r
13	472.5	77.0	128 2 S31514	Ig heavy chain - h
14	472	76.9	137 2 S31676	Ig heavy chain v r
15	469	76.4	99 2 S26803	Ig heavy chain v r
16	467.5	76.1	123 2 S30530	Ig heavy chain v r
17	467	76.1	99 2 S26801	Ig heavy chain v r
18	467	76.1	122 2 S69912	Ig V-D-J region (N
19	465	75.7	133 2 S31586	Ig heavy chain v r
20	464	75.6	99 2 S26802	Ig heavy chain v r
21	461	75.1	145 2 S78055	Ig heavy chain v r
22	460.5	75.0	109 2 PH1673	Ig heavy chain pre
23	459	74.8	110 2 S44110	Ig heavy chain v-D
24	458	74.6	139 2 A41287	Ig heavy chain v-D
25	457	74.4	118 2 A26340	Ig heavy chain pre
26	454	73.9	97 2 PLO118	Ig heavy chain v r
27	454	73.9	99 2 S26899	Ig heavy chain v r
28	452	73.6	135 2 S31604	Ig heavy chain v r
29	451	73.5	118 2 S20780	Ig heavy chain v r

30	451	73.5	129 2 S44114	Ig heavy chain v r
31	448	73.0	99 2 S12418	Ig heavy chain v r
32	447.5	72.9	139 2 S31696	Ig heavy chain v r
33	445.5	72.6	137 2 S31585	Ig heavy chain v r
34	445.5	72.6	140 2 A49045	Ig heavy chain v r
35	445	72.5	120 2 P70370	Ig mu chain precu
36	444	72.3	126 2 S47010	Ig heavy chain V4.
37	443	72.1	99 2 S26800	Ig heavy chain v r
38	442	72.0	99 2 S12412	Ig heavy chain v r
39	442	72.0	105 2 S44125	Ig lambda chain v
40	442	72.0	118 2 S24443	Ig heavy chain v r
41	442	72.0	140 2 S78052	Ig heavy chain pre
42	441.5	71.9	98 2 S12421	Ig heavy chain v r
43	441.5	71.9	132 2 A38911	Ig heavy chain v r
44	441.5	71.9	140 2 A24770	hypothetical hdbri
45	441	71.8	97 2 S26906	Ig heavy chain v r

## ALIGNMENTS

RESULT 1  
S78051  
Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C:Accession: S78051, S23716  
R:Harindranath, N.  
Submitted to the EMBL Data Library, August 1990  
A:Reference number: S78051  
A:Accession: S78051  
A:Molecule type: mRNA  
A:Residues: 1-135 <HAR>  
A:Cross-references: EMBL:X54437, NID:937814, PIDD:CA38306.1, PID:9930117  
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burratello, S.E.; Wilder, R.L.; Notkins  
Int. Immunol. 3, 865-875, 1991  
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h  
patient.  
A:Reference number: S23716, MUID:92031262, PMID:11718404  
A:Accession: S23716  
A:Molecule type: mRNA  
A:Residues: 13-111 <HAM>  
A:Cross-references: EMBL:X54437  
C:Superfamily: immunoglobulin V region, immunoglobulin homology  
C:Keywords: immunoglobulin  
F:1-13/Domains: signal sequence (fragment) #status predicted <SIG>  
F:14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F:127-111/Domains: immunoglobulin homology <IMM>  
Query Match 81.7% Score 501.5; DB 2; Length 135;  
Best local similarity 82.2% Pred. No. 3.1e-38;  
Matches 97; Conservative 6; Mismatches 10; Indels 5; Gaps 2;  
OY 2 ESFGPLVPSQTLSTCTVSGSIRSGGYWMTROPKGLMIGVYHSNGTYNPSL 61  
DB 18 ESFGPLVPSQTLSTCTVSGSIRSGHYWMTROPKGLMIGVYHSNGTYNPSL 77  
OY 62 KSRVTMSVDISKNFPSRLSLSVTAADTAIVYCAR--SDGYTLDN---WGQGLTVTVSS 114  
DB 78 KSRVTMSVDISKNFPSRLSLSVTAADTAIVYCARLGPDDYTLDDGMDVWGQGLTVTVSS 135  
RESULT 2  
S13519  
Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S13519  
R:Morlat, P.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
Nucleic Acids Res. 19, 673, 1991  
A:Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
A:Reference number: S13519, MUID:91187691, PMID:2011536  
A:Accession: S13519





Qy	62	KSRVMSVDTSKMHSESLRSSVTAADTAVYYCARSDG-----	YTLDMGQGLTVV	112
		:		
Db	69	KSRVTSVDTSKNGSLKLRSSVTAADTAVYYCARSGSVLLMFEGELLV	YFDYWGQGLTVV	128
Qy	113	SS	114	
Db	129	SS	130	

RESULT 7  
S4413  
IG heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C:Accession: S44113  
R:Hawkins, R.E.; Zhu, D.; Owecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
Submitted to the EMBL Data Library, March 1994  
A:Description: Idiolytic vaccination against human B-cell lymphoma: rescue of variable r  
A:Reference number: S44105  
A:Accession: S44113  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-121 <HAW>  
A:Cross-references: EMBL:Z31389; NID:9472967; PIDD:CAA83264.1; PID:940524  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterodimer; immunoglobulin  
I:15-99/Domain: immunoglobulin homology <IWM>

Query Match	78.3%	Score 480.5	DB 2	Length 121
Best Local Similarity	80.2%	Pred No. 2.2e-36		
Matches 93	Conservative 14	Mismatches 6	Indels 3	Gaps 2

Qy 2 ESAGGLVKEPSGTTSLTCTVSGGSIIRSGGYWSWRQCPGGGLGEMIGIYIHSGATTNPST 61

Db 6 ESAGGLVKEPSGTTSLTCTVSGGSIIRSGGYWSWRQCPGGGLGEMIGIYIHSGATTNPST 65

Qy 62 KSRITMSVDPSKHFSLRLSSVTPADPAVYVCAR-SNGY--TLDNMGCGTLTVTSS 114

Db 66 KSRITLSDVDSKDFSLRLSSVTPADPAVYVCARSLSGGYSDPFWSSQGLTLTVTSS 121

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RESULT 8
S31511
Ig heavy chain - human
C|Species: Homo sapiens (man)
C|Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C|Accession: S31511
R|Chastagner, P.; Demaison, C.; There, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A|Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA
A|Accession: S31511
A|Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-155 <CHA>
A|Cross-References: EMBL:X69866; NID:g33094; PDB:CAA4500.1; PID:g33095
C|Superfamily: immunoglobulin V region; immunoglobulin homology
C|Keywords: heterotetramer; immunoglobulin
F|47-Domain: immunoglobulin homology <IMM>

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	Query Match	Similarity	Score	DB 2	Length
Best Local	78.1%	77.5%	479.5	155	
Matches	93	Conservative	8	Mismatches	10
				Indels	9
				Gaps	2

  

	Query	DB	Score	DB 2	Length
1	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
2	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
3	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
4	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
5	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
6	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
7	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
8	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
9	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
10	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
11	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
12	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
13	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
14	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
15	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
16	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
17	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
18	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
19	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
20	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
21	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
22	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
23	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
24	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
25	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
26	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
27	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
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29	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
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33	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
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35	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
36	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
37	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
38	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
39	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
40	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
41	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
42	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
43	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
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46	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
47	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL	61			
48	ESGPGIVKRSQTLSTCTCTVSGSISGCGYVWMIROPKPKGLEWIGTYIHSQNTNPNL				

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RESULT 9
S09710
Ig heavy chain V region - human
C.Species: Homo sapiens (man)
C.Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C.Accession: S09710
R.Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A.Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A.Reference number: S09710; PMID:90262535; PMID:2111699
A.Accession: S09710
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-146 <HUG>
A.Cross-references: GB:X52110; NID:G31447; PIDN:CA36344.1; PID:G31448
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
E:34-118/Domain: immunoglobulin homology <IMM>

```

Query Match	77.8%;	Score 477.5;	DB 2;	Length 146;
Best Local Similarity	74.0%;	Pred. No. 4.9e-36;		
Matches 91;	Conservative 11;	Mismatches 10;	Indels 11;	Gaps 2;

[illegible]

QY	112	VSS	114
Db	144	VSS	146

RESULT 10  
S31512  
IG heavy chain - human  
C.Species: Homo sapiens (man)  
C.Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C.Accession: S31512  
R.Character: P.; Demaison, C.; Theze, J.; Zouali, M.  
Submitted to the EMBL Data Library, December 1992  
A.Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto-  
A.Reference number: S31509  
A.Accession: S31512  
A.Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 1-155 <CHA>  
A.Cross-references: EMBL:X69860; NID:G33082; PIDN:CAA49494.1; PID:G33083  
C.Superfamily: Immunoglobulin V region; immunoglobulin homology  
C.Keywords: heterotetramer; immunoglobulin  
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match	77.8%	Score 477.5	DB 2	Length 155
Best Local Similarity	76.7%	Pred. No. 5,2e-36		
Matches	92	Conservative	9	Mismatches 10, Indels 9, Gaps 2
QY	2	ESGPELWKPQSLTCTCTGSGSISFSGGYVMSWIFQPKGLEWIGYIYHSANTYVNSL	61	
DB	38	ESGPELWKPSESLTCTCTGSGSIS--YMSWIKQPEKGLEWIGYIYHSATYVNPPI	95	
QY	62	KSRVTVMSVDTSKNHPSLRLSVTAADTAIVVYCARSDG-----YTLNMGQGLTVTVSS	114	
DB	96	KSRVTVISVDTSKNQPSLKVYSSVTADTAIVVYCARSGGJSISWVYVYGMDVWGQGITVTVSS	155	

```
RESULT 11
S09711
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
```

C:Accession: S09711  
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of  
A:Reference number: S09710; MUID:90262535; PMID:2111699  
A:Accession: S09711  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-146 <HUG>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 473.5; DB 2; Length 146;  
Best Local Similarity 73.8%; Pred. No. 1.1e-35;  
Matches 90; Conservative 10; Mismatches 13; Indels 9; Gaps 1;

Qy 2 ESGGGLVPSQTSLTCTVSGGSIRSGYWSWIRPGKLEWIGYIHSGNTYNSL 61  
Db 25 ESGGGLVPSQTSLTCTVSGGSIRSGYWSWIRPGKLEWIGYIHSGNTYNSL 84  
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCAR-----SDGYTLDMNGGTLVTV 112  
Db 85 KSRVTISVDTSENQFSLRLTSVTPADTAAYVYCARIGVNFQGFDPWCGTLVTV 144

Qy 113 SS 114  
Db 145 SS 146

## RESULT 12

S19668  
Ig heavy chain V region (VH4D9H6) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 12-Apr-1996 #text\_change 20-Jun-2000  
C:Accession: S19668; S24445  
R:Markx, U.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991  
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage  
A:Reference number: S19663; MUID:92085276; PMID:1748994  
A:Accession: S19668  
A:Molecule type: mRNA  
A:Residues: 1-127 <MAR>  
A:Cross-references: EMBL:X61648  
R:Jones, P.T.  
submitted to the EMBL Data Library, October 1991  
A:Reference number: S24442  
A:Accession: S24445  
A:Molecule type: mRNA  
A:Residues: 1-118, 'E', 120-121, 'T', 123-126, 'P' <DON>  
A:Cross-references: EMBL:X61648; NID:937722; PIDN:CAA43829.1; PID:g1335380  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 127;  
Best Local Similarity 74.6%; Pred. No. 1.2e-35;  
Matches 91; Conservative 9; Mismatches 13; Indels 9; Gaps 1;

Qy 2 ESGGGLVPSQTSLTCTVSGGSIRSGYWSWIRPGKLEWIGYIHSGNTYNSL 61  
Db 6 QSGGGLVPSQTSLTCTVSGGSIRSGYWSWIRPGKLEWIGYIHSGNTYNSL 65  
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCARSDG-----YTLDMNGGTLVTV 112  
Db 66 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCARSDG-----YTLDMNGGTLVTV 125

Qy 113 SS 114  
Db 126 SS 127

## RESULT 13

S31514  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31514  
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoantibodies  
A:Reference number: S31509  
A:Accession: S31514  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-128 <CHA>  
A:Cross-references: EMBL:X59862; NID:933086; PIDN:CAA49496.1; PID:g33087  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:22-106/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 128;  
Best Local Similarity 78.4%; Pred. No. 1.2e-35;  
Matches 91; Conservative 8; Mismatches 14; Indels 3; Gaps 1;

Qy 2 ESGGGLVPSQTSLTCTVSGGSIRSGYWSWIRPGKLEWIGYIHSGNTYNSL 61  
Db 13 ESGGGLVPSQTSLTCTVSGGSIRSGYWSWIRPGKLEWIGYIHSGNTYNSL 72  
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCAR-----SDGYTLDMNGGTLVTV 114  
Db 73 KSRVTISVDTSENQFSLRLTSVTPADTAAYVYCARIGVNFQGFDPWCGTLVTV 128

## RESULT 14

S31676  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31676  
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31885  
A:Accession: S31676  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-137 <COI>  
A:Cross-references: EMBL:Z14182; NID:931031; PIDN:CAA78551.1; PID:g31032  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 472; DB 2; Length 137;  
Best Local Similarity 82.6%; Pred. No. 1.4e-35;  
Matches 95; Conservative 4; Mismatches 12; Indels 4; Gaps 2;

Qy 2 ESGGGLVPSQTSLTCTVSGGSIRSGYWSWIRPGKLEWIGYIHSGNTYNSL 61  
Db 25 ESGGGLVPSQTSLTCTVSGGSIRSGYWSWIRPGKLEWIGYIHSGNTYNSL 82  
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCARSDG-----YTLDMNGGTLVTV 114  
Db 83 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCARSDG-----YTLDMNGGTLVTV 137

## RESULT 15

S26803  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26803  
R:Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A:Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.  
A:Reference number: S26800; MUID:92201299; PMID:1348029

A;Accession: S26803  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-99 <MEN>  
 C;Cross-references: EMBL:Z14238; NID:937710; PIDN:CAA78607.1; PID:g1335374  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 469; DB 2; Length 99;  
 Best Local Similarity 92.6%; Pred. No. 1.9e-35;  
 Matches 87; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 ESGPGLVPSQTLSTCTVSGGSIRSGYWSWIRPGKGLWIGYIYHSGNTYINPSL 61  
 Db 6 ESGPGLVPSQTLSTCTVSGGSIRSGYWSWIRPGKGLWIGYIYHSGNTYINPSL 65  
 QY 62 KSRVTMSVDTSKNHPSLRSSVTADTAIVYYCAR 95  
 Db 66 KSRVTISVDTSKNQFSLKSSVTADTAIVYYCAR 99

Search completed: July 26, 2005, 09:27:49  
 Job time : 15.6818 secs

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Thu Jul 28 05:42:34 2005

GenCore version 5.1.5  
Copyright (c) 1993 - 2005  
Time 71.6818 Seconds  
Chout alignments  
using sw m04.391 Million cell updates/sec

OM protein - protein search, July 26, 2005, 08:57  
.....RSDGYTLDMWGQGLTVVSS 114

Run on: us-10-027-725a-9

Title: Perfect score: 1 LEF  
Sequence: 614  
Scoring table: 2000000000  
Maximum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

UniProt\_03: \*  
1: uniprot\_prot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	504.5	82.2	476	2	O6GMX1
2	480	78.2	465	2	O6GMX6
3	480	78.2	478	2	O7Z379
4	470.5	76.6	119	2	O9UL73
5	469.5	76.5	492	2	O7Z374
6	469	76.4	477	2	O6GMX7
7	468	76.2	150	2	O9S973
8	460	74.9	496	2	O96KX8
9	460	74.9	620	2	O96KX8
10	452	73.6	576	2	O6P418
11	441	71.8	139	2	O86SX2
12	439.5	71.6	129	1	HV2F_HUMAN
13	431	70.2	130	2	O81ZD7
14	429.5	70.0	595	2	O8WUX4
15	428.5	70.0	597	2	O6GMX5
16	429.5	70.0	597	2	O9BUI0
17	429.5	70.0	625	2	O96A66
18	425.5	69.3	597	2	O9BQB8
19	424.5	69.1	478	2	O6NTH3
20	420	68.4	146	1	HV2I_HUMAN
21	412	67.1	473	2	O8TC63
22	393.5	64.1	117	1	HV2G_HUMAN
23	392.5	63.9	479	2	O99M22
24	389	63.4	116	2	O7Z3Y6
25	387	63.0	136	2	O6LBO5
26	377.5	61.5	476	2	O6MZX7
27	372.5	60.7	137	1	HV4E_MOUSE
28	370.5	60.3	262	2	O6S2I1
29	364	59.3	122	2	O9UL75
30	357.5	58.2	113	1	HV4I_MOUSE
31	349.5	56.9	144	1	HV4J_MOUSE

32	348.5	56.8	116	1	HV6I_MOUSE
33	347	56.5	117	1	HV6J_MOUSE
34	344.5	56.1	121	2	O9UL96
35	343	55.9	118	2	O81IUS
36	342.5	55.8	116	1	HV6O_MOUSE
37	340	55.4	121	2	O99NG4
38	336	54.7	482	2	O91X92
39	330	53.7	135	1	HV02_XENLA
40	314.5	51.2	118	2	O9UL74
41	313	51.0	120	1	HV2H_HUMAN
42	303.5	49.4	240	2	O6S2C9
43	302.5	49.3	119	1	HV2C_HUMAN
44	301.5	49.1	466	2	O6IN78
45	299	48.7	473	2	O6MZV7

## ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	476 AA.
O6GMX1			
AC	O6GMX1		
DT	05-JUL-2004 (TREMBlrel. 27, Created)		
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)		
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
NCBI	NCBI_Taxid=9606;		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Splice.		
RK	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stappleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Faley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S., Krzywinski M.I., Skalek U., Smallos D.E., Scherch A., Schein J.E., Jones S.J., Warr M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Splice.		
RA	Strausberg R.L.		
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC073773; AAH73773.1; -		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003597; IG-cl.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF07654; Cl-sec; 3.		
DR	Pfam; PF00047; Ig; 4.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00407; IGcl; 3.		
DR	SMART; SM00406; IGv; 1.		
DR	PROSITE; PS00835; IG_LIKE; 4.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.		

KW Hypothetical protein.  
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE5D CRC64;  
Query Match 82.2%; Score 504.5; DB 2; Length 476;  
Best Local Similarity 76.6%; Pred. No. 1e-43;  
Matches 95; Conservative 12; Mismatches 4; Indels 13; Gaps 2;

QY 2 ESGPGLVPSQTLSTLTCTVSGGSIIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSL 61  
DB 25 ESGPGLVPSQTLSTLTCTVSGGSIIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSL 84  
QY 62 KSRVTMSVDSKXHFSLRLSSVTADTAAYVYCARSDGVTLDNMGCGTLVTWSS 110  
DB 85 KSRVTMSVDSKXHFSLRLSSVTADTAAYVYCARSDGVTLDNMGCGTLVTWSS 142  
QY 111 TVSS 114  
DB 143 TVSS 146

RESULT 2  
Q6GMX6 PRELIMINARY; PRT; 465 AA.  
ID Q6GMX6  
AC Q6GMX6  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul R.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Chao S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Pheasant M., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA [12] Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA SEQUENCE Touchman J.W., Green E.D., Dickson M.C.,  
RA TISSUE=Epitheloid J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Straube R., Kalka U., Smallus D.E., Scherch A., Schein J.E.,  
RA Submitted (JUN-2003);  
DR EMBL; BC073766; AAH3.A. 99:16899-16903(2002).  
DR InterPro; IPR003597; IG\_1.  
DR InterPro; IPR007110; IG\_1.  
DR InterPro; IPR003597; IG\_1.  
DR InterPro; IPR003597; IG\_1.  
DR Pfam; PF07654; IG\_MHC.  
DR SMART; SM00409; IG\_4.  
DR SMART; SM00409; IG\_4.  
DR SMART; SM00409; IG\_4.  
DR PROSITE; PS50835; IG\_LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;  
Query Match 78.2%; Score 480; DB 2; Length 465;  
Best Local Similarity 84.1%; Pred. No. 3.4e-41;  
Matches 95; Conservative 3; Mismatches 13; Indels 2; Gaps 1;

QY 2 ESGPGLVPSQTLSTLTCTVSGGSIIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSL 61  
DB 25 ESGPGLVPSQTLSTLTCTVSGGSIIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSL 82  
QY 62 KSRVTMSVDSKXHFSLRLSSVTADTAAYVYCARSDGVTLDNMGCGTLVTWSS 114  
DB 83 KSRVTMSVDSKXHFSLRLSSVTADTAAYVYCARSDGVTLDNMGCGTLVTWSS 135

RESULT 3  
Q72379 PRELIMINARY; PRT; 478 AA.  
ID Q72379  
AC Q72379  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein DKFZp686K04218 (Fragment).  
GN Name=DKFZp686K04218;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Mleemann S.,  
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX338066; CAD97996.1; -.  
DR HSSP; P01820; 1G7J.  
DR InterPro; IPR007110; IG\_LIKE.  
DR InterPro; IPR003597; IG\_MHC.  
DR InterPro; IPR003597; IG\_MHC.  
DR Pfam; PF07654; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
FT NON TER  
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217C41 CRC64;  
Query Match 78.2%; Score 480; DB 2; Length 478;  
Best Local Similarity 77.4%; Pred. No. 3.5e-41;  
Matches 89; Conservative 14; Mismatches 10; Indels 2; Gaps 1;

QY 2 ESGPGLVPSQTLSTLTCTVSGGSIIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSL 61  
DB 24 ESGPGLVPSQTLSTLTCTVSGGSIIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSL 83  
QY 62 KSRVTMSVDSKXHFSLRLSSVTADTAAYVYCARSDGVTLDNMGCGTLVTWSS 114  
DB 84 ESRVLSIDTSKQFSLRLSSVTADTAAYVYCARSDGVTLDNMGCGTLVTWSS 138

RESULT 4  
Q9UL73 PRELIMINARY; PRT; 119 AA.  
ID Q9UL73  
AC Q9UL73  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98271139; PubMed=9614934; DOI=10.1006/cjlin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Betney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035041; AAD56277.1; -.  
 DR PIR; PH0876; PH0876.  
 DR PIR; S12416; S12416.  
 DR HSSP; P01820; 1G7J.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV\_1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 FT NON\_TER 1  
 FT TER 1  
 SQ SEQUENCE 119 AA; 13219 MM; 1BDB86B6420EAOBE CRC64;

Query Match 76.6%; Score 470.5; DB 2; Length 119;  
 Best Local Similarity 79.3%; Pred. No. 7.4e-41;  
 Matches 92; Conservative 8; Mismatches 11; Indels 5; Gaps 2;

OY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGYIHSGNTYNSPL 61  
 DB 6 ESGPGLVPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGYIHSGNTYNSPL 63  
 OY 62 KSRVTSVDTSKNHFSLRLSSVTADTAVYYCAR---SDGYTLDMWGQGLTVTSS 114  
 DB 64 KSRVTSVDTSKNHFSLRLSSVTADTAVYYCAR---SDGYTLDMWGQGLTVTSS 119

RESULT 5  
 Q72374 PRELIMINARY; PRT; 492 AA.  
 AC Q72374;  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Hypothetical protein DKFZp686C02218 (Fragment).  
 GN Name=DKFZp686C02218;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human rectum tumor;  
 RA Bloeker H., Boeher M., Mewes H.W., Well B., Amd C., Oeanger A.,  
 RA Rob G., Han M., Wiemann S.;  
 RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BX538077; CAD98001.1; -.  
 DR HSSP; P01820; 1G7J.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; CL-sect; 2.  
 DR SMART; SM00406; IGV\_1.  
 DR PROSITE; PS50835; IG-LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 FT TER 1  
 SQ SEQUENCE 492 AA; 53776 MM; 1E7A15760FOCA74B CRC64;

Query Match 76.5%; Score 469.5; DB 2; Length 492;  
 Best Local Similarity 76.9%; Pred. No. 4.4e-40;  
 Matches 90; Conservative 10; Mismatches 12; Indels 5; Gaps 2;

OY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGYIHSGNTYNSPL 61  
 DB 37 ESGPGLVPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGYIHSGNTYNSPL 96  
 OY 62 KSRVTSVDTSKNHFSLRLSSVTADTAVYYCAR---SDGYTLDMWGQGLTVTSS 114  
 DB 97 KSRVTSVDTSKNHFSLRLSSVTADTAVYYCAR---SDGYTLDMWGQGLTVTSS 152

RESULT 6  
 Q6GKX7 PRELIMINARY; PRT; 477 AA.  
 AC Q6GKX7;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Deris J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marisica K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stadler M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Topolycki S., Carninci P., Pange C.,  
 RA Rana S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.U., McKernan K.U., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulty S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.B., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BC073765; AAH73765.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; CL-sect; 2.  
 DR SMART; SM00407; IGV\_3.  
 DR SMART; SM00409; IGV\_4.  
 DR SMART; SM00407; IGV\_3.  
 DR SMART; SM00406; IGV\_1.  
 DR PROSITE; PS50835; IG-LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 FT TER 1  
 SQ SEQUENCE 477 AA; 51631 MM; 9FB59C09C50CF85 CRC64;

Query Match 76.4%; Score 469; DB 2; Length 477;  
 Best Local Similarity 80.0%; Pred. No. 4.8e-40;  
 Matches 92; Conservative 6; Mismatches 13; Indels 4; Gaps 2;

OY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGYIHSGNTYNSPL 61  
 DB 25 ESGPGLVPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGYIHSGNTYNSPL 82

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Qy      62 KSRVTMSVDTSKNHFSLRLSSVTADTAVVYCCASDGG--YTLDNWGQGLTVTVSS 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      83 KSRVTLSLDTSKNPFSLRLNSVTADTAVVYCAHGGSSWDFADYWGQGLTVTVSS 137

RESULT 7
ID      095973      PRELIMINARY;      PRT;      150 AA.
AC      095973;
DT      01-MAY-1999 (TRENBLrel. 10, Created)
DT      01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT      01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE      VH4 heavy chain variable region precursor (fragment).
DN      Name=IGM;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RL      Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF103795; AAC79084.1; -.
DR      PIR; S31673; S31673.
DR      HSSP; P01820; S78056.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003596; IG_v.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Signal.
FT      SIGNAL      1      19      Potential.
FT      CHAIN      20      >150      VH4 heavy chain variable region.
FT      NON_TER      150      150
SQ      SEQUENCE      150 AA; 16315 MW; 8566404938AA7C9 CRC64;

Query Match      76.2%; Score 468; DB 2; Length 150;
Best Local Similarity 78.8%; Pred. No. 1.7e-40;
Matches 89; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy      2 ESGGGLVKSQTLSTCTVSGSGSIRSGGYWMTROPKGLKEMIGYIHSGNTYPSL 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      25 ESGGGLVKSQTLSTCTVSGSGSISSTNYWGMROPEKGLKEMIGSLHNSGSDVPSL 84

Qy      62 KSRVTMSVDTSKNHFSLRLSSVTADTAVVYCCASDGGTTLDNWGQGLTVTVSS 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      85 KSRVTISVDTSKNPFSLRLNSVTADTAVVYCAHGGSSWDFADYWGQGLTVTVSS 137

RESULT 8
ID      096KX8      PRELIMINARY;      PRT;      496 AA.
AC      096KX8;
DT      01-DEC-2001 (TRENBLrel. 19, Created)
DT      01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT      01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE      MGC27165 protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Tissue=Lung;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein W.J., Ueudin T.B., Toshlyuki S., Carninci P., Prange C.,
RA      Brownstein W.J., Ueudin T.B., Toshlyuki S., Carninci P., Prange C.,

Qy      62 KSRVTMSVDTSKNHFSLRLSSVTADTAVVYCCASDGGTTLDNWGQGLTVTVSS 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      85 KSRVTISVDTSKNPFSLRLNSVTADTAVVYCAHGGSSWDFADYWGQGLTVTVSS 137

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RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Maiz M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Tissue=Lung;
RX      Strausberg R.;
RL      Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC016369; AAH16369.1; -.
DR      HSSP; P01876; IOW0.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003597; IG_c1.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; Pf07654; CI-sec; 2.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ      SEQUENCE      496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match      74.9%; Score 460; DB 2; Length 496;
Best Local Similarity 75.0%; Pred. No. 4.3e-39;
Matches 90; Conservative 8; Mismatches 14; Indels 8; Gaps 2;

Qy      2 ESGGGLVKSQTLSTCTVSGSGSIRSGGYWMTROPKGLKEMIGYIHSGNTYPSL 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      25 ESGGGLVKSQTLSTCTVSGSGSISSTNYWGMROPEKGLKEMIGYIHSGNTYPSL 84

Qy      62 KSRVTMSVDTSKNHFSLRLSSVTADTAVVYCCASDGGTTLDNWGQGLTVTVSS 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      85 KSRVTISVDTSKNPFSLRLNSVTADTAVVYCAHGGSSWDFADYWGQGLTVTVSS 143

RESULT 9
ID      096EY0      PRELIMINARY;      PRT;      620 AA.
AC      096EY0;
DT      01-DEC-2001 (TRENBLrel. 19, Created)
DT      01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT      01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE      IGHM protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Tissue=Primary B-Cells;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein W.J., Ueudin T.B., Toshlyuki S., Carninci P., Prange C.,
RA      Brownstein W.J., Ueudin T.B., Toshlyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smalhus D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011857; AAH11857.2; -.  
DR PIR; S15590; S15590.  
DR HSSP; P01820; 1G7J.  
DR InterPro; IPR003599; 1G.  
DR InterPro; IPR007110; 1G-1like.  
DR InterPro; IPR003597; 1G-cl.  
DR InterPro; IPR003596; 1G-v.  
DR Pfam; PF07654; C1-set; 4.  
DR SMART; SM00409; 1G; 2.  
DR SMART; SM00407; 1Gcl; 4.  
DR SMART; SM00406; 1Gv; 1.  
DR PROSITE; PS50835; 1G-LIKE; 5.  
DR PROSITE; PS00290; 1G-MHC; UNKNOWN 3.  
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FE27B CRC64;  
  
Query Match 74.9%; Score 460; DB 2; Length 620;  
Best Local Similarity 80.5%; Pred. No. 5.5e-39;  
Matches 95; Conservative 4; Mismatches 11; Indels 8; Gaps 3;  
  
Qy 2 ESGGLVPSQTLSTCTVSGSGSIRSGGYWMSWIRPGKGLMIGVYHSGNTYNSL 61  
Db 32 ESGGLVPSQTLSTCTVSGSGSIS--YMSWIRPGKGLMIGVYHSGNTYNSL 89  
Qy 62 KSRVYMSVDSKMFSLRLSSVTADTAVYVCARSDGYTLDN-----WGQGLTVTVSS 114  
Db 90 KSRVYMSVDSKMFSLRLSSVTADTAVYVCARSDGYTLDN-----WGQGLTVTVSS 146  
  
RESULT 10  
Q6P418 PRELIMINARY; PRT; 576 AA.  
ID Q6P418; PRELIMINARY; PRT; 576 AA.  
AC Q6P418;  
DT 05-JUN-2004 (TREMBLrel. 27, Created)  
DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)  
DE IGHG protein.  
GN Name=IGHG;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smalhus D.E., Scherch A., Schein J.E.,

RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC063384; AAH63384.1; -.  
DR HSSP; P01820; 1A7N.  
DR InterPro; IPR003599; 1G.  
DR InterPro; IPR007110; 1G-1like.  
DR InterPro; IPR003597; 1G-cl.  
DR InterPro; IPR003596; 1G-MHC.  
DR InterPro; IPR003596; 1G-v.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00409; 1G; 1.  
DR SMART; SM00407; 1Gcl; 3.  
DR SMART; SM00406; 1Gv; 1.  
DR PROSITE; PS50835; 1G-LIKE; 4.  
DR PROSITE; PS00290; 1G-MHC; UNKNOWN 2.  
SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;  
  
Query Match 73.6%; Score 452; DB 2; Length 576;  
Best Local Similarity 77.6%; Pred. No. 3.4e-38;  
Matches 90; Conservative 6; Mismatches 16; Indels 4; Gaps 2;  
  
Qy 2 ESGGLVPSQTLSTCTVSGSGSIRSGGYWMSWIRPGKGLMIGVYHSGNTYNSL 61  
Db 32 ESGGLVPSQTLSTCTVSGSGSIS--YMSWIRPGKGLMIGVYHSGNTYNSL 90  
Qy 62 KSRVYMSVDSKMFSLRLSSVTADTAVYVCARSDGYTLDN-----YTLDNMGQTLTVSS 114  
Db 91 KSRVYMSVDSKMFSLRLSSVTADTAVYVCARSDGYTLDN-----YTLDNMGQTLTVSS 146  
  
RESULT 11  
Q6SXX2 PRELIMINARY; PRT; 139 AA.  
ID Q6SXX2; PRELIMINARY; PRT; 139 AA.  
AC Q6SXX2;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Full-length cDNA clone CSDDL004YML9 of B cells (Ramos cell line) of  
DE Homo sapiens (human) (fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B cells;  
RA Li W.B., Gruber C., Jeesee J., Polayes D.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B cells;  
RA Genoscope;  
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX248300; CAD62627.1; -.  
DR HSSP; P01820; 1G7J.  
DR InterPro; IPR007110; 1G-1like.  
DR InterPro; IPR003597; 1G-cl.  
DR SMART; SM00406; 1Gv; 1.  
DR PROSITE; PS50835; 1G-LIKE; 1.  
FT NON TER 1  
SQ SEQUENCE 139 AA; 15573 MW; 7D1E202410B4F8C CRC64;  
  
Query Match 71.8%; Score 441; DB 2; Length 139;  
Best Local Similarity 89.4%; Pred. No. 9.9e-38;  
Matches 84; Conservative 5; Mismatches 3; Indels 2; Gaps 1;

```

QY      2  ESGPGLVKSQTLSTCTVSGSGSIRSGGYWMIROPKGLKLEWIGYIHSGNTYNSPL 61
DB      38  ESGPGLVKSQTLSTCTVSGSGSIS--YYWMIROPKGLKLEWIGYIHSGNTYNSPL 95
QY      62  KSRVTMSVDTSKNHFSLRLSSVTADPAVYCAR 95
DB      96  KSRVTISVDTSKNPFSLKSSVTADPAVYCAR 129

RESULT 12
HV2F HUMAN
ID      HV2F HUMAN      STANDARD;      PRT;      129 AA.
AC      P01824;
DT      21-JUL-1986 (Rel. 01, Created)
DT      05-JUL-1986 (Rel. 01, Last sequence update)
DE      IG heavy chain V-II region WAH.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=8222235; PubMed=6806818;
RA      Takahashi N., Tetaert D., Deboutte B., Lin L.-C., Putnam F.W.;
RT      "Complete amino acid sequence of the delta heavy chain of human
RT      immunoglobulin D.";
RL      Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854 (1982).
CC      -1- MSCELANEOUS: This chain was isolated from an Igd myeloma
CC      protein.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR      PIR; A02099; D2HWA.
DR      HSSP; P01820; 1G7J.
DR      GlycoSuiteDB; P01824; -.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0003823; F:antigen binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      InterPro; IPR007110; Ig-like.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; Igv; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Direct protein sequencing; Immunoglobulin V region.
FT      DOMAIN 1 113
FT      NON TER 129
SQ      SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match      71.6%; Score 439.5; DB 1; Length 129;
Best Local Similarity 66.7%; Pred. No. 1.3e-37;
Matches 84; Conservative 12; Mismatches 15; Indels 15; Gaps 2;

QY      2  ESGPGLVKSQTLSTCTVSGSGSIRSGGYWMIROPKGLKLEWIGYIHSGNTYNSPL 61
DB      6  ESGPGLVKSQTLSTCTVSGSGSIRSGGYWMIROPKGLKLEWIGYIHSGNTYNSPL 65
QY      62  KSRVTMSVDTSKNHFSLRLSSVTADPAVYCAR-----SDGYTLDNWGQGT 108
DB      66  RGRVTISVDTSKNPFSLKSSVTADPAVYCAR-----IDVWGQGT 123
QY      109  LVTYSS 114
DB      124  TVHVS 129

RESULT 13
Q81ZD7
ID      Q81ZD7      PRELIMINARY;      PRT;      130 AA.
AC      Q81ZD7;
DT      01-MAR-2003 (TREMBlrel. 23, Created)
DT      01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE      Anti-choyroglobulin heavy chain variable region (Fragment).

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OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Jiang Y.-J., Chung J., Park J.-Y.;
RL      Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AY145445; AAN64329.1; -.
DR      HSSP; P01820; 1G7J.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Igv.
DR      SMART; SM00406; Igv; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
FT      NON TER 1
FT      NON TER 130
SQ      SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match      70.2%; Score 431; DB 2; Length 130;
Best Local Similarity 71.2%; Pred. No. 1e-36;
Matches 89; Conservative 8; Mismatches 16; Indels 12; Gaps 4;

QY      2  ESGPGLVKSQTLSTCTVSGSGSIRSGGYWMIROPKGLKLEWIGYIHSGNT-----Y 56
DB      6  QSGPGLVKSQTLSTCTVSGSGSISSSSYWMIROPKGLKLEWIGYIHSGNTSPY 65
QY      57  YNPSLKSRVTMSVDTSKNHFSLRLSSVTADPAVYCAR---SDG--YT-LDNWGQGT 109
DB      66  YAPFLSRVTISVDTSKNQLSLRLSSVTADPAVYCARPTHCGGGCAAFQWGGQFL 125
QY      110  VTYSS 114
DB      126  TVVSS 130

RESULT 14
Q8WUX4
ID      Q8WUX4      PRELIMINARY;      PRT;      595 AA.
AC      Q8WUX4;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lymph;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.;
RA      Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA      Datchenko L., Marulita K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Uebin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Lottuliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smalins D.B., Schermer A., Schein J.E.,
RA      Jones S.J., Maira M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN      [2]
RP      SEQUENCE FROM N.A.

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RC TISSUE=Lymph;  
RA Strauberg R.;  
RL Submitted (BEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC019235; AAH19235.2; -.  
DR PIR; G34964; G34964.  
DR HSSP; P01861; 1ADQ.  
DR Pfam; PF07654; CI-sec; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Hypothetical protein.  
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;  
  
Query Match 70.0%; Score 429.5; DB 2; Length 595;  
Best Local Similarity 72.5%; Pred. No. 7.6e-36;  
Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;  
  
QY 4 GPGIVKPSQTLSTLCYVSGSIRSGYVSWIRPPGKGLKLEIGIYHSGNTYVNPISKS 63  
DB 34 GAGLLKPSSETLSTLCGYVGSF--SGYVSWIRPPGKGLKLEIGIYHSGNTYVNPISKS 91  
QY 64 RVTWSVDTSKNHFSLRLSSVTAADTAVYYCAR-----SDG-YTLDMNCGGLTVYSS 114  
DB 92 RVTISVDTSKKQSLKLSVNAADTAVYYCARVITRASPGTDGRYGMVWCGTIVYSS 151  
  
RESULT 15  
06GKM5 PRELIMINARY; PRT; 597 AA.  
AC 06GKM5;  
DT 05-JUL-2004 (TREMblrel. 27, Created)  
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RS TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rata S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.B.,  
RA Jones S.J., Maira M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RS TISSUE=Lymph;  
RA Strauberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073767; AAH73767.1; -.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG\_LIKE.  
DR InterPro; IPR003597; IG\_cl.

DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; CI-sec; 4.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;  
  
Query Match 70.0%; Score 429.5; DB 2; Length 597;  
Best Local Similarity 72.5%; Pred. No. 7.6e-36;  
Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;  
  
QY 4 GPGIVKPSQTLSTLCYVSGSIRSGYVSWIRPPGKGLKLEIGIYHSGNTYVNPISKS 63  
DB 27 GAGLLKPSSETLSTLCGYVGSF--SGYVSWIRPPGKGLKLEIGIYHSGNTYVNPISKS 84  
QY 64 RVTWSVDTSKNHFSLRLSSVTAADTAVYYCAR-----SDG-YTLDMNCGGLTVYSS 114  
DB 85 RVTISVDTSKKQSLKLSVNAADTAVYYCARVITRASPGTDGRYGMVWCGTIVYSS 144  
  
Search completed: July 26, 2005, 09:26:19  
Job time : 72.6818 secs

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PT diagnosing or passive immunotherapy of type I allergy, for environmental  
XX allergen detection.  
XX  
PS Disclosure; Page 38; 45pp; English.  
XX  
CC This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE Fabs and methods for their use. The proteins  
CC of the invention may have anti-allergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE  
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific Fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The Fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific Fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergic patients  
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
CC Fab, clone 100 heavy chain protein of the invention  
CC  
XX Sequence 114 AA;  
SQ

Query Match 98.5%; Score 605; DB 5; Length 114;  
Best Local Similarity 99.1%; Pred. No. 3.4e-44;  
Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTLCTVSGGSIKSGGYWMSWIRPPGKLEWIGYIHSGNTYVNS 60  
1 LESGPGLVKPSQTLSTLCTVSGGSIKSGGYWMSWIRPPGKLEWIGYIHSGNTYVNS 60  
DB 1 LESGPGLVKPSQTLSTLCTVSGGSIKSGGYWMSWIRPPGKLEWIGYIHSGNTYVNS 60  
QY 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAAYYCARSDGYTLDMNGQGLTVTVSS 114  
61 LKSRVTMSVDTSKNHFSLRLSVTAADTAAYYCARSDGYTLDMNGQGLTVTVSS 114  
DB 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAAYYCARSDGYTLDMNGQGLTVTVSS 114

RESULT 2  
ABG30446  
ID ABG30446 standard; protein; 114 AA.  
XX  
AC ABG30446;  
XX  
XX 21-OCT-2002 (first entry)  
XX  
DE Human IgE Fab clone 60 heavy chain protein.  
XX  
KM Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;  
KW timothy grass pollen allergen; passive immunotherapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH Region 1..26  
FT /note= "FR1 region"  
FT 27..33  
FT /note= "CDR1 region"  
FT 34..47  
FT /note= "FR2 region"  
FT 48..63  
FT /note= "CDR2 protein"  
FT 64..95  
FT /note= "FR3 region"  
FT 96..103  
FT /note= "CDR2 region"  
FT 104..114  
FT /note= "FR4 region"  
XX  
PN WO200253595-A1.  
XX  
PD 11-JUL-2002.  
XX  
PE 27-DEC-2001; 2001WO-SE002908.  
XX

PR 29-DEC-2000; 2000SE-00004892.  
XX  
XX (PHEA ) PHARMACIA DIAGNOSTICS AB.  
XX  
PI Flicker S, Steindberger P, Kraft D, Valenta R;  
XX  
XX WPI, 2002-583604/62.  
DR N-PSDB; ABK89638.  
XX  
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
XX variable region of group 2 allergen specific-human IgE Fabs, useful for  
PT diagnosing or passive immunotherapy of type I allergy, for environmental  
PT allergen detection.  
XX  
XX Disclosure; Page 37; 45pp; English.  
XX  
XX  
CC This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE Fabs and methods for their use. The proteins  
CC of the invention may have anti-allergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE  
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific Fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The Fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific Fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergic patients  
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
CC Fab, clone 60 heavy chain protein of the invention  
CC  
XX Sequence 114 AA;  
SQ

Query Match 97.7%; Score 600; DB 5; Length 114;  
Best Local Similarity 96.5%; Pred. No. 9.1e-44;  
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTLCTVSGGSIKSGGYWMSWIRPPGKLEWIGYIHSGNTYVNS 60  
1 LESGPGLVKPSQTLSTLCTVSGGSIKSGGYWMSWIRPPGKLEWIGYIHSGNTYVNS 60  
DB 1 LESGPGLVKPSQTLSTLCTVSGGSIKSGGYWMSWIRPPGKLEWIGYIHSGNTYVNS 60  
QY 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAAYYCARSDGYTLDMNGQGLTVTVSS 114  
61 LKSRVTMSVDTSKNHFSLRLSVTAADTAAYYCARSDGYTLDMNGQGLTVTVSS 114  
DB 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAAYYCARSDGYTLDMNGQGLTVTVSS 114

RESULT 3  
ABG30445  
ID ABG30445 standard; protein; 114 AA.  
XX  
AC ABG30445;  
XX  
XX 21-OCT-2002 (first entry)  
XX  
DE Human IgE Fab clone 94 heavy chain protein.  
XX  
KM Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;  
KW timothy grass pollen allergen; passive immunotherapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH Region 1..26  
FT /note= "FR1 region"  
FT 27..33  
FT /note= "CDR1 region"  
FT 34..47  
FT /note= "FR2 region"  
FT 48..63  
FT /note= "CDR2 protein"  
FT 64..95  
FT /note= "FR3 region"  
FT  
FT Region

FT	Region	96..103
PT	/note= "CDR2 region"	
FT	Region	104..114
FT	/note= "FRA region"	
XX		
XX	WO200253595-A1.	
PD		
PD	11-JUL-2002.	
XX		
XX	27-DEC-2001; 2001WO-SE002908.	
XX		
XX	29-DEC-2000; 2000SE-00004892.	
XX		
PA	(PHAA ) PHARMACIA DIAGNOSTICS AB.	
PI	Flicker S, Steiberger P, Kraft D, Valenta R;	
DR	WPI; 2002-583604/62.	
DR	N-PADB; ABR89637.	
XX		
XX	Disclosure; Page 36; 45pp; English.	
CC	This invention relates to the DNA and protein sequences of group 2	
CC	allergen-specific human IgE Fabs and methods for their use. The proteins	
CC	of the invention may have antiallergic activities and may be used as a	
CC	vaccine or an inhibitor of binding of grass pollen allergen patient's IgE	
CC	antibodies to Phl p 2 (a major Timothy grass pollen allergen). The group	
CC	2 allergen-specific fads of the invention may be useful for environmental	
CC	allergen detection and for standardisation of allergen extracts. The fads	
CC	- or a vaccine against a type I allergy is useful for passive	
CC	immunotherapy of type I allergy, it is also useful for diagnosing a type	
CC	I allergy. The allergen-specific fads of the invention are useful for	
CC	inter alia, diagnosis, therapy and prevention of type I allergy. They are	
CC	also useful for identification of group 2 allergen-containing pollen and	
CC	may be used for blocking the binding of grass pollen allergic patients	
CC	IgE antibodies to Phl p 2. The present sequence represents the human IgG	
CC	fab, clone 94 heavy chain protein of the invention	
XX		
SQ	Sequence 114 AA;	
	Query Match 90.6%; Score 556; DB 5; Length 114;	
	Best Local Similarity 90.4%; Pred. No. 5.3e-40;	
	Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0	
OY	1 LESGPGLVPSQTLSLTCTVSGSIRSGGYWSMIRDPKGLEIMIGIYHSGNTYYNS 60	
DB	1 LESGPGLVPSQTLSLTCSAVSGSIRSGGYWSMIRDPKGLEIMIGIYHSGNTYYNS 60	
OY	61 LKSRYTMSVDTSKNHPSTRLSSVTADPRTVVCASDGTLLDNNGCGLTVTYSS 114	
DB	61 LKSRIAMSVDTSKNKFSRLINSVTADPRTVVCARDLDTLLDWGGTLTVTYSS 114	
ID	ADP03982 standard; protein; 121 AA.	
XX	ADP03982;	
XX		
DT	29-JUL-2004 (first entry)	
DE	Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 152.	
XX		
KW	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;	
KW	cystostatic; colorectal neoplasia; renal cell carcinoma;	
KW	cervical intraepithelial squamous neoplasia;	
KW	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;	
KW	gene therapy; murine; mouse; human; heavy chain variable domain.	

[illegible]

XX 02-DEC-2002; 2002WO-US038550.  
PF 03-DEC-2001; 2001US-0337275P.  
XX (ABGE-) ABGENIX INC.  
PA Gudas J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
XX Example 2; SEQ ID NO 138; 89pp; English.  
XX  
XX The invention relates to a novel isolated monoclonal antibody (mab)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cyostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
SQ Sequence 118 AA;  
Query Match 85.3%; Score 524; DB 7; Length 118;  
Best Local Similarity 88.5%; Pred. No. 3e-37;  
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;  
Qy 2 ESGGGLVKEPSQTLSTCTVSGSGSIRSGGYWMSWIRPGKGLWIGYIHSGNTYNPSTL 61  
Db 6 ESGGGLVKEPSQTLSTCTVSGSGSIRSGGYWMSWIRPGKGLWIGYIHSGNTYNPSTL 65  
Qy 62 KSRVTMSVDSKKNFSLRLSSVTAADTAAYVYCARSDGTYLDMWGQGLTVTVSS 114  
Db 66 KSRVTISVDSKKNFSLRLSSVTAADTAAYVYCARSDGTYLDMWGQGLTVTVSS 118  
RESULT 6  
ADP03870 ID ADP03870 standard; protein; 123 AA.  
XX  
AC ADP03870;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DB Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.  
XX  
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cyostatic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
XX Unidentified.  
OS  
XX WO2003048328-A2.  
XX  
XX 12-JUN-2003.  
XX  
XX 02-DEC-2002; 2002WO-US038550.  
XX  
XX 03-DEC-2001; 2001US-0337275P.  
XX  
XX (ABGE-) ABGENIX INC.  
PA

XX Gudas J, Foltz I, Handa M, Gallo M;  
PI WPI; 2003-523295/49.  
XX  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
XX Claim 1; SEQ ID NO 10; 89pp; English.  
XX  
XX The invention relates to a novel isolated monoclonal antibody (mab)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cyostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
SQ Sequence 123 AA;  
Query Match 85.3%; Score 523.5; DB 7; Length 123;  
Best Local Similarity 85.6%; Pred. No. 3.4e-37;  
Matches 101; Conservative 5; Mismatches 7; Indels 5; Gaps 1;  
Qy 2 ESGGGLVKEPSQTLSTCTVSGSGSIRSGGYWMSWIRPGKGLWIGYIHSGNTYNPSTL 61  
Db 6 ESGGGLVKEPSQTLSTCTVSGSGSIRSGGYWMSWIRPGKGLWIGYIHSGNTYNPSTL 65  
Qy 62 KSRVTMSVDSKKNFSLRLSSVTAADTAAYVYCARSDGTYLDMWGQGLTVTVSS 114  
Db 66 KSRVTISVDSKKNFSLRLSSVTAADTAAYVYCARSDGTYLDMWGQGLTVTVSS 123  
RESULT 7  
ADP03974 ID ADP03974 standard; protein; 120 AA.  
XX  
AC ADP03974;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DB Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.  
XX  
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cyostatic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
XX Unidentified.  
OS  
XX WO2003048328-A2.  
XX  
XX 12-JUN-2003.  
XX  
XX 02-DEC-2002; 2002WO-US038550.  
XX  
XX 03-DEC-2001; 2001US-0337275P.  
XX  
XX (ABGE-) ABGENIX INC.  
PA Gudas J, Foltz I, Handa M, Gallo M;  
PI WPI; 2003-523295/49.  
XX  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT



PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
PS Example 2; SEQ ID NO 144; 89pp; English.  
XX  
CC The invention relates to a novel isolated monoclonal antibody (mab)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
CC  
SQ Sequence 120 AA;  
XX  
Query Match 84.9%; Score 521; DB 7; Length 120;  
Best Local Similarity 87.1%; Pred. No. 5.5e-37;  
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;  
QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRQPGKLEWIGYTHSGNTYYNPSL 61  
DB 6 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRQPGKLEWIGYTHSGNTYYNPSL 65  
QY 62 KSRVTMSVDYTSKNHFSRLSSVTADTAIVYYCARSDGYT--LDNMGGGTLVTYSS 114  
DB 66 KSRVTISVDTSKNQFSLKLSVTADTAIVYYCAR-DGYNVYVFDLMGRGTLVTYSS 120  
Db  
QY 62 KSRVTMSVDYTSKNHFSRLSSVTADTAIVYYCARSDGYT--LDNMGGGTLVTYSS 114  
DB 66 KSRVTISVDTSKNQFSLKLSVTADTAIVYYCAR-DGYNVYVFDLMGRGTLVTYSS 120  
Db  
RESULT 8  
ADP03873  
ID ADP03873 standard; protein; 120 AA.  
XX  
AC ADP03873;  
XX  
DT 29-JUN-2004 (first entry)  
XX  
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.  
XX  
KM monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KM cytosstatic; colorectal neoplasm; renal cell carcinoma;  
KM cervical intraepithelial squamous neoplasia;  
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KM gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
OS Unidentified.  
XX  
PN WO2003048328-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 02-DEC-2002; 2002WO-US038550.  
XX  
PR 03-DEC-2001; 2001US-0337275P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J, Foltz I, Handa M, Gallo M;  
XX  
DR WPI; 2003-523295/49.  
XX  
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
PS Claim 1; SEQ ID NO 13; 89pp; English.  
XX  
CC The invention relates to a novel isolated monoclonal antibody (mab)

CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
CC  
SQ Sequence 120 AA;  
XX  
Query Match 84.9%; Score 521; DB 7; Length 120;  
Best Local Similarity 87.1%; Pred. No. 5.5e-37;  
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;  
QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRQPGKLEWIGYTHSGNTYYNPSL 61  
DB 6 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRQPGKLEWIGYTHSGNTYYNPSL 65  
QY 62 KSRVTMSVDYTSKNHFSRLSSVTADTAIVYYCARSDGYT--LDNMGGGTLVTYSS 114  
DB 66 KSRVTISVDTSKNQFSLKLSVTADTAIVYYCAR-DGYNVYVFDLMGRGTLVTYSS 120  
Db  
RESULT 9  
ADP03977  
ID ADP03977 standard; protein; 122 AA.  
XX  
AC ADP03977;  
XX  
DT 29-JUN-2004 (first entry)  
XX  
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.  
XX  
KM monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KM cytosstatic; colorectal neoplasm; renal cell carcinoma;  
KM cervical intraepithelial squamous neoplasia;  
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KM gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
OS Unidentified.  
XX  
PN WO2003048328-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 02-DEC-2002; 2002WO-US038550.  
XX  
PR 03-DEC-2001; 2001US-0337275P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J, Foltz I, Handa M, Gallo M;  
XX  
DR WPI; 2003-523295/49.  
XX  
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
PS Example 2; SEQ ID NO 147; 89pp; English.  
XX  
CC The invention relates to a novel isolated monoclonal antibody (mab)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,

CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
SQ Sequence 122 AA;  
  
Query Match 84.9%; Score 521; DB 7; Length 122;  
Best Local Similarity 85.5%; Pred. No. 5,6e-37;  
Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;  
  
QY 2 ESGGGLVKEPQTLSTCTVSGSGSIRSGYWSWIRPPGKLEWIGYIHSGNTYNPSTL 61  
DB 6 ESGGGLVKEPQTLSTCTVSGSGSIRSGYWSWIRPPGKLEWIGYIHSGNTYNPSTL 65  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCAR-----SDGYTLDMNGOGTLVTYSS 114  
DB 66 KSRVTISVDTSKNHFSLRLSSVTADTAVYYCARGDYDILTGYGMDVWGQGITVTYSS 122  
  
RESULT 10  
AAB36206  
ID AAB36206 standard; protein; 473 AA.  
XX  
AC AAB36206;  
XX  
DT 15-FEB-2001 (first entry)  
XX  
DE Human immune system associated protein HISAP-4.  
XX  
KW Human; immune system associated protein; HISAP-4; immune disorder;  
KM infection; autoimmune disease; cancer.  
XX  
OS Homo sapiens.  
XX  
PN US6135941-A.  
XX  
PD 24-OCT-2000.  
XX  
PF 27-MAR-1998; 98US-00049672.  
XX  
PR 27-MAR-1998; 98US-00049672.  
XX  
PA (INCY-) INCYTE PHARM INC.  
XX  
PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;  
PI Hillman JL, Au-Young J;  
DR WPI; 2001-030926/04.  
DR N-PSDB; AAC66522.  
XX  
PT New human immune system associated proteins (HISAP) and polynucleotides  
PT encoding the HISAP, useful for diagnosing, treating or preventing immune  
PT or cell proliferative disorders or infections.  
XX  
PS Claim 1; Col 53-56; 54pp; English.  
XX  
CC The present invention provides the coding and protein sequences for a  
CC number of human immune system associated proteins (HISAPs). These can be  
CC used in the diagnosis and treatment of various autoimmune disorders,  
CC infections and cell proliferation diseases. The diseases include AIDS,  
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,  
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia  
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus  
CC erythematosus, arteriosclerosis, cirrhosis and cancer  
XX  
SQ Sequence 473 AA;  
  
Query Match 84.9%; Score 521; DB 4; Length 473;  
Best Local Similarity 83.2%; Pred. No. 2.3e-36;  
Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

QY 2 ESGGGLVKEPQTLSTCTVSGSGSIRSGYWSWIRPPGKLEWIGYIHSGNTYNPSTL 61  
DB 25 ESGGGLVKEPQTLSTCTVSGSGSIRSGYWSWIRPPGKLEWIGYIHSGNTYNPSTL 84  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSD-----GYTLDMNGOGTLVTYSS 114  
DB 85 KSRVTISVDTSKNHFSLRLSSVTADTAVYYCARDDVGLRGANYGMDVWGQGITVTYSS 143  
  
RESULT 11  
ADJ32126  
ID ADJ32126 standard; protein; 221 AA.  
XX  
AC ADJ32126;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Human interferon-gamma antibody heavy chain amino acid sequence SeqID80.  
XX  
KW antibody; antigen binding domain; interferon-gamma; INF-gamma;  
KM antagonist antibody; antiinflammatory; immunosuppressive;  
KM autoimmune disease; inflammatory condition; human; heavy chain.  
XX  
OS Homo sapiens.  
XX  
PN US2003099647-A1.  
XX  
PD 29-MAY-2003.  
XX  
PF 05-OCT-2001; 2001US-00972656.  
XX  
PR 05-OCT-2001; 2001US-00972656.  
XX  
PA (DESH/) DESHPANDE R V.  
PA (TSAI/) TSAI M.  
XX  
PI Deshpande RV, Tsai M;  
PI WPI; 2003-696068/66.  
DR N-PSDB; ADJ32125.  
XX  
PT New antibody or antigen binding domain, or its fragment, variant or  
PT derivative, which binds to an interferon-gamma protein, useful for  
PT preparing a composition for preventing or treating inflammatory or  
PT autoimmune disorders.  
XX  
PS Claim 10; SEQ ID NO 80; 113pp; English.  
XX  
CC This invention relates to a novel antibody or antigen binding domain, or  
CC its fragment, variant or derivative, which binds to an interferon-gamma  
CC (INF-gamma) protein, and is an antagonist antibody. The invention may be  
CC useful for the development of compounds with an antiinflammatory or  
CC immunosuppressive activity through action as interferon-gamma agonists. A  
CC composition containing the antibody is useful for preventing or treating  
CC an autoimmune disease and an inflammatory condition. The present sequence  
CC is that of an antibody heavy chain of a human IFN-gamma antibody which  
CC may be part of the invention.  
XX  
SQ Sequence 221 AA;  
  
Query Match 84.7%; Score 520; DB 7; Length 221;  
Best Local Similarity 86.7%; Pred. No. 1.3e-36;  
Matches 98; Conservative 4; Mismatches 11; Indels 0; Gaps 0;  
  
QY 2 ESGGGLVKEPQTLSTCTVSGSGSIRSGYWSWIRPPGKLEWIGYIHSGNTYNPSTL 61  
DB 6 ESGGGLVKEPQTLSTCTVSGSGSIRSGYWSWIRPPGKLEWIGYIHSGNTYNPSTL 65  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGYTLDMNGOGTLVTYSS 114  
DB 66 KSRVTISVDTSKNHFSLRLSSVTADTAVYYCARGDYDILTGYGMDVWGQGITVTYSS 118

RESULT 12  
ADP03981  
ID ADP03981 standard; protein, 121 AA.  
XX  
AC ADP03981;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 151.  
XX  
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
OS Unidentified.  
XX  
PN MO2003048328-A2.  
XX  
PD 12-JUN-2003.  
XX  
PP 02-DEC-2002; 2002WO-US038550.  
XX  
PR 03-DEC-2001; 2001US-0337275P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J, Foltz I, Handa M, Gallo M;  
XX  
DR WPI; 2003-523295/49.  
XX  
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
PS Example 2; SEQ ID NO 151; 89pp; English.  
XX  
CC The invention relates to a novel isolated monoclonal antibody (mAb)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
SQ Sequence 121 AA;  
XX  
Query Match 84.6%; Score 519.5; DB 7; Length 121;  
Best Local Similarity 86.2%; Pred. No. 7.4e-37;  
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;  
XX  
QY 2 ESGPGLVPSQTLSTLTCTVSGSIRSGGYMSWIRQPGKLEWIGYTHSGNTYNNPSL 61  
DB 6 ESGPGLVPSQTLSTLTCTVSGSIRSGGYMSWIRQPGKLEWIGYTHSGNTYNNPSL 65  
XX  
QY 62 KSRVTMSYDTSKNHPSRLSSSVTAADTAIVYICARS---DGYTLDNWGGTILVTVSS 114  
DB 66 KSRVTISYDTSKNQPSLKLSSVTADTAIVYICARVILWFVGMDVWGQGITVTVSS 121  
XX  
RESULT 13  
ADP03871  
ID ADP03871 standard; protein, 125 AA.  
XX  
AC ADP03871;  
XX

XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.  
XX  
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
KW cervical intraepithelial squamous neoplasia;  
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KW gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
OS Unidentified.  
XX  
PN MO2003048328-A2.  
XX  
PD 12-JUN-2003.  
XX  
PP 02-DEC-2002; 2002WO-US038550.  
XX  
PR 03-DEC-2001; 2001US-0337275P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J, Foltz I, Handa M, Gallo M;  
XX  
DR WPI; 2003-523295/49.  
XX  
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
PS Claim 1; SEQ ID NO 11; 89pp; English.  
XX  
CC The invention relates to a novel isolated monoclonal antibody (mAb)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
SQ Sequence 125 AA;  
XX  
Query Match 84.6%; Score 519.5; DB 7; Length 125;  
Best Local Similarity 83.3%; Pred. No. 7.7e-37;  
Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;  
XX  
QY 2 ESGPGLVPSQTLSTLTCTVSGSIRSGGYMSWIRQPGKLEWIGYTHSGNTYNNPSL 61  
DB 6 ESGPGLVPSQTLSTLTCTVSGSIRSGGYMSWIRQPGKLEWIGYTHSGNTYNNPSL 65  
XX  
QY 62 KSRVTMSYDTSKNHPSRLSSSVTAADTAIVYICARS---DGY--TLDNWGGTILVTVSS 114  
DB 66 KSRVTISYDTSKNQPSLKLSSVTADTAIVYICARTYVDFLTGYDPAFDIMGQGITVTVSS 125  
XX  
RESULT 14  
ADP03970  
ID ADP03970 standard; protein, 119 AA.  
XX  
AC ADP03970;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 140.  
XX  
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KW

KM cytosstatic; colorectal neoplasm; renal cell carcinoma;  
KM cervical intraepithelial squamous neoplasia;  
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KM gene therapy; murine; mouse; human; heavy chain variable domain.  
XX Unidentified.  
OS  
XX MO2003048328-A2.  
PN  
XX 12-JUN-2003.  
PD  
XX  
XX 02-DEC-2002; 2002WO-US038550.  
PF  
XX  
XX 03-DEC-2001; 2001US-0337275P.  
PR  
XX  
XX (ABGE-) ABGENIX INC.  
PA  
XX  
XX Gudas J, Foltz I, Handa M, Gallo M;  
PI  
XX WPI; 2003-523295/49.  
DR  
XX  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or oesophageal tumors.  
PS  
XX Example 2; SEQ ID NO 140; 89pp; English.  
XX  
XX The invention relates to a novel isolated monoclonal antibody (mAb)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention  
CC demonstrates cytosstatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
CC  
XX  
SQ Sequence 119 AA;  
  
Query Match 84.3%; Score 517.5; DB 7; Length 119;  
Best Local Similarity 86.8%; Pred. No. 1.1e-36;  
Matches 99; Conservative 6; Mismatches 8; Indels 1; Gaps 1;  
  
QY 2 ESGPGLVWPSPQTLSTCTVSGSIRSGGYWMIROPKGLGEMIGYIYHSGNTYVNSL 61  
Db 6 ESGPGLVWPSPQTLSTCTVSGSIRSGGYWMIROPKGLGEMIGYIYHSGNTYVNSL 65  
  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVVYCARSD--GYTLDNMGQGLTVTVSS 114  
Db 66 KSRVTISVDTSKNHFSLRLSSVTADTAIVVYCARSD--GYTLDNMGQGLTVTVSS 119

RESULT 15  
AAW78433  
ID AAW78433 standard; protein; 123 AA.  
XX  
XX AAW78433;  
AC  
XX 11-MAY-1999 (first entry)  
DT  
XX  
XX Antibody heavy chain targeted to obr clone 26.  
DE  
XX  
XX Variant; antibody; heavy chain; light chain; immunoassay;  
KM diagnosis; cancer; primer; PCR; amplification; diagnostic.  
XX  
XX Synthetic.  
OS  
XX  
XX W09850431-A2.  
XX

PD 12-NOV-1998.  
XX  
XX 30-APR-1998; 98WO-US008762.  
PF  
XX  
XX 02-MAY-1997; 97US-00850058.  
PR 24-JUN-1997; 97US-0050661P.  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX  
XX Arathoon R, Carter PJ, Merchant AM, Presta LG;  
PI  
XX WPI; 1999-070091/06.  
DR  
XX  
XX  
XX Selective preparation of multispecific antibodies - with heteromultimeric  
PT heavy chain and common light chain components, useful for, e.g. in vivo  
PT diagnosis of cancer.  
PS  
XX  
XX Example 4; Fig 5; 69pp; English.  
XX  
XX This sequence represents the heavy chain variable region for an antibody  
CC that binds to the obr clone 26 protein. The sequence encoding the chain  
CC is generated by a new method for preparing a multispecific Ab comprising  
CC a first polypeptide (P1) and at least 1 extra P, where: (i) the first P  
CC comprises a multimerisation domain (MD) forming an interface positioned  
CC to interact with an interface of a MD of the extra P; and (ii) the first  
CC and extra P each have a binding domain, which comprises a heavy chain  
CC and a light chain, where the variable light chains of the first and extra  
CC Ps comprise a common sequence. The method comprises: (a) culturing a  
CC host cell comprising nucleic acid encoding the first P and extra P, and  
CC the variable light chain, such that the nucleic acid is expressed; and  
CC (b) recovering the multispecific Ab from the culture. The method prepares  
CC heteromultimeric Ps, such as bispecific Abs, bispecific immunoassays  
CC and Ab-immunoassay chimeras. The method allows for the enhanced  
CC formation of the desired heteromultimer relative to the undesired  
CC heteromultimers and homomultimers. The Abs can be used in immunoassays  
CC and for the in vitro or in vivo diagnosis of various diseases, such as  
CC cancer.  
CC  
XX  
SQ Sequence 123 AA;  
  
Query Match 84.1%; Score 516.5; DB 2; Length 123;  
Best Local Similarity 84.0%; Pred. No. 1.4e-36;  
Matches 100; Conservative 5; Mismatches 9; Indels 5; Gaps 1;  
  
QY 1 LESGPGLVWPSPQTLSTCTVSGSIRSGGYWMIROPKGLGEMIGYIYHSGNTYVNS 60  
Db 5 VESGPGLVWPSPQTLSTCTVSGSIRSGGYWMIROPKGLGEMIGYIYHSGNTYVNS 64  
  
QY 61 LKSRVTMSVDTSKNHFSLRLSSVTADTAIVVYCARSD-----GYTLDNMGQGLTVTVSS 114  
Db 65 LKSRVTISVDTSKNHFSLRLSSVTADTAIVVYCARSD-----GYTLDNMGQGLTVTVSS 123

Search completed: July 26, 2005, 09:19:19  
Job time : 86.3273 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:26:32 ; Search time 72.5455 Seconds

(without alignments)  
611.274 Million cell updates/sec

Title: US-10-027-725A-9

Perfect score: 614  
Sequence: 1 LESGPGLVKPSQTLSTCTV.....RSDGYTLDMGQGLTVTVSS 114

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications MA:  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
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20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	114	US-10-027-725A-9	Sequence 9, Appl1
2	600	97.7	114	US-10-027-725A-8	Sequence 8, Appl1
3	556	90.6	114	US-10-027-725A-7	Sequence 7, Appl1
4	524.5	85.4	121	US-10-309-762-152	Sequence 152, App
5	524	85.3	118	US-10-309-762-138	Sequence 138, App
6	523.5	85.3	123	US-10-309-762-130	Sequence 10, Appl
7	521	84.9	120	US-10-309-762-113	Sequence 13, Appl
8	521	84.9	120	US-10-309-762-144	Sequence 144, App
9	521	84.9	122	US-10-309-762-147	Sequence 147, App
10	520	84.7	221	US-09-972-656-80	Sequence 80, Appl
11	519.5	84.6	121	US-10-309-762-151	Sequence 151, App

12	519.5	84.6	125	US-10-309-762-11	Sequence 11, Appl
13	518	84.4	121	US-10-805-177-56	Sequence 56, Appl
14	517.5	84.3	119	US-10-309-762-140	Sequence 140, App
15	517	84.2	125	US-10-805-177-53	Sequence 53, Appl
16	516.5	84.1	123	US-10-309-762-12	Sequence 12, Appl
17	516.5	84.1	144	US-10-893-576-35	Sequence 35, Appl
18	516	84.0	124	US-10-309-762-75	Sequence 75, Appl
19	516	84.0	143	US-10-309-762-96	Sequence 96, Appl
20	515.5	84.0	117	US-10-330-613-13	Sequence 13, Appl
21	515.5	84.0	117	US-10-330-613-13	Sequence 13, Appl
22	515.5	84.0	117	US-10-660-357-13	Sequence 13, Appl
23	514	83.7	120	US-10-309-762-128	Sequence 128, App
24	514	83.7	120	US-10-309-762-139	Sequence 139, App
25	514	83.7	121	US-10-308-817-137	Sequence 137, App
26	514	83.7	121	US-10-453-698-137	Sequence 137, App
27	514	83.7	122	US-10-984-960A-56	Sequence 56, Appl
28	513	83.6	116	US-10-309-762-127	Sequence 127, App
29	512.5	83.5	125	US-10-309-762-8	Sequence 8, Appl1
30	512.5	83.5	125	US-10-309-762-16	Sequence 16, Appl
31	512.5	83.5	480	US-10-910-901-6	Sequence 6, Appl1
32	511.5	83.3	119	US-10-309-762-131	Sequence 131, App
33	511.5	83.3	140	US-10-893-576-41	Sequence 41, Appl
34	511	83.2	110	US-10-309-762-74	Sequence 74, Appl
35	510.5	83.1	123	US-10-309-762-9	Sequence 9, Appl1
36	510.5	83.1	127	US-10-893-576-14	Sequence 14, Appl
37	510.5	83.1	148	US-10-910-901-22	Sequence 31, Appl
38	509	82.9	149	US-10-910-901-22	Sequence 22, Appl
39	508.5	82.8	123	US-10-893-576-190	Sequence 150, App
40	508.5	82.8	125	US-10-309-762-153	Sequence 153, App
41	508	82.7	128	US-10-727-155-2	Sequence 2, App
42	508	82.7	128	US-10-727-155-10	Sequence 10, Appl
43	508	82.7	128	US-10-727-155-30	Sequence 30, Appl
44	508	82.7	172	US-10-153-382-21	Sequence 21, Appl
45	508	82.7	172	US-10-612-497-7	Sequence 7, Appl1

## ALIGNMENTS

RESULT 1  
US-10-027-725A-9  
; Sequence 9, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific Ige-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-9

Query Match 100.0%; Score 614; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.1e-47;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTCTVSGSGIRSGCYWWSWRPPGKLEWIGYTHSGNTYNS 60  
DB 1 LESGPGLVKPSQTLSTCTVSGSGIRSGCYWWSWRPPGKLEWIGYTHSGNTYNS 60

QY 61 LKSRVTMSVDYSKHFSLRLSGVTADAVVYCARSDGYTLDMGQGLTVTVSS 114  
DB 61 LKSRVTMSVDYSKHFSLRLSGVTADAVVYCARSDGYTLDMGQGLTVTVSS 114

RESULT 2

US-10-027-725A-8  
; Sequence 8, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027, 725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-8

Query Match 97.7%; Score 600; DB 14; Length 114;  
Best Local Similarity 96.5%; Pred. No. 2e-46;  
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKLEWIGIYHSGNTYVPS 60  
DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKLEWIGIYHSGNTYVPS 60  
QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDGYTLDMNGQGLTVTVSS 114  
DB 61 LKSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDGYTLDMNGQGLTVTVSS 114

RESULT 3  
US-10-027-725A-7  
; Sequence 7, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027, 725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-7

Query Match 90.6%; Score 556; DB 14; Length 114;  
Best Local Similarity 90.4%; Pred. No. 1.8e-42;  
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKLEWIGIYHSGNTYVPS 60  
DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKLEWIGIYHSGNTYVPS 60  
QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDGYTLDMNGQGLTVTVSS 114  
DB 61 LKSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDGYTLDMNGQGLTVTVSS 114

RESULT 4  
US-10-309-762-152  
; Sequence 152, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudus, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa

; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: AGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309, 762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 152  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-152

Query Match 85.4%; Score 524.5; DB 15; Length 121;  
Best Local Similarity 86.2%; Pred. No. 1.3e-39;  
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKLEWIGIYHSGNTYVPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKLEWIGIYHSGNTYVPSL 65  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSD--GYTLDMNGQGLTVTVSS 114  
DB 66 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCAYDILITGAFDIDWQGLTVTVSS 121

RESULT 5  
US-10-309-762-138  
; Sequence 138, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudus, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: AGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309, 762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 138  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-138

Query Match 85.3%; Score 524; DB 15; Length 118;  
Best Local Similarity 86.5%; Pred. No. 1.4e-39;  
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKLEWIGIYHSGNTYVPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKLEWIGIYHSGNTYVPSL 65  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDGYTLDMNGQGLTVTVSS 114  
DB 66 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCAYDILITGAFDIDWQGLTVTVSS 118

RESULT 6  
US-10-309-762-10  
; Sequence 10, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudus, Jean  
; APPLICANT: Foltz, Ian

```
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-309-762-10
```

```
Query Match      85.3%; Score 523.5; DB 15; Length 123;
Best Local Similarity 85.6%; Pred. No. 1.7e-39;
Matches 101; Conservative 5; Mismatches 7; Indels 5; Gaps 1;
```

```
Qy 2 ESGGGLVPSQTLTLCTVSGSIRSGGYWSWIRQPPGKLEWIGYIYHSGNTYINPSL 61
Db 6 ESGGGLVPSQTLTLCTVSGSIRSGGYWSWIRQHPGKLEWIGYIYHSGNTYINPSL 65
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYVCARS---DGYTLDNWGGTLVTYSS 114
Db 66 KSRVTISVDTSKNPFSLKLSVTADTAIVYVCARAGKAYGSGSYLDYWGQGTTLVTYSS 123
```

```
RESULT 7
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-309-762-13
```

```
Query Match      84.9%; Score 521; DB 15; Length 120;
Best Local Similarity 87.1%; Pred. No. 2.7e-39;
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;
```

```
Qy 2 ESGGGLVPSQTLTLCTVSGSIRSGGYWSWIRQPPGKLEWIGYIYHSGNTYINPSL 61
Db 6 ESGGGLVPSQTLTLCTVSGSIRSGGYWSWIRQHPGKLEWIGYIYHSGNTYINPSL 65
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYVCARS---DGYTLDNWGGTLVTYSS 114
Db 66 KSRVTISVDTSKNPFSLKLSVTADTAIVYVCAR-DGYNVYFIDMGRLVTYSS 120
```

```
RESULT 8
US-10-309-762-14
; Sequence 14, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-309-762-14
```

```
Query Match      84.9%; Score 521; DB 15; Length 120;
Best Local Similarity 87.1%; Pred. No. 2.7e-39;
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;
```

```
Qy 2 ESGGGLVPSQTLTLCTVSGSIRSGGYWSWIRQPPGKLEWIGYIYHSGNTYINPSL 61
Db 6 ESGGGLVPSQTLTLCTVSGSIRSGGYWSWIRQHPGKLEWIGYIYHSGNTYINPSL 65
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYVCARS---DGYTLDNWGGTLVTYSS 114
Db 66 KSRVTISVDTSKNPFSLKLSVTADTAIVYVCAR-DGYNVYFIDMGRLVTYSS 120
```

```
RESULT 9
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-309-762-147
```

```
Query Match      84.9%; Score 521; DB 15; Length 122;
Best Local Similarity 85.5%; Pred. No. 2.8e-39;
Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;
```

```
Qy 2 ESGGGLVPSQTLTLCTVSGSIRSGGYWSWIRQPPGKLEWIGYIYHSGNTYINPSL 61
Db 6 ESGGGLVPSQTLTLCTVSGSIRSGGYWSWIRQHPGKLEWIGYIYHSGNTYINPSL 65
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCAR---SDGYTLDNWGGTLVTYSS 114
Db 66 KSRVTISVDTSKNPFSLKLSVTADTAIVYCARYYDILNQGMDWGGTLVTYSS 122
```

```
RESULT 10
US-09-972-656-80
; Sequence 80, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
```



```

; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Wei-Wei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-80
```

```

Query Match      84.7%; Score 520; DB 10; Length 221;
Best Local Similarity 86.7%; Pred. No. 6.2e-39;
Matches 98; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
```

```

Qy      2  ESGPGLVPSQTLSLTCTVSGGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61
      6  ESGPGLVPSQTLSLTCTVSGGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 65
Db      6  KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDGYTLDNWGCGTLVTYSS 114
      66 KSRVTISVDTSKNHFSLRLSSVTADTAAYVYCARSDGYFDYWGCGTLVTYSS 118
```

## RESULT 11

```

US-10-309-762-151
; Sequence 151, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-151
```

```

Query Match      84.6%; Score 519.5; DB 15; Length 121;
Best Local Similarity 86.2%; Pred. No. 3.7e-39;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;
```

```

Qy      2  ESGPGLVPSQTLSLTCTVSGGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61
      6  ESGPGLVPSQTLSLTCTVSGGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 65
Qy      62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDGYTLDNWGCGTLVTYSS 114
      66 KSRVTISVDTSKNHFSLRLSSVTADTAAYVYCARVLMFGYGMVWGCGTLVTYSS 121
Db
```

## RESULT 12

```

US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
```

```

; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-11
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Query Match      84.6%; Score 519.5; DB 15; Length 125;
Best Local Similarity 83.3%; Pred. No. 3.9e-39;
Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;
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Qy      2  ESGPGLVPSQTLSLTCTVSGGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61
      6  ESGPGLVPSQTLSLTCTVSGGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 65
Db      6  KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDGYTLDNWGCGTLVTYSS 114
      66 KSRVTISVDTSKNHFSLRLSSVTADTAAYVYCARSDGYFDYWGCGTLVTYSS 125
```

## RESULT 13

```

US-10-805-177-56
; Sequence 56, Application US/10805177
; Publication No. US2005008449A1
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Chen, Francine
; APPLICANT: Berzabeh, Binyam
; APPLICANT: Foltz, Ian
; APPLICANT: Tse, Kam Fai
; APPLICANT: Measri, Michael
; APPLICANT: Measri, Mehdi
; APPLICANT: Starling, Gary
; APPLICANT: Mezes, Peter
; APPLICANT: Khramtsov, Nikolai
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
; FILE REFERENCE: ABXCUR.006A
; CURRENT APPLICATION NUMBER: US/10/805,177
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/456,652
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-56
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```

Query Match      84.4%; Score 518; DB 17; Length 121;
Best Local Similarity 84.3%; Pred. No. 5.1e-39;
Matches 97; Conservative 9; Mismatches 7; Indels 2; Gaps 1;
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Qy      2  ESGPGLVPSQTLSLTCTVSGGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61
      6  ESGPGLVPSQTLSLTCTVSGGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 65
Qy      62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDGYTLDNWGCGTLVTYSS 114
      66 KSRVTISVDTSKNHFSLRLSSVTADTAAYVYCARNNNNNNNNFVWGCGTLVTYSS 120
Db
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## RESULT 14



US-10-309-762-140  
; Sequence 140, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: AGENIX, 027A  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 140  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-140

Query Match 84.3%; Score 517.5; DB 15; Length 119;  
Best Local Similarity 86.8%; Pred. No. 5.6e-39;  
Matches 99; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGGYWWSWIRQPPKGLWETGYTHSGNTYYNPSL 61  
Db 6 ESGGGLVPSQTLSTCTVSGSGSISGGYWWSWIRQHPKGLWETGYTHSGNTYYNPSL 65  
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYYCARSD-GYTLDMGQGLVTVSS 114  
Db 66 KSRVTISVDTSKNQPSLKLSSVTADTAIVYYCARNNNNSSSWYNNFDYWGQGLVTVSS 119

RESULT 15  
US-10-805-177-53  
; Sequence 53, Application US/10805177  
; Publication No. US20050084449A1  
; GENERAL INFORMATION:  
; APPLICANT: Landes, Gregory M.  
; APPLICANT: Chen, Francine  
; APPLICANT: Bezabeh, Binyam  
; APPLICANT: Foltz, Ian  
; APPLICANT: Tse, Kam Fai  
; APPLICANT: Jeffers, Michael  
; APPLICANT: Meeri, Mehdi  
; APPLICANT: Starling, Gary  
; APPLICANT: Mezes, Peter  
; APPLICANT: Khramtsov, Nikolai  
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN  
; FILE REFERENCE: ABXCUR.006A  
; CURRENT FILING DATE: 2004-03-19  
; PRIOR FILING DATE: 2003-03-19  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 125  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-805-177-53

Query Match 84.2%; Score 517; DB 17; Length 125;  
Best Local Similarity 83.2%; Pred. No. 6.5e-39;  
Matches 99; Conservative 7; Mismatches 7; Indels 6; Gaps 1;

Qy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGGYWWSWIRQPPKGLWETGYTHSGNTYYNPSL 61  
Db 6 ESGGGLVPSQTLSTCTVSGSGSISGGYWWSWIRQHPKGLWETGYTHSGNTYYNPSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYYCARSDGYT-----LDNMGQGLVTVSS 114  
Db 66 KSRVTISVDTSKNQPSLKLSSVTADTAIVYYCARNNNNSSSWYNNFDYWGQGLVTVSS 124

Search completed: July 26, 2005, 10:05:19  
Job time : 73.7121 secs

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## OM protein - protein search, using sw model

Run on: July 26, 2005, 09:09:56 ; Search time 21.5909 Seconds  
(without alignments)  
394.147 Million cell updates/sec

Title: US-10-027-725a-8  
Perfect score: 614  
Sequence: 1 LBSGPIVKPSQTLSTCTV.....RSDGYLDMNGGTLTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

## Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCrus.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	507	82.6	473	US-09-049-672A-4	Sequence 4, Appl1
2	494	80.5	122	US-08-360-125-11	Sequence 11, Appl1
3	494	80.5	122	US-08-450-578-11	Sequence 11, Appl1
4	494	80.5	122	US-09-017-628-11	Sequence 11, Appl1
5	494	80.5	122	US-09-014-880-11	Sequence 11, Appl1
6	494	80.5	122	US-08-450-363-11	Sequence 11, Appl1
7	494	80.5	122	US-09-467-903-11	Sequence 11, Appl1
8	494	80.5	172	US-09-472-087-7	Sequence 11, Appl1
9	494	80.5	172	US-09-472-087-86	Sequence 86, Appl1
10	490.5	79.9	117	US-09-720-493-2	Sequence 2, Appl1
11	488.5	79.6	119	US-09-025-769B-39	Sequence 39, Appl1
12	488.5	79.6	119	US-09-025-769B-65	Sequence 65, Appl1
13	488.5	79.6	119	US-09-430-070A-39	Sequence 39, Appl1
14	488.5	79.6	119	US-09-430-070A-65	Sequence 65, Appl1
15	488.5	79.6	119	US-09-430-153-39	Sequence 39, Appl1
16	488.5	79.6	119	US-09-430-153-65	Sequence 65, Appl1
17	488.5	79.6	119	US-09-430-324-39	Sequence 39, Appl1
18	488.5	79.6	119	US-09-430-324-65	Sequence 65, Appl1
19	488	79.5	118	US-09-025-769B-25	Sequence 25, Appl1
20	488	79.5	118	US-09-430-070A-25	Sequence 25, Appl1
21	488	79.5	118	US-09-430-153-25	Sequence 25, Appl1
22	488	79.5	118	US-09-430-324-25	Sequence 25, Appl1
23	478	77.9	487	US-09-800-729-145	Sequence 145, App
24	477	77.7	120	US-09-424-840B-20	Sequence 20, Appl1
25	473.5	77.1	119	US-08-360-125-5	Sequence 5, Appl1
26	473.5	77.1	119	US-08-450-578-5	Sequence 5, Appl1
27	473.5	77.1	119	US-09-017-628-5	Sequence 5, Appl1

28	473.5	77.1	119	2	US-09-014-880-5	Sequence 5, Appl1
29	473.5	77.1	119	4	US-08-450-363-5	Sequence 5, Appl1
30	473.5	77.1	119	4	US-09-467-903-5	Sequence 5, Appl1
31	459.5	74.8	142	2	US-08-480-774A-2	Sequence 2, Appl1
32	458	74.6	244	3	US-08-918-148-79	Sequence 79, Appl1
33	458	74.6	244	4	US-09-138-091A-77	Sequence 77, Appl1
34	453	73.8	118	3	US-08-545-809A-116	Sequence 116, App
35	453	73.8	126	1	US-08-276-852-142	Sequence 142, App
36	453	73.8	126	1	US-08-899-575-142	Sequence 142, App
37	453	73.8	126	1	US-08-899-575-142	Sequence 142, App
38	453	73.8	126	5	PCT-US95-08743-142	Sequence 142, App
39	451.5	73.5	155	4	US-09-471-276-888	Sequence 888, App
40	446.5	72.7	119	2	US-08-652-816A-10	Sequence 10, Appl1
41	446	72.6	118	3	US-08-545-809A-123	Sequence 123, Appl1
42	446	72.6	278	3	US-09-260-527-3	Sequence 3, Appl1
43	445.5	72.6	123	3	US-08-793-450-4	Sequence 4, Appl1
44	445.5	72.6	472	3	US-08-793-450-8	Sequence 8, Appl1
45	445	72.5	118	4	US-09-343-698-6	Sequence 6, Appl1

## ALIGNMENTS

RESULT 1  
US-09-049-672A-4  
; Sequence 4, Application US/09049672A  
; Patent No. 6135941  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/049,672A  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ceirone, Michael C  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0497 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 473 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PANTU01

CLONE: 1513264  
US-09-049-672a-4

Query Match 82.6%; Score 507; DB 3; Length 473;  
Best Local Similarity 79.8%; Pred. No. 1e-42;  
Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;

Qy 2 ESGPGLVKEPSQTLSTCTVSGGSIIRSGGYMSWVRQPGKGLWIGNIYHSGNTYVPSL 61  
Db 25 ESGPGLVKEPSQTLSTCTVSGGSIIRSGGYMSWVRQPGKGLWIGNIYHSGNTYVPSL 84

Qy 62 KSRITMSVDPSTSKHFSRLTSTVTAADTAAYVYCARSD-----GYTLDMNGGGLTVTVSS 114  
Db 85 KSRVITISVDTSKQFSLKLSSTVTAADTAAYVYCARSDVGLRGNGYGMVWGGLTVTVSS 143

RESULT 2  
US-08-360-125-11  
Sequence 11, Application US/08360125  
Patent No. 5767246  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5767246ihiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Mordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360.125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905.534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-11

Query Match 80.5%; Score 494; DB 1; Length 122;  
Best Local Similarity 78.6%; Pred. No. 4.1e-42;  
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

Qy 2 ESGPGLVKEPSQTLSTCTVSGGSIIRSGGYMSWVRQPGKGLWIGNIYHSGNTYVPSL 61  
Db 6 ESGPGLVKEPSQTLSTCTVSGGSIIRSGGYMSWVRQPGKGLWIGNIYHSGNTYVPSL 65

Qy 62 KSRITMSVDPSTSKHFSRLTSTVTAADTAAYVYCARSD-----GYTLDMNGGGLTVTVSS 114  
Db 66 KSRVITISVDTSKQFSLKLSSTVTAADTAAYVYCARSGYIGYGMVWGGLTVTVSS 122

RESULT 3  
US-08-450-578-11  
Sequence 11, Application US/08450578  
Patent No. 5837845  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845ihiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Mordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450.578



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
US-09-014-880-11

Query Match 80.5%; Score 494; DB 2; Length 122;  
Best Local Similarity 78.6%; Pred. No. 4,1e-42;  
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVKEPSQTLSTLTCTVSGSIRSGGYWVWROPKGLMIGNIYHSGNTYVPSL 61  
DB 6 ESGPGLVKEPSQTLSTLTCTVSGSIRSGGYWVWROPKGLMIGNIYHSGNTYVPSL 65  
QY 62 KSRITMSVDTSKXHFSLRLTSVTAADTAAYVYCARSD---GYTLDMWGCGTLTVVSS 114  
DB 66 KSRVITISVDTSKXHFSLRLTSVTAADTAAYVYCARSGYGYGMDWVGCGTLTVVSS 122

RESULT 6  
US-08-450-363-11  
Sequence 11, Application US/08450363  
Patent No. 6436434  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 6436434ihiko ITO  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,363  
FILING DATE: May 25, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-363-11

Query Match 80.5%; Score 494; DB 4; Length 122;  
Best Local Similarity 78.6%; Pred. No. 4,1e-42;  
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVKEPSQTLSTLTCTVSGSIRSGGYWVWROPKGLMIGNIYHSGNTYVPSL 61  
DB 6 ESGPGLVKEPSQTLSTLTCTVSGSIRSGGYWVWROPKGLMIGNIYHSGNTYVPSL 65  
QY 62 KSRITMSVDTSKXHFSLRLTSVTAADTAAYVYCARSD---GYTLDMWGCGTLTVVSS 114  
DB 66 KSRVITISVDTSKXHFSLRLTSVTAADTAAYVYCARSGYGYGMDWVGCGTLTVVSS 122

RESULT 7  
US-09-467-903-11  
Sequence 11, Application US/09467903  
Patent No. 6787153  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA

No. 6781531hiko ITO  
Kazuhiko NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
Specifically Binding to Surface Antigen of Cancer  
Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 203 K Street, N.W., #800  
City: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/467,903  
FILING DATE: 21-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,363  
FILING DATE: May 25, 1995  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER: JP158859/1991  
FILING DATE: June 28, 1991  
APPLICATION NUMBER: JP158860/1991  
FILING DATE: June 28, 1991  
APPLICATION NUMBER: JP158861/1991  
FILING DATE: June 28, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: <Unknown>  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: protein  
HYPOTHEICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: <Unknown>  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL LINE: Hybridoma producing human antibody 1-3-1  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:

OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-467-903-11  
Query Match 80.5%; Score 494; DB 4; Length 122;  
Best Local Similarity 78.6%; Pred. No. 4,1e-42;  
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;  
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DB 6 ESQGLVPSQTLSTCTVSGSIRSGGYWVWVROPGKLEWIGNIYHSGNTYVPSL 65  
QY 62 KSRITMSVDTSKNHFSLRTSVTAADTVAVYVCARSD---GYLDNMGQGLTVVSS 114  
DB 66 KSRITMSVDTSKNHFSLRTSVTAADTVAVYVCARSDGYVYGVMDVWGQGLTVVSS 122  
RESULT 8  
US-09-472-087-7  
Sequence 7, Application US/09472087  
Patent No. 6682736  
GENERAL INFORMATION:  
APPLICANT: HANSON, DOUGLAS C.  
APPLICANT: NEVEU, MARK J.  
APPLICANT: MUELLER, BILLEN E.  
APPLICANT: HANKS, JEFFREY H.  
APPLICANT: GILMAN, STEVEN C.  
APPLICANT: DAVIS, C. GEOFFREY  
APPLICANT: CORVALAN, JOSE R.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
FILE REFERENCE: ABX-PFI  
CURRENT APPLICATION NUMBER: US/09/472,087  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/113,647  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-472-087-7  
Query Match 80.5%; Score 494; DB 4; Length 172;  
Best Local Similarity 81.6%; Pred. No. 6,1e-42;  
Matches 93; Conservative 8; Mismatches 11; Indels 2; Gaps 1;  
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DB 1 SGPGLVPSQTLSTCTVSGSIRSGGYWVWVROPGKLEWIGNIYHSGNTYVPSL 60  
QY 63 SRTMSVDTSKNHFSLRTSVTAADTVAVYVCARSDG---YLDNMGQGLTVVSS 114  
DB 61 SRTMSVDTSKNHFSLRTSVTAADTVAVYVCARSDGYVYGVMDVWGQGLTVVSS 114  
RESULT 9  
US-09-472-087-86  
Sequence 86, Application US/09472087  
Patent No. 6682736  
GENERAL INFORMATION:

Query Match	80.5%	Score 494	DB 4	Length 172
Best Local Similarity	81.6%	Pred. No. 6.1e-42		
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Db	1	SGPLVLRPQRLTLSTCTVSGSGSIRSGGYVMSVIRHPKGLGLEIYIYIGNIYVNSLX	60	
Qy	63	SRIMSVDTSKNHFSLRLTSTYADPVTAVYYCARSPG--YTLDDNGGGLTAVYS	114	
Db	61	SRVITSVDTSKNQFLKLSSTVTAAPVTAVYYCARDSDYDGIDVWGGLTAVYS	114	

	Query Match	79.9%	Score 490.5;	DB 4;	Length 117;
	Best Local Similarity	81.4%;	Pred.	Nm.8-7e+2;	
Matches	92; Conservative	8;	Ph.Matches	12;	Indels 1; Gaps 1
Oy	2	ESGPGLVSPSTLLTCTVSGGSINSGGYMWSWROPPEKGLIEWIIGNITSHSNGTYNPSL	61		
Dd	6	ESGPGLVPSESLTLTCALVSQYISLSGGYMWMIRPCKGLEMIIGSIHSSGTYYNPBL	64		
Oy	62	KSRITMSVDTSKNHPFLRLITSVTADLTAVYYCARSDGYRLDMWGGOQLTVYS	114		
Dd	65	KSRVVISDVDTSKNQPSLKLISSVTADLTAVYYCARGRWKSFEEDVGGOQLTVYS	117		

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1      MEDIUM TYPE: FLOPPY disk
2      COMPUTER: IBM PC compatible
3      OPERATING SYSTEM: PC-DOS/MS-DOS
4      SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
5      CURRENT APPLICATION DATA:
6      APPLICATION NUMBER: US/09/025,769B
7      FILING DATE: 18-FEB-1998
8      PRIOR APPLICATION DATA:
9      APPLICATION NUMBER: EP 95 11 3021.0
10     FILING DATE: 18-AUG-1995
11     ATTORNEY/AGENT INFORMATION:
12     NAME: James F. Haley, Jr., Esq.
13     REGISTRATION NUMBER: 27,794
14     REFERENCE/DOCKET NUMBER: MORPHO/5
15     TELECOMMUNICATION INFORMATION:
16     TELEPHONE: (212)596-9000
17     TELEFAX: (212)596-9090
18     INFORMATION FOR SEQ ID NO: 39:
19     SEQUENCE CHARACTERISTICS:
20     LENGTH: 119 amino acids
21     TYPE: amino acid
22     STRANDEDNESS:
23     TOPOLOGY: linear
24     MOLECULE TYPE: protein
25     US-09-025-769B-39

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RESULT 12
US-09-025-769B-65
; Sequence 65, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373

```



CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-65

Query Match 79.6%; Score 488.5; DB 3; Length 119;  
Best Local Similarity 81.9%; Pred. No. 1,4e-41;  
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

QY 2 ESGGGLVPSQTLSTCTVSGSIRSGGYMSWVROPKGLEWIGNIYHSGNTYNSPL 61  
DB 6 ESGGGLVPSQTLSTCTVSGSIRSGGYMSWVROPKGLEWIGNIYHSGNTYNSPL 63

QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAIVYYCAR--SDG-YTLDNMGQGLTVTVSS 114  
DB 64 KSRVTTISVDTSKNHFSLRTSVTAADTAIVYYCARMGDGFYAMDYWGQGLTVTVSS 119

RESULT 13  
US-09-490-070A-39  
Sequence 39, Application US/09490070A  
Patent No. 6696248

GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthum, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
White & McLaughlin  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-070A-39

Query Match 79.6%; Score 488.5; DB 4; Length 119;  
Best Local Similarity 81.9%; Pred. No. 1,4e-41;  
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

QY 2 ESGGGLVPSQTLSTCTVSGSIRSGGYMSWVROPKGLEWIGNIYHSGNTYNSPL 61  
DB 6 ESGGGLVPSQTLSTCTVSGSIRSGGYMSWVROPKGLEWIGNIYHSGNTYNSPL 63

QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAIVYYCAR--SDG-YTLDNMGQGLTVTVSS 114  
DB 64 KSRVTTISVDTSKNHFSLRTSVTAADTAIVYYCARMGDGFYAMDYWGQGLTVTVSS 119

RESULT 14  
US-09-490-070A-65  
Sequence 65, Application US/09490070A  
Patent No. 6696248

GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthum, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
White & McLaughlin  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:26:32 ; Search time 72.5455 Seconds  
(without alignments)  
611.274 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614  
Sequence: 1 LBSGPGLVKXPSQTLSTLCTV.....RSDGYTLDMWGQGLTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubppaa/PCTUS\_NEW\_PUB.pep:\*  
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4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*  
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21: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	100.0	114	US-10-027-725A-8	Sequence 8, Appl1
2	600	97.7	114	US-10-027-725A-9	Sequence 9, Appl1
3	546	88.9	114	US-10-027-725A-7	Sequence 7, Appl1
4	514.5	83.8	140	US-10-893-576-41	Sequence 41, Appl1
5	511	83.2	128	US-10-727-155-2	Sequence 2, Appl1
6	511	83.2	128	US-10-727-155-10	Sequence 10, Appl1
7	511	83.2	128	US-10-727-155-30	Sequence 30, Appl1
8	510.5	83.1	121	US-10-309-762-152	Sequence 152, App
9	510	83.1	118	US-10-309-762-138	Sequence 138, App
10	509.5	83.0	123	US-10-309-762-10	Sequence 10, Appl1
11	507.5	82.7	125	US-10-309-762-11	Sequence 11, Appl1

12	507	82.6	120	US-10-309-762-13	Sequence 13, Appl1
13	507	82.6	120	US-10-309-762-14	Sequence 14, Appl1
14	507	82.6	122	US-10-309-762-147	Sequence 147, App
15	506.5	82.5	119	US-10-893-576-189	Sequence 189, App
16	506	82.4	221	US-09-972-656-80	Sequence 80, Appl1
17	505.5	82.3	121	US-10-309-762-151	Sequence 151, App
18	505	82.2	128	US-10-727-155-26	Sequence 26, Appl1
19	504.5	82.2	117	US-10-330-613-13	Sequence 13, Appl1
20	504.5	82.2	117	US-10-330-530-13	Sequence 13, Appl1
21	504.5	82.2	117	US-10-660-357-13	Sequence 56, Appl1
22	504	82.1	121	US-10-805-177-56	Sequence 140, App
23	503.5	82.0	125	US-10-309-762-140	Sequence 53, App
24	503	81.9	125	US-10-805-177-53	Sequence 12, Appl1
25	502.5	81.8	123	US-10-309-762-112	Sequence 35, Appl1
26	502.5	81.8	144	US-10-893-576-35	Sequence 75, Appl1
27	502	81.8	122	US-10-984-660A-56	Sequence 56, Appl1
28	502	81.8	124	US-10-309-762-75	Sequence 96, Appl1
29	502	81.8	143	US-10-309-762-96	Sequence 1329, App
30	501	81.6	252	US-09-880-748-1329	Sequence 1329, App
31	501	81.6	252	US-10-293-418-1329	Sequence 128, App
32	500	81.4	120	US-10-309-762-128	Sequence 137, App
33	500	81.4	120	US-10-309-762-139	Sequence 137, App
34	500	81.4	121	US-10-308-817-137	Sequence 137, App
35	500	81.4	121	US-10-453-698-137	Sequence 6, Appl1
36	500	81.4	126	US-09-974-449-6	Sequence 18, Appl1
37	500	81.4	16	US-10-652-502A-18	Sequence 34, Appl1
38	499.5	81.4	135	US-10-388-214A-34	Sequence 127, App
39	499	81.3	116	US-10-309-762-127	Sequence 40, Appl1
40	499	81.3	120	US-10-706-689-40	Sequence 40, Appl1
41	499	81.3	120	US-10-988-360-40	Sequence 8, Appl1
42	498.5	81.2	125	US-10-309-762-8	Sequence 16, Appl1
43	498.5	81.2	125	US-10-309-762-16	Sequence 6, Appl1
44	498.5	81.2	480	US-10-910-901-6	Sequence 23, Appl1
45	498	81.1	135	US-10-910-901-23	

#### ALIGNMENTS

RESULT 1  
US-10-027-725A-8  
; Sequence 8, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OR INVENTION: Group 2 Allergen Specific IGF-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027, 725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259, 436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-8  
Query Match 100.0%; Score 614; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7, 8e-48;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cy 1 LBSGPGLVKXPSQTLSTLCTVSGSIRSGGYWVWRPQKGLWMIGNIYHSNTYNNPS 60  
Db 1 LBSGPGLVKXPSQTLSTLCTVSGSIRSGGYWVWRPQKGLWMIGNIYHSNTYNNPS 60  
Cy 61 LKSRITSVPTSKNHFSLRTSVTAADTAVYYCARSDGYTLDMWGQGLTVSS 114  
Db 61 LKSRITSVPTSKNHFSLRTSVTAADTAVYYCARSDGYTLDMWGQGLTVSS 114  
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US-10-027-725A-9  
; Sequence 9, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-9

Query Match 97.7%; Score 600; DB 14; Length 114;  
Best Local Similarity 96.5%; Pred. No. 1,4e-46;  
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYNNPS 60

QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114  
DB 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114

RESULT 3  
US-10-027-725A-7  
; Sequence 7, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-7

Query Match 88.9%; Score 546; DB 14; Length 114;  
Best Local Similarity 89.5%; Pred. No. 1.1e-41;  
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYNNPS 60

QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114  
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RESULT 4  
US-10-893-576-41  
; Sequence 41, Application US/10893576  
; Publication No. US20050118643A1  
; GENERAL INFORMATION:  
; APPLICANT: BURGESS, TERESA L.  
; APPLICANT: COXON, ANGELA  
; APPLICANT: GREEN, LARRY L.

; APPLICANT: ZHANG, KE  
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR  
; FILE REFERENCE: 06843.0051-00000  
; CURRENT APPLICATION NUMBER: US/10/893,576  
; CURRENT FILING DATE: 2004-07-16  
; PRIOR APPLICATION NUMBER: US 60/488,681  
; PRIOR FILING DATE: 2003-07-18  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 41  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HGF 2.40.1  
; OTHER INFORMATION: Heavy chain V region (Vh, Vg 4-31)-hnlgs2 C region  
US-10-893-576-41

Query Match 83.8%; Score 514.5; DB 17; Length 140;  
Best Local Similarity 84.5%; Pred. No. 9.3e-39;  
Matches 98; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYNNPSL 61  
DB 25 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYNNPSL 84

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114  
DB 85 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 140

RESULT 5  
US-10-727-155-2  
; Sequence 2, Application US/10727155  
; Publication No. US20050049402A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. Babcock  
; APPLICANT: Jaspal S. Kang  
; APPLICANT: Orit Foord  
; APPLICANT: Larry Green  
; APPLICANT: Xiao Feng  
; APPLICANT: Scott Klakamp  
; APPLICANT: Mary Haak-Frendsch  
; APPLICANT: Palaniswami Ratnaswami  
; APPLICANT: Craig Pigott  
; APPLICANT: Meina Liang  
; APPLICANT: Rozanne Lee  
; APPLICANT: Kathy Manchulenko  
; APPLICANT: Raffaela Fegioni  
; APPLICANT: Giorgio Senaldi  
; APPLICANT: Qiaojuan Jane Su  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
; FILE REFERENCE: AGENIX 073A  
; CURRENT APPLICATION NUMBER: US/10/727,155  
; CURRENT FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: 60/430729  
; PRIOR FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 320  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-727-155-2

Query Match 83.2%; Score 511; DB 17; Length 128;  
Best Local Similarity 78.9%; Pred. No. 1.8e-38;  
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYNNPSL 65



Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSD---GTYLDNMGCGTLVTYSS 114  
Db 66 KSRVITISVDTSKNQFSLKLSSTVTAADTAIVYCCAYYDILTGAFDIMGCGTMTYSS 121

RESULT 9  
US-10-309-762-138

/ Sequence 138, Application US/10309762  
/ Publication No. US20040018198A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Gudas, Jean  
/ APPLICANT: Foltz, Ian  
/ APPLICANT: Handa, Masahisa  
/ APPLICANT: Gallo, Michael  
/ TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
/ FILE REFERENCE: ABGENIX.027A  
/ CURRENT APPLICATION NUMBER: US/10/309,762  
/ PRIOR FILING DATE: 2002-12-02  
/ PRIOR APPLICATION NUMBER: 60/337275  
/ PRIOR FILING DATE: 2001-12-03  
/ NUMBER OF SEQ ID NOS: 246  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 138  
/ LENGTH: 118  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-309-762-138

Query Match 83.1%; Score 510; DB 15; Length 118;  
Best Local Similarity 85.0%; Pred. No. 2e-38;

Matches 96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGYYWSWVROPKGKLEWIGNIYHSGNTYYNPSL 61  
Db 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGYYWSWVROPKGKLEWIGNIYHSGNTYYNPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSDGYTLDNMGCGTLVTYSS 114  
Db 66 KSRVITISVDTSKNQFSLKLSSTVTAADTAIVYCCAYYSGSDYWGCGTLVTYSS 118

RESULT 10  
US-10-309-762-10

/ Sequence 10, Application US/10309762  
/ Publication No. US20040018198A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Gudas, Jean  
/ APPLICANT: Foltz, Ian  
/ APPLICANT: Handa, Masahisa  
/ APPLICANT: Gallo, Michael  
/ TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
/ FILE REFERENCE: ABGENIX.027A  
/ CURRENT APPLICATION NUMBER: US/10/309,762  
/ CURRENT FILING DATE: 2002-12-02  
/ PRIOR APPLICATION NUMBER: 60/337275  
/ PRIOR FILING DATE: 2001-12-03  
/ NUMBER OF SEQ ID NOS: 246  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 10  
/ LENGTH: 123  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-309-762-10

Query Match 83.0%; Score 509.5; DB 15; Length 123;  
Best Local Similarity 82.2%; Pred. No. 2.3e-38;

Matches 97; Conservative 8; Mismatches 8; Indels 5; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGYYWSWVROPKGKLEWIGNIYHSGNTYYNPSL 61  
Db 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGYYWSWVROPKGKLEWIGNIYHSGNTYYNPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSD---DGYTLDNMGCGTLVTYSS 114  
Db 66 KSRVITISVDTSKNQFSLKLSSTVTAADTAIVYCCARAGKYSGSDYWGCGTLVTYSS 123

RESULT 11  
US-10-309-762-11

/ Sequence 11, Application US/10309762  
/ Publication No. US20040018198A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Gudas, Jean  
/ APPLICANT: Foltz, Ian  
/ APPLICANT: Handa, Masahisa  
/ APPLICANT: Gallo, Michael  
/ TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
/ FILE REFERENCE: ABGENIX.027A  
/ CURRENT APPLICATION NUMBER: US/10/309,762  
/ CURRENT FILING DATE: 2002-12-02  
/ PRIOR APPLICATION NUMBER: 60/337275  
/ PRIOR FILING DATE: 2001-12-03  
/ NUMBER OF SEQ ID NOS: 246  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 11  
/ LENGTH: 125  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-309-762-11

Query Match 82.7%; Score 507.5; DB 15; Length 125;  
Best Local Similarity 81.7%; Pred. No. 3.5e-38;

Matches 98; Conservative 7; Mismatches 8; Indels 7; Gaps 2;

Qy 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGYYWSWVROPKGKLEWIGNIYHSGNTYYNPSL 61  
Db 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGYYWSWVROPKGKLEWIGNIYHSGNTYYNPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSD---DGYTLDNMGCGTLVTYSS 114  
Db 66 KSRVITISVDTSKNQFSLKLSSTVTAADTAIVYCCARTYYDFLTGYPDAFDIMGCGTMTYSS 125

RESULT 12  
US-10-309-762-13

/ Sequence 13, Application US/10309762  
/ Publication No. US20040018198A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Gudas, Jean  
/ APPLICANT: Foltz, Ian  
/ APPLICANT: Handa, Masahisa  
/ APPLICANT: Gallo, Michael  
/ TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
/ FILE REFERENCE: ABGENIX.027A  
/ CURRENT APPLICATION NUMBER: US/10/309,762  
/ CURRENT FILING DATE: 2002-12-02  
/ PRIOR APPLICATION NUMBER: 60/337275  
/ PRIOR FILING DATE: 2001-12-03  
/ NUMBER OF SEQ ID NOS: 246  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 13  
/ LENGTH: 120  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-309-762-13

Query Match 82.6%; Score 507; DB 15; Length 120;  
Best Local Similarity 83.6%; Pred. No. 3.8e-38;

Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;

Qy 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGYYWSWVROPKGKLEWIGNIYHSGNTYYNPSL 61  
Db 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGYYWSWVROPKGKLEWIGNIYHSGNTYYNPSL 65

Db 6 ESGPGLVKSQTLSTLCTVSGGSISGCGYWSMIRQHPGKLEWIGITYYSGSTYYP SL 65  
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGT---LDNMGQGLTVTVSS 114  
Db 66 KSRVTVSDTSKNQFSLKLSSTVTAADTAAYYCAR-DGYNMYFPLMGRGLTVTVSS 120

## RESULT 13

US-10-309-762-144  
; Sequence 144, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: AGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 144  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-144

Query Match 82.6%; Score 507; DB 15; Length 120;  
Best Local Similarity 83.6%; Pred. No. 3.8e-38;  
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;

Qy 2 ESGPGLVKSQTLSTLCTVSGGSIRSGGYWSWVROPKGLWIGINYHSGNTYYP SL 61  
Db 6 ESGPGLVKSQTLSTLCTVSGGSISGCGYWSMIRQHPGKLEWIGITYYSGSTYYP SL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGT---LDNMGQGLTVTVSS 114  
Db 66 KSRVTVSDTSKNQFSLKLSSTVTAADTAAYYCAR-DGYNMYFPLMGRGLTVTVSS 120

## RESULT 14

US-10-309-762-147  
; Sequence 147, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: AGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 147  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-147

Query Match 82.6%; Score 507; DB 15; Length 122;  
Best Local Similarity 82.1%; Pred. No. 3.8e-38;  
Matches 96; Conservative 8; Mismatches 9; Indels 4; Gaps 1;

Qy 2 ESGPGLVKSQTLSTLCTVSGGSIRSGGYWSWVROPKGLWIGINYHSGNTYYP SL 61

Db 6 ESGPGLVKSQTLSTLCTVSGGSISGCGYWSMIRQHPGKLEWIGITYYSGSTYYP SL 65  
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCAR---SDGYTLDMWGQGLTVTVSS 114  
Db 66 KSRVTVSDTSKNQFSLKLSSTVTAADTAAYYCARYYDILLYGMDVWGQGLTVTVSS 122

## RESULT 15

US-10-893-576-189  
; Sequence 189, Application US/10893576  
; Publication No. US20050118643A1  
; GENERAL INFORMATION:  
; APPLICANT: BURGESS, TERESA L.  
; APPLICANT: COXON, ANGELA  
; APPLICANT: GREEN, LARRY L.  
; APPLICANT: ZHANG, KE  
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR  
; FILE REFERENCE: 06843.0051-00000  
; CURRENT APPLICATION NUMBER: US/10/893,576  
; CURRENT FILING DATE: 2004-07-16  
; PRIOR APPLICATION NUMBER: US 60/488,681  
; PRIOR FILING DATE: 2003-07-18  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 189  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic gamma heavy  
US-10-893-576-189

Query Match 82.5%; Score 506.5; DB 17; Length 119;  
Best Local Similarity 84.2%; Pred. No. 4.1e-38;  
Matches 96; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

Qy 2 ESGPGLVKSQTLSTLCTVSGGSIRSGGYWSWVROPKGLWIGINYHSGNTYYP SL 61  
Db 6 ESGPGLVKSQTLSTLCTVSGGSISGCGYWSMIRQHPGKLEWIGITYYSGSTYYP SL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGT---DGYTLDMWGQGLTVTV 112  
Db 66 KSRVTVSDTSKNQFSLKLSSTVTAADTAAYYCARDPYGDYGFDPWGQGLTVTV 119

Search completed: July 26, 2005, 10:05:18  
Job time : 72.7121 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:09:56 ; Search time 21.5909 Seconds  
(without alignment)  
394.147 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609  
Sequence: 1 LESGPGLVKPAQTLSICAV.....RLDGYTIDWQGTLYTSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: Issued Patents AA:\*  
2: /cgn2\_6/ptodata/1/aa/5A\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/aa/6A\_COMB.pep:\*  
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6: /cgn2\_6/ptodata/1/aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	499	81.9	473	3	US-09-049-672A-4
2	496	81.4	172	4	US-09-472-087-7
3	496	81.4	172	4	US-09-472-087-86
4	482	79.1	487	1	US-09-800-729-145
5	471.5	77.4	119	1	US-08-360-125-5
6	471.5	77.4	119	2	US-08-450-578-5
7	471.5	77.4	119	2	US-09-017-628-5
8	471.5	77.4	119	2	US-09-014-880-5
9	471.5	77.4	119	3	US-09-025-769B-39
10	471.5	77.4	119	3	US-09-025-769B-65
11	471.5	77.4	119	3	US-08-450-363-5
12	471.5	77.4	119	4	US-09-490-070A-39
13	471.5	77.4	119	4	US-09-490-070A-65
14	471.5	77.4	119	4	US-09-490-153-39
15	471.5	77.4	119	4	US-09-490-153-65
16	471.5	77.4	119	4	US-09-467-903-5
17	471.5	77.4	119	4	US-09-490-324-39
18	471.5	77.4	119	4	US-09-490-324-65
19	468	76.8	120	4	US-09-424-840B-20
20	466	76.5	122	1	US-08-360-125-11
21	466	76.5	122	2	US-08-450-578-11
22	466	76.5	122	2	US-09-017-628-11
23	466	76.5	122	2	US-09-014-880-11
24	466	76.5	122	4	US-08-450-363-11
25	466	76.5	122	4	US-09-467-903-11
26	465.5	76.4	117	4	US-09-720-493-2
27	455	74.7	118	3	US-09-025-769B-25

28	455	74.7	118	4	US-09-490-070A-25	Sequence 25, Appl
29	455	74.7	118	4	US-09-490-153-25	Sequence 25, Appl
30	455	74.7	118	4	US-09-490-324-25	Sequence 25, Appl
31	453	74.4	118	3	US-08-545-809A-116	Sequence 116, App
32	445	73.1	244	3	US-08-918-148-79	Sequence 79, Appl
33	445	73.1	244	4	US-09-138-091A-77	Sequence 77, Appl
34	442.5	72.7	142	2	US-08-480-774A-2	Sequence 2, Appl
35	441.5	72.5	155	4	US-09-471-276-888	Sequence 888, App
36	438	71.9	278	3	US-09-260-527-3	Sequence 3, Appl
37	429.5	70.5	119	2	US-08-652-816A-10	Sequence 10, Appl
38	429	70.4	150	4	US-09-582-337-14	Sequence 14, Appl
39	427	70.1	118	4	US-09-343-698-6	Sequence 6, Appl
40	427	70.1	118	4	US-08-325-955-6	Sequence 6, Appl
41	425.5	69.9	119	4	US-09-424-840B-2	Sequence 2, Appl
42	425.5	69.9	476	3	US-08-487-550-12	Sequence 12, Appl
43	425.5	69.9	476	4	US-09-526-098-12	Sequence 12, Appl
44	425.5	69.9	476	4	US-09-383-916-12	Sequence 12, Appl
45	424.5	69.7	117	4	US-09-232-290-47	Sequence 47, Appl

# ALIGNMENTS

RESULT 1  
US-09-049-672A-4  
; Sequence 4, Application US/09049672A  
; Patent No. 6135941  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/049,672A  
; FILING DATE: HEREMITH  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ceirone, Michael C  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PR-0497 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 473 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PANTUT01

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; CLONE: 1513264
US-09-049-672A-4
Query Match      81.4%; Score 499; DB 3; Length 473;
Best Local Similarity 78.2%; Pred. No. 6,3e-43;
Matches 93; Conservative 13; Mismatches 7; Indels 6; Gaps 1;

QY 2  ESGGLVPAQTLTSLSCAVSGSGSIRSGGYWMSWIRHDPKGLGEMIGYIYHSGNTYNPSTL 61
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DB 25  ESGGLVPAQTLTSLTCTVSGSGSISGGHYWMSWIRHDPKGLGEMIGYIYHSGNTYNPSTL 84

QY 62  KSRIAMSVDTSENKFSRLNSVTADTAADTAAYVYCARLDG--YTLDIWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 85  KSRVTISVDTSKNPSLKLSSVTADTAADTAAYVYCARLDGVLRCGNYGMDVWGQGLTVTVSS 143

RESULT 2
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      81.4%; Score 496; DB 4; Length 172;
Best Local Similarity 79.8%; Pred. No. 3.8e-43;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY 3  SGPGLVPAQTLTSLSCAVSGSGSIRSGGYWMSWIRHDPKGLGEMIGYIYHSGNTYNPSTL 62
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1  SGPGLVPAQTLTSLTCTVSGSGSISGGHYWMSWIRHDPKGLGEMIGYIYHSGNTYNPSTL 60

QY 63  SRIAMSVDTSENKFSRLNSVTADTAADTAAYVYCARLDG--YTLDIWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61  KSRVTISVDTSKNPSLKLSSVTADTAADTAAYVYCARLDGVDYGDVWGQGLTVTVSS 114

RESULT 3
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
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; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-86

Query Match      81.4%; Score 496; DB 4; Length 172;
Best Local Similarity 79.8%; Pred. No. 3.8e-43;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY 3  SGPGLVPAQTLTSLSCAVSGSGSIRSGGYWMSWIRHDPKGLGEMIGYIYHSGNTYNPSTL 62
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1  SGPGLVPAQTLTSLTCTVSGSGSISGGHYWMSWIRHDPKGLGEMIGYIYHSGNTYNPSTL 60

QY 63  SRIAMSVDTSENKFSRLNSVTADTAADTAAYVYCARLDG--YTLDIWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61  KSRVTISVDTSKNPSLKLSSVTADTAADTAAYVYCARLDGVDYGDVWGQGLTVTVSS 114

RESULT 4
US-09-800-729-145
; Sequence 145, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-145

Query Match      79.1%; Score 482; DB 4; Length 487;
Best Local Similarity 74.8%; Pred. No. 3.6e-41;
Matches 92; Conservative 12; Mismatches 9; Indels 10; Gaps 2;

QY 2  ESGGLVPAQTLTSLSCAVSGSGSIRSGGYWMSWIRHDPKGLGEMIGYIYHSGNTYNPSTL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 25  ESGGLVPAQTLTSLTCTVSGSGSISGGHYWMSWIRHDPKGLGEMIGYIYHSGNTYNPSTL 84

QY 62  KSRIAMSVDTSENKFSRLNSVTADTAADTAAYVYCARLDG--YTLDIWGQGLTVTVSS 111
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 85  KSRVTISVDTSKNPSLKLSSVTADTAADTAAYVYCARLDGVDYGDVWGQGLTVTVSS 144

QY 112 VSS 114
    |||
DB 145 VSS 147

RESULT 5
US-08-360-125-5
; Sequence 5, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: SAIKO HOSOKAWA
; APPLICANT: TOSHIAKI INAGAWA
; APPLICANT: YOKO HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: KAZUHIRO NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
```

NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Menderoth, Lind & Ponack  
 STREET: 805 Fifteenth Street, N.W., #700  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/360,125  
 FILING DATE:  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/905,534  
 FILING DATE: June 29, 1992  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek, Jr.  
 REGISTRATION NUMBER: 33,367  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-8850  
 TELEFAX:  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 119 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHEICAL:  
 ANTI-SENSE:  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM:  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 RAPID TYPE:  
 TISSUE TYPE:  
 CELL TYPE: Hybridoma producing human  
 CELL LINE: antibody GAH  
 ORGANELLE:  
 IMMEDIATE SOURCE:  
 LIBRARY:  
 CLONE:  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT:  
 MAP POSITION:  
 UNITS:  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:  
 VOLUME:  
 ISSUE:  
 PAGES:  
 DATE:  
 DOCUMENT NUMBER:  
 FILING DATE:

PUBLICATION DATE:  
 RELEVANT RESIDUES IN SEQ ID NO:  
 US-08-360-125-5  
 Query Match 77.4%; Score 471.5; DB 1; Length 119;  
 Best Local Similarity 75.9%; Pred. No. 7.9e-41;  
 Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;  
 QY 2 ESGPGLVPAQTSLSCAVSGSIRSGYVSWIRHHPGKLEWIGYIYHSGNTYVPSL 61  
 DB 6 ESGPGLVPSQTLSTCTVSGGSISSCGFYNNWRHHPGKLEWIGYIYHSGNTYVPSL 65  
 QY 62 KSRIAMSVDTSENKFSRLNSVTADTAIVYCA--RIDGYTLDIWGGTILVTSS 114  
 DB 66 KSRVTISLDTSKSQFSIKLSLTADTAIVYCARSTLRG--ADYWGQGTWVTVSS 119  
 RESULT 6  
 US-08-450-578-5  
 Sequence 5, Application US/08450578  
 Patent No. 5837845  
 GENERAL INFORMATION:  
 APPLICANT: Saiko HOSOKAWA  
 APPLICANT: Toshiaki TAGAWA  
 APPLICANT: Yoko HIRAKAWA  
 APPLICANT: No. 5837845hiko ITO  
 APPLICANT: Kazuhito NAGAIKE  
 TITLE OF INVENTION: Human Monoclonal Antibody  
 TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Menderoth, Lind & Ponack  
 STREET: 805 Fifteenth Street, N.W., #700  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/450,578  
 FILING DATE: May 25, 1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/360,125  
 FILING DATE: December 20, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/905,534  
 FILING DATE: June 29, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek, Jr.  
 REGISTRATION NUMBER: 33,367  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-8850  
 TELEFAX:  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 119 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHEICAL:  
 ANTI-SENSE:  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM:

STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL LINE: antibody GAH  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-5

Query Match 77.4%; Score 471.5; DB 2; Length 119;  
Best Local Similarity 75.9%; Pred. No. 7.9e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

Qy 2 ESGPGLVPAQTLTSLSCAVSGSIRSGYWSWIRQHPGKLEWIGYTHSGNTYVNSL 61  
Db 6 ESGPGLVPAQTLTSLTCTVSGSGSISCGFYNNMIRQHPGKLEWIGYTHSGNTYVNSL 65

Qy 62 KSRVAMVDTSSENKFSRLNSVTADTAIVYCA---RLDGYTLDIWGGTLVTVSS 114  
Db 66 KSRVTISLDTSKQFSLKSLSTRADTAIVYCASTRLRG--ADYWGCGTMTVTVSS 119

RESULT 7  
US-09-017-628-5  
Sequence 5, Application US/09017628  
Patent No. 5990287  
GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saiko  
APPLICANT: TAGAWA, Toshiaki  
APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITO, No. 5990287hiko  
APPLICANT: NAGAIKE, Kazuhiko  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
FILE REFERENCE: 177/527361KH  
CURRENT APPLICATION NUMBER: US/09/017, 628  
CURRENT FILING DATE: 1998-02-02  
EARLIER APPLICATION NUMBER: 08/360,125  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 119  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody GAH

US-09-017-628-5

Query Match 77.4%; Score 471.5; DB 2; Length 119;  
Best Local Similarity 75.9%; Pred. No. 7.9e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

Qy 2 ESGPGLVPAQTLTSLSCAVSGSIRSGYWSWIRQHPGKLEWIGYTHSGNTYVNSL 61  
Db 6 ESGPGLVPAQTLTSLTCTVSGSGSISCGFYNNMIRQHPGKLEWIGYTHSGNTYVNSL 65

Qy 62 KSRVAMVDTSSENKFSRLNSVTADTAIVYCA---RLDGYTLDIWGGTLVTVSS 114  
Db 66 KSRVTISLDTSKQFSLKSLSTRADTAIVYCASTRLRG--ADYWGCGTMTVTVSS 119

RESULT 8  
US-09-014-880-5  
Sequence 5, Application US/09014880  
Patent No. 5990297  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA et al.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014,880  
FILING DATE: January 28, 1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,578  
FILING DATE: May 25, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
US-09-014-880-5

Query Match 77.4%; Score 471.5; DB 2; Length 119;  
Best Local Similarity 75.9%; Pred. No. 7.9e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;



STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,363  
FILING DATE: May 25, 1995  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL LINE:  
CELL TYPE: antibody G4H  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-363-5

Query Match 77.4%; Score 471.5; DB 4; Length 119;  
Best Local Similarity 75.9%; Pred. No. 7.9e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;  
Qy 2 ESGPGLVPAQOTLSLSCAVSGGSIKSGYWSWIRQHPGKLEWIGYIYHSGNTYVPSL 61  
Db 6 ESGPGLVPSQTLSTLTVSGGSISSCGFYWMWIRQHPGKLEWIGYIYHSGNTYVPSL 65  
Qy 62 KSRIVMSVDTSENKFSRLNSVTPADPAVYCA---RLDGYTLDIWOGTLVTVSS 114  
Db 66 KSRVTISLDTSKSQFSLKSLTPADPAVYCAKSTLRG--ADYWGQGMVTVSS 119  
RESULT 12  
US-09-490-070A-39  
Sequence 39, Application US/09490070A  
Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pach, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
White & McCauliffe  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-070A-39  
Query Match 77.4%; Score 471.5; DB 4; Length 119;  
Best Local Similarity 77.6%; Pred. No. 7.9e-41;  
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;  
Qy 2 ESGPGLVPAQOTLSLSCAVSGGSIKSGYWSWIRQHPGKLEWIGYIYHSGNTYVPSL 61  
Db 6 ESGPGLVPSQTLSTLTVSGGSISS--YVMSWIRQHPGKLEWIGYIYHSGNTYVPSL 63  
Qy 62 KSRIVMSVDTSENKFSRLNSVTPADPAVYCARLDG---YTDIDWOGTLVTVSS 114  
Db 64 KSRVTISVDTSKQFSLKSLTPADPAVYCARWGDGFYAMDWOGTLVTVSS 119



## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-153-65

## Query Match

77.4%; Score 471.5; DB 4; Length 119;

Best Local Similarity 77.6%; Pred. No. 7.9e-41;

Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

Qy	2	ESGGLVPAQTLSLSCAVSGSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYVNSL	61
Db	6	ESGGLVPAQTLSLSCAVSGSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYVNSL	63
Qy	62	KSRIAMSVDTSENKFSRLNSVTADTAIVYCARLDG--YTLDIWGQGLVTVSS	114
Db	64	KSRYTISVDTSKNOFSLKLSVTADTAIVYCARWGDDGFYAMDYWGQGLVTVSS	119

Search completed: July 26, 2005, 09:29:58

Job time : 22.5909 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:07:26 ; Search time 14.6818 Seconds

(without alignments)  
747.095 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614  
Sequence: 1 LESGPGLVKPSQTLSTCTV.....RSDGYTLDMGQGLTVVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapect 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	499.5	81.4	135	2 S78051	Ig heavy chain pre
2	495.5	80.7	147	2 S13519	Ig heavy chain V r
3	487	79.3	130	2 S30534	Ig heavy chain V r
4	480.5	78.3	121	2 S44113	Ig heavy chain V r
5	478.5	77.9	140	2 S37782	Ig variable region
6	477.5	77.8	146	2 S09710	Ig heavy chain V r
7	474.5	77.3	116	2 S37456	Ig mu chain - huma
8	474.5	77.3	130	2 S31690	Ig heavy chain V r
9	474	77.2	122	2 S69912	Ig heavy chain V r
10	473.5	77.1	128	2 S31514	Ig V-D-J region (N
11	472.5	77.0	127	2 S19668	Ig heavy chain - h
12	469	76.4	137	2 S31676	Ig heavy chain V r
13	468.5	76.3	123	2 S30530	Ig heavy chain V r
14	465.5	75.8	155	2 S31511	Ig heavy chain - h
15	463.5	75.5	155	2 S31512	Ig heavy chain - h
16	462	75.2	139	2 S31586	Ig heavy chain V r
17	460.5	75.0	146	2 S09711	Ig heavy chain V r
18	460	74.9	145	2 S78055	Ig heavy chain pre
19	459.5	74.8	109	2 PH1673	Ig heavy chain V r
20	457	74.4	110	2 S44110	Ig heavy chain V-D
21	455	74.1	99	2 S26803	Ig heavy chain V r
22	454	73.9	139	2 A41287	Ig heavy chain pre
23	453	73.8	99	2 S26801	Ig heavy chain V r
24	452	73.6	129	2 S44114	Ig heavy chain V r
25	450	73.3	99	2 S26802	Ig heavy chain V r
26	450	73.3	135	2 S31604	Ig heavy chain V r
27	447	72.8	118	2 S20780	Ig heavy chain V r
28	446	72.6	99	2 S12418	Ig heavy chain V r
29	444.5	72.4	139	2 S31696	Ig heavy chain V r

30	443	72.1	118	2 A26340	Ig heavy chain pre
31	442.5	71.9	140	2 A49045	Ig heavy chain V r
32	441.5	71.9	132	2 A38911	Ig heavy chain V r
33	441	71.8	99	2 S26800	Ig heavy chain V r
34	441	71.8	126	2 S47010	Ig heavy chain V4.
35	440.5	71.7	129	1 D2HWA	Ig heavy chain V-I
36	440	71.7	97	2 PK0118	Ig heavy chain V-I
37	440	71.7	99	2 S26859	Ig heavy chain V r
38	439.5	71.6	98	2 S12421	Ig heavy chain V r
39	439.5	71.6	140	2 A24770	Ig heavy chain V r
40	439	71.5	140	2 S78052	Ig heavy chain pre
41	438.5	71.4	123	2 S30529	Ig heavy chain V r
42	438	71.3	120	2 P70370	Ig mu chain precu
43	437	71.2	124	2 S31684	Ig heavy chain V r
44	435.5	70.9	134	2 S54906	Ig heavy chain V r
45	434.5	70.8	98	2 S26902	Ig heavy chain V r

## ALIGNMENTS

## RESULT 1

S78051

Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)  
C/Species: Homo sapiens (man)

C/Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999

C/Accession: S78051; S23716

R/Harindranath, N.

Submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78051

A/Molecule type: mRNA

A/Residues: 1-135 <HAR>

A/Cross-references: EMBL:X54437; NID:937814; PIDN:CA38306.1; PID:9930117

R/Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burratello, S.E.; Wilder, R.L.; Notkins

Int. Immunol. 3, 865-875, 1991

A/Title: Complete sequence of the gene encoding the V(H) and V(L) regions of low- and h

patient.

A/Reference number: S23716; MUID:92031262; PMID:1718404

A/Accession: S23716

A/Molecule type: mRNA

A/Residues: 13-111 <HAW>

A/Cross-references: EMBL:X54437

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F/1-13/Domain: signal sequence (fragment) #status predicted <SIG>

F/14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>

F/27-111/Domain: immunoglobulin homology <IMM>

## Query Match

Best Local Similarity 79.7%; Pred. No. 1.2e-37;  
Matches 94; Conservative 10; Mismatches 9; Indels 5; Gaps 2;

## QY

2 ESGPGLVPSQTLSTCTVSGSGIRSGYVSWNPQPGKLEWIGNIYHSNTYNDL 61

18 ESGPGLVPSQTLSTCTVSGSGIRSGYVSWNPQPGKLEWIGNIYHSNTYNDL 77

## QY

62 KSRTMSVDTSKNHSFLSTVTAADTVVYCAR--SPQGYLDN---WGQGLTVVSS 114

78 KSRVTISVDTSKNPSLKLSTVTAADTVVYCARLGPDPDTLDGMDVWGQGLTVVSS 135

## RESULT 2

S13519

Ig heavy chain V region precursor - human

C/Species: Homo sapiens (man)

C/Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S13519

R/Morari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.

Nucleic Acids Res. 19, 673, 1991

A/Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked

A/Reference number: S13519; MUID:91187691; PMID:2011536

A/Accession: S13519

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-147 <MOR>  
A:Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:41-125/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 495.5; DB 2; Length 147;  
Best Local Similarity 80.2%; Pred. No. 3.1e-37;  
Matches 93; Conservative 9; Mismatches 11; Indels 3; Gaps 1;

Qy 2 ESGGGLVKSPTSLTCTVSGGSIIRSGGYMSWRQPGKLEWIGNIGHSGNTYNPSTL 61  
Db 32 ESGGGLVKSPTSLTCTVSGGSIIRSGGYMSWRQPGKLEWIGNIGHSGNTYNPSTL 91

Qy 62 KSRITMSVDTSKNHPSRLTSVTADTAIVYYCARSDG---DGYTLDMWGQGLTVTVSS 114  
Db 92 KSRVTISVDTSKNQPSLKLSSVTADTAIVYYCARFLMFGSLFDYWGQGLTVTVSS 147

RESULT 3  
S30534  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
C:Accession: S30534  
R:Marielette, X.  
Submitted to the EMBL Data Library, October 1992  
A:Reference number: S30520  
A:Accession: S30534  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-130 <MAR>  
A:Cross-references: EMBL:Z18320  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 487; DB 2; Length 130;  
Best Local Similarity 76.0%; Pred. No. 1.5e-36;  
Matches 95; Conservative 7; Mismatches 11; Indels 12; Gaps 2;

Qy 2 ESGGGLVKSPTSLTCTVSGGSIIRSGGYMSWRQPGKLEWIGNIGHSGNTYNPSTL 61  
Db 6 ESGGGLVKSPTSLTCTVSGGSIIRSGGYMSWRQPGKLEWIGNIGHSGNTYNPSTL 65

Qy 62 KSRITMSVDTSKNHPSRLTSVTADTAIVYYCARSDG-----YTLDMWGQGLTVTVSS 109  
Db 66 KSRVTISVDTSKNQPSLKLSSVTADTAIVYYCARDKGFGFGGYTRNSRAAFDWMGQGLTV 125

Qy 110 VTSS 114  
Db 126 VTSS 130

RESULT 4  
S44113  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C:Accession: S44113  
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
Submitted to the EMBL Data Library, March 1994  
A:Description: Idiolytic vaccination against human B-cell lymphoma: rescue of variable r  
A:Reference number: S44105  
A:Accession: S44113  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-121 <HAW>  
A:Cross-references: EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PID:g940524  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 480.5; DB 2; Length 121;  
Best Local Similarity 78.4%; Pred. No. 5.4e-36;  
Matches 91; Conservative 9; Mismatches 13; Indels 3; Gaps 2;

Qy 2 ESGGGLVKSPTSLTCTVSGGSIIRSGGYMSWRQPGKLEWIGNIGHSGNTYNPSTL 61  
Db 6 ESGGGLVKSPTSLTCTVSGGSIIRSGGYMSWRQPGKLEWIGNIGHSGNTYNPSTL 65

Qy 62 KSRITMSVDTSKNHPSRLTSVTADTAIVYYCAR-SPGY--TLDMWGQGLTVTVSS 114  
Db 66 KSRVTISVDTSKNQPSLKLSSVTADTAIVYYCARLSGSGYISDFPYWGQGLTVTVSS 121

RESULT 5  
I37782  
Ig variable region (VDJ) (clone T23-9) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C:Accession: I37782; S25476  
R:Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A:Title: Somatic diversification in the heavy chain variable region genes expressed by h  
A:Reference number: A36876; MUID:94119917; PMID:8290556  
A:Accession: I37782  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140 <RES>  
A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:46-128/Domain: immunoglobulin homology <IMM>

Query Match 77.9%; Score 478.5; DB 2; Length 140;  
Best Local Similarity 78.8%; Pred. No. 9.5e-36;  
Matches 93; Conservative 9; Mismatches 9; Indels 7; Gaps 2;

Qy 2 ESGGGLVKSPTSLTCTVSGGSIIRSGGYMSWRQPGKLEWIGNIGHSGNTYNPSTL 61  
Db 25 ESGGGLVKSPTSLTCTVSGGSIIRSGGYMSWRQPGKLEWIGNIGHSGNTYNPSTL 82

Qy 62 KSRITMSVDTSKNHPSRLTSVTADTAIVYYCARSD-----GYTLDMWGQGLTVTVSS 114  
Db 83 KSRVTISVDTSKNQPSLKLSSVTADTAIVYYCARHSSSWYGRFYDWMGQGLTVTVSS 140

RESULT 6  
S09710  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S09710  
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains o  
A:Reference number: S09710; MUID:90262535; PMID:2111699  
A:Accession: S09710  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-146 <HUG>  
A:Cross-references: GB:X52110; NID:g31447; PIDN:CAA36344.1; PID:g31448  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 477.5; DB 2; Length 146;  
Best Local Similarity 73.2%; Pred. No. 1.2e-35;  
Matches 90; Conservative 13; Mismatches 9; Indels 11; Gaps 2;

Qy 2 ESGGGLVKSPTSLTCTVSGGSIIRSGGYMSWRQPGKLEWIGNIGHSGNTYNPSTL 61  
Db 25 ESGGGLVKSPTSLTCTVSGGSIIRSGGYMSWRQPGKLEWIGNIGHSGNTYNPSTL 84



C:Accession: S19668; S24445  
C:Marker: U.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991  
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on pH A:Reference number: S19663; MUID:92085276; PMID:1748994  
A:Accession: S19668  
A:Molecule type: mRNA  
A:Residues: 1-127 <MAR>  
A:Cross-references: EMBL:X61648  
R:Jones, P.T.  
Submitted to the EMBL Data Library, October 1991  
A:Reference number: S24442  
A:Accession: S24445  
A:Molecule type: mRNA  
A:Residues: 1-118, 'E', 120-121, 'T', 123-126, 'F' <DON>  
A:Cross-references: EMBL:X61648; NID:g37722; PIDN:CAA43829.1; PID:g1335380  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 127;  
Best Local Similarity 73.0%; Pred. No. 2.9e-35;  
Matches 89; Conservative 12; Mismatches 12; Indels 9; Gaps 1;

Qy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGYVSWVRQPPGKGLVIGTINYSNTYYNPDL 61  
Db 6 QSGGGLVPSQTLSTCTVSGSDSISSGYVSWVRQPPGKGLVIGTINYSNTYYNPDL 65

Qy 62 KSRITMSVDTSKHFSLRLTSVTADTAIVYCARSDG-----YTLDMNGGTLVTV 112  
Db 66 KSRITMSVDTSKHFSLRLTSVTADTAIVYCARSDG-----YTLDMNGGTLVTV 125

Qy 113 SS 114  
Db 126 SS 127

RESULT 12  
S31676  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31676  
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Pougereau, M.; Tonnelie, C.  
Submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the A:Reference number: S31585  
A:Accession: S31676  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-137 <CU>  
A:Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 469; DB 2; Length 137;  
Best Local Similarity 80.0%; Pred. No. 6.5e-35;  
Matches 92; Conservative 7; Mismatches 12; Indels 4; Gaps 2;

Qy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGYVSWVRQPPGKGLVIGTINYSNTYYNPDL 61  
Db 25 ESGGGLVPSQTLSTCTVSGSIS--YVSWVRQPPGKGLVIGTINYSNTYYNPDL 82

Qy 62 KSRITMSVDTSKHFSLRLTSVTADTAIVYCARSDG-----YTLDMNGGTLVTVSS 114  
Db 83 KSRITMSVDTSKHFSLRLTSVTADTAIVYCARSDG-----YTLDMNGGTLVTVSS 137

RESULT 13  
S30530  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)

C:Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C:Accession: S30530  
R:Marieje, X.  
Submitted to the EMBL Data Library, October 1992  
A:Reference number: S30520  
A:Accession: S30530  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-123 <MAR>  
A:Cross-references: EMBL:Z18316  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 468.5; DB 2; Length 123;  
Best Local Similarity 75.6%; Pred. No. 6.4e-35;  
Matches 90; Conservative 11; Mismatches 11; Indels 7; Gaps 2;

Qy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGYVSWVRQPPGKGLVIGTINYSNTYYNPDL 61  
Db 6 ESGGGLVPSQTLSTCTVSGYSI--SSGYVSWVRQPPGKGLVIGTINYSNTYYNPDL 64

Qy 62 KSRITMSVDTSKHFSLRLTSVTADTAIVYCAR-----SDGYTLDMNGGTLVTVSS 114  
Db 65 KSRITMSVDTSKHFSLRLTSVTADTAIVYCAR-----SDGYTLDMNGGTLVTVSS 123

RESULT 14  
S31511  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31511  
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
Submitted to the EMBL Data Library, December 1992.  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto:  
A:Reference number: S31509  
A:Accession: S31511  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 75.8%; Score 465.5; DB 2; Length 155;  
Best Local Similarity 74.2%; Pred. No. 1.5e-34;  
Matches 89; Conservative 11; Mismatches 11; Indels 9; Gaps 2;

Qy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGYVSWVRQPPGKGLVIGTINYSNTYYNPDL 61  
Db 38 ESGGGLVPSQTLSTCTVSGSIS--YVSWVRQPPGKGLVIGTINYSNTYYNPDL 95

Qy 62 KSRITMSVDTSKHFSLRLTSVTADTAIVYCARSDG-----YTLDMNGGTLVTVSS 114  
Db 96 KSRITMSVDTSKHFSLRLTSVTADTAIVYCARSDG-----YTLDMNGGTLVTVSS 155

RESULT 15  
S31512  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31512  
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
Submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto:  
A:Reference number: S31509  
A:Accession: S31512  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>

A:Cross-references: EMBL:X69860; NID:g33082; PID:CAA49494.1; PID:g33083  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 463.5; DB 2; Length 155;  
Best Local Similarity 73.3%; Pred. No. 2,3e-34;  
Matches 88; Conservative 12; Mismatches 11; Indels 9; Gaps 2;  
Qy 2 ESGPGLVLPSPQTLSTCTVSGGSGIRSGGYWVWRQPPGKLEWIGNIYHSGNTYYNPQL 61  
Db 38 ESGPGLVLPSPETLSLCTVSGGSSIS--YVSMIRQPPGKLEWIGIYITGSATYNPPI 95  
Qy 62 KSRITMSYDTSKNHPSLRILTSYTAADTAIVYYCARSDG-----YTLDNMGQTLVTVSS 114  
Db 96 KSRVTISYDTSKNQPSLKVSVTAADTAIVYYCARGGGISWVYVYGMDDVMGQTLVTVSS 155

Search completed: July 26, 2005, 09:27:48  
Job time : 14.6818 secs

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KW Hypothetical protein.  
 SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;  
 Query Match 80.2%; Score 492.5; DB 2; Length 476;  
 Best Local Similarity 74.2%; Pred. No. 2.5e-41;  
 Matches 92; Conservative 13; Mismatches 6; Indels 13; Gaps 2;

QY 2 ESGGGLVPSQGLTSLTCTVSGSGSIRSGGYWVWVRQPPGKGLWIGNIYHSGNTYNPSTL 61  
 DB 25 ESGGGLVPSQGLTSLTCTVSGSGSIRSGGYWVWVRQPPGKGLWIGNIYHSGNTYNPSTL 84  
 QY KSRITMSVDSKQHFSLRLTSVTADPAVYYCARSDYTLDMNGGTLVTVSS 110  
 DB 85 KSRITMSVDSKQHFSLRLTSVTADPAVYYCARSDYTLDMNGGTLVTVSS 142  
 QY 111 TVSS 114  
 DB 143 TVSS 146

RESULT 2  
 Q6GKX6 PRELIMINARY; PRT; 465 AA.  
 AC 06GKX6;  
 DT 05-JUN-2004 (TReMBLrel. 27, Created)  
 DT 05-JUN-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUN-2004 (TReMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Tomshy L.S., Carrinci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Jones S.D., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073766; AAH73766.1; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF07654; C1-set; 3.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; Igcl; 3.  
 DR SMART; SM00406; Igv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;  
 Query Match 77.7%; Score 477; DB 2; Length 465;  
 Best Local Similarity 81.4%; Pred. No. 9e-40;  
 Matches 92; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 2 ESGGGLVPSQGLTSLTCTVSGSGSIRSGGYWVWVRQPPGKGLWIGNIYHSGNTYNPSTL 61  
 DB 25 ESGGGLVPSQGLTSLTCTVSGSGSIRSGGYWVWVRQPPGKGLWIGNIYHSGNTYNPSTL 82  
 QY KSRITMSVDSKQHFSLRLTSVTADPAVYYCARSDYTLDMNGGTLVTVSS 114  
 DB 83 KSRITMSVDSKQHFSLRLTSVTADPAVYYCARSDYTLDMNGGTLVTVSS 135

RESULT 3  
 Q72374 PRELIMINARY; PRT; 492 AA.  
 AC Q72374;  
 DT 01-OCT-2003 (TReMBLrel. 25, Created)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Hypothetical protein DKFZp686C02218 (Fragment).  
 GN Name=DKFZp686C02218;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human rectum tumor;  
 RA Bloecher H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX538077; CAB98001.1; -.  
 DR HSSP; P01820; 167J.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF07654; C1-set; 2.  
 DR SMART; SM00406; Igv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 FT NON TER  
 SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;  
 Query Match 77.6%; Score 476.5; DB 2; Length 492;  
 Best Local Similarity 76.9%; Pred. No. 1.1e-39;  
 Matches 90; Conservative 11; Mismatches 11; Indels 5; Gaps 2;

QY 2 ESGGGLVPSQGLTSLTCTVSGSGSIRSGGYWVWVRQPPGKGLWIGNIYHSGNTYNPSTL 61  
 DB 37 ESGGGLVPSQGLTSLTCTVSGSGSIRSGGYWVWVRQPPGKGLWIGNIYHSGNTYNPSTL 96  
 QY KSRITMSVDSKQHFSLRLTSVTADPAVYYCARSDYTLDMNGGTLVTVSS 114  
 DB 97 KSRITMSVDSKQHFSLRLTSVTADPAVYYCARSDYTLDMNGGTLVTVSS 152

RESULT 4  
 Q72379 PRELIMINARY; PRT; 478 AA.  
 AC Q72379;  
 DT 01-OCT-2003 (TReMBLrel. 25, Created)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Hypothetical protein DKFZp686C04218 (Fragment).  
 GN Name=DKFZp686C04218;  
 OS Homo sapiens (Human).



```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloembergen H., Boeher M., Wewes H.W., Weil B., Amid C., Oanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538066; CAD97996.1; -.
DR HSP; P01820; IGI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00406; IGV.1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG-MHC; UNKNOWN_2.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFB541F3217C61 CRC64;

Query Match 76.5%; Score 470; DB 2; Length 478;
Best Local Similarity 75.7%; Pred. No. 4.7e-39;
Matches 87; Conservative 14; Mismatches 12; Indels 2; Gaps 1;

QY 2 ESGGLVPSQTLSTCTVSGSGSIRSGYVSWRQPGKLEWIGNIYHSGNTYVPSL 61
DB 24 ESGGLVPSQTLSTCTVSGSGSIRSGYVSWRQPGKLEWIGNIYHSGNTYVPSL 83
QY 62 KSRITVSDTSKQNFSLRLTSVTADPAVYVCARSDGV--TLDNMGGTLTVVSS 114
DB 84 KSRITVSDTSKQNFSLRLTSVTADPAVYVCARSDGV--TLDNMGGTLTVVSS 138

RESULT 5
095973 PRELIMINARY; PRT; 150 AA.
AC 095973;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE VHA heavy chain variable region precursor (Fragment).
GN Name=IGH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR PIR; S31673; S31673.
DR HSP; P01820; IGI.
DR HSP; P01820; IGI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG-V.
DR SMART; SM00406; IGV.1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 >150 VHA heavy chain variable region.
FT NON TER 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 75.9%; Score 466; DB 2; Length 150;
Best Local Similarity 76.1%; Pred. No. 3.4e-39;
Matches 86; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 2 ESGGLVPSQTLSTCTVSGSGSIRSGYVSWRQPGKLEWIGNIYHSGNTYVPSL 61
DB 24 ESGGLVPSQTLSTCTVSGSGSIRSGYVSWRQPGKLEWIGNIYHSGNTYVPSL 83
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DB 25 ESGGLVPSQTLSTCTVSGSGSIRSGYVSWRQPGKLEWIGNIYHSGNTYVPSL 84
QY 62 KSRITVSDTSKQNFSLRLTSVTADPAVYVCARSDGV--TLDNMGGTLTVVSS 114
DB 85 KSRITVSDTSKQNFSLRLTSVTADPAVYVCARSDGV--TLDNMGGTLTVVSS 137

RESULT 6
096KX8 PRELIMINARY; PRT; 496 AA.
AC 096KX8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshlyak S., Carinini P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smaluk D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strauberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1; -.
DR HSP; P01876; IGM.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00406; IGV.1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG-MHC; UNKNOWN_1.
SQ SEQUENCE 496 AA; 53391 MW; D3469294849040D69 CRC64;

Query Match 75.9%; Score 466; DB 2; Length 496;
Best Local Similarity 74.2%; Pred. No. 1.2e-38;
Matches 89; Conservative 10; Mismatches 13; Indels 8; Gaps 2;

QY 2 ESGGLVPSQTLSTCTVSGSGSIRSGYVSWRQPGKLEWIGNIYHSGNTYVPSL 61
DB 25 ESGGLVPSQTLSTCTVSGSGSIRSGYVSWRQPGKLEWIGNIYHSGNTYVPSL 84
QY 62 KSRITVSDTSKQNFSLRLTSVTADPAVYVCARSDGV--TLDNMGGTLTVVSS 114
DB 85 KSRITVSDTSKQNFSLRLTSVTADPAVYVCARSDGV--TLDNMGGTLTVVSS 143
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RESULT 7
Q9UL73 PRELIMINARY; PRT; 119 AA.
ID Q9UL73
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827713; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EAOBE CRC64;

Query Match 75.5%; Score 463.5; DB 2; Length 119;
Best Local Similarity 77.6%; Pred. No. 4.8e-39;
Matches 90; Conservative 9; Mismatches 12; Indels 5; Gaps 2;

Qy 2 ESGGGLVKKPQTLSTLTCTVSGGSGIRSGYMSWRQPGKGLKLEWIGNIYHSGNTYNPSTL 61
Db 6 ESGGGLVKKPSETLSTLTCTVSGGSGIS--YMSWRQPGKGLKLEWIGNIYHSGNTYNPSTL 63
Qy 62 KSRITMSVDTSKNPSRLTSTVTAADTAVYYCARSDG--YTLDNWGGGLVTYSS 114
Db 64 KSRVTISVDRSKNPSTLSTLTADTAVYFCARLSNMGPFYFDWGGGLVTYSS 119

RESULT 8
Q6GMX7 PRELIMINARY; PRT; 477 AA.
ID Q6GMX7
AC Q6GMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshitsuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalton D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skaleja U., Smalms D.E., Schercher A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
   and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Straubeberg R.;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073765; AAH73765.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sect; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00409; IGV; 4.
DR SMART; SM00407; IGV; 3.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFE85 CRC64;

Query Match 74.4%; Score 457; DB 2; Length 477;
Best Local Similarity 77.4%; Pred. No. 9.7e-38;
Matches 89; Conservative 7; Mismatches 15; Indels 4; Gaps 2;

Qy 2 ESGGGLVKKPQTLSTLTCTVSGGSGIRSGYMSWRQPGKGLKLEWIGNIYHSGNTYNPSTL 61
Db 25 ESGGGLVKKPSETLSTLTCTVSGGSGIS--YMSWRQPGKGLKLEWIGNIYHSGNTYNPSTL 82
Qy 62 KSRITMSVDTSKNPSRLTSTVTAADTAVYYCARSDG--YTLDNWGGGLVTYSS 114
Db 83 KSRVTISVDRSKNPSTLSTLTADTAVYFCARLSNMGPFYFDWGGGLVTYSS 137

RESULT 9
Q96EY0 PRELIMINARY; PRT; 620 AA.
ID Q96EY0
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshitsuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strauberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC011857; AAH11857.2; -.  
 DR PIR; S15590; S15590.  
 DR HSSP; P01820; 1G7J.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; CI-set; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00407; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
 SQ SEQUENCE 620 AA; 68125 MW; 990A1A4AE8FF27B CRC64;  
 Query Match 74.4%; Score 457; DB 2; Length 620;  
 Best Local Similarity 78.0%; Pred. No. 1.3e-37;  
 Matches 92; Conservative 7; Mismatches 11; Indels 8; Gaps 3;  
 Oy 2 ESGGLVPSQTLSTCTVSGSIRSGGYWVRQPGKLEWIGNTYHSGNTYNSL 61  
 Db 32 ESGGLVPSQTLSTCTVSGSIRSGGYWVRQPGKLEWIGNTYHSGNTYNSL 89  
 Oy 62 KSRITMSVDTSKNPSLRITSVTAADTAIVYVCASDGYTLDN-----WGQGLVTVSS 114  
 Db 90 KSRITMSVDTSKNPSLRITSVTAADTAIVYVCASDGYTLDN-----WGQGLVTVSS 146  
 RESULT 10  
 Q6P418 PRELIMINARY; PRT; 576 AA.  
 ID Q6P418; PRELIMINARY; PRT; 576 AA.  
 AC Q6P418;  
 DT 05-JUL-2004 (TRENDEL. 27, Created)  
 DT 05-JUL-2004 (TRENDEL. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENDEL. 27, Last annotation update)  
 DE IGH protein.  
 GN Name=IGHD;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA MEDLINE=22288257; PubMed=12477932; DOI=10.1073/pnae.242603899;  
 RA Strauberg R.;  
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stadelon M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shechenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,

RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strauberg R.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC063384; AAH63384.1; -.  
 DR HSSP; P01820; 1A7N.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; CI-set; 2.  
 DR SMART; SM00407; IG; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00407; IGV; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;  
 Query Match 73.5%; Score 451; DB 2; Length 576;  
 Best Local Similarity 76.7%; Pred. No. 4.8e-37;  
 Matches 89; Conservative 7; Mismatches 16; Indels 4; Gaps 2;  
 Oy 2 ESGGLVPSQTLSTCTVSGSIRSGGYWVRQPGKLEWIGNTYHSGNTYNSL 61  
 Db 32 ESGGLVPSQTLSTCTVSGSIRSGGYWVRQPGKLEWIGNTYHSGNTYNSL 90  
 Oy 62 KSRITMSVDTSKNPSLRITSVTAADTAIVYVCASDGYTLDN-----YTLDNMGITLVTVSS 114  
 Db 91 KSRITMSVDTSKNPSLRITSVTAADTAIVYVCASDGYTLDN-----YTLDNMGITLVTVSS 146  
 RESULT 11  
 H2F\_HUMAN STANDARD; PRT; 129 AA.  
 ID H2F\_HUMAN STANDARD; PRT; 129 AA.  
 AC P01824;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig heavy chain V-II region WHH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=8222235; PubMed=6806818;  
 RA Takahashi N., Teraert D., Debutre B., Lin L.-C., Putnam F.W.;  
 RT "Complete amino acid sequence of the delta heavy chain of human  
 RT immunoglobulin D.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).  
 CC -I- MUSCLE/LAMBDOUS: This chain was isolated from an Igd myeloma  
 CC protein.  
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02099; D2HUMA.  
 DR HSSP; P01820; 1G7J.  
 DR GlycoSiteDB; P01824; -.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 113 Ig-like.



RC TISSUE=Lymph;  
RA Strauberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC019235; AAH19235.2; -.  
DR PIR; G34964; G34964.  
DR HSP; P01861; IADQ.  
DR Pfam; PF07654; Cl-sec; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Hypothetical protein.  
SQ SEQUENCE 595 AA; 65290 MW; 0D4B5076545714E CRC64;  
  
Query Match 69.5%; Score 426.5; DB 2; Length 595;  
Best Local Similarity 70.0%; Pred. No. 1.5e-34;  
Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;  
  
Cy 4 GPGVKSQTLSTCTVSGSIRSGYVSWVROPKGLGEMIGNIYHSGNTYNNPSLKS 63  
Db 34 GAGLLKSETLSTCTGVYGSF--SGYVSWVIRPPKGLGEMIGNIYHSGNTYNNPSLKS 91  
Cy 64 RITMSVDTSKKHFSRLTSVTAADTAVYYCAR-----SDG-YTLDNMGGTLVTVSS 114  
Db 92 RVTISVDTSKKQLSLKLSVNAADTAVYYCARVITRASPGTDGRYGMVWGQITVTVSS 151  
  
RESULT 15  
Q6GMX5 PRELIMINARY; PRT; 597 AA.  
AC Q6GMX5;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.F.,  
RA Jones S.J., Maira M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strauberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073767; AAH73767.1; -.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG\_LIKE.  
DR InterPro; IPR003597; IG\_cl.

DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-sec; 4.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;  
  
Query Match 69.5%; Score 426.5; DB 2; Length 597;  
Best Local Similarity 70.0%; Pred. No. 1.5e-34;  
Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;  
  
Cy 4 GPGVKSQTLSTCTVSGSIRSGYVSWVROPKGLGEMIGNIYHSGNTYNNPSLKS 63  
Db 27 GAGLLKSETLSTCTGVYGSF--SGYVSWVIRPPKGLGEMIGNIYHSGNTYNNPSLKS 84  
Cy 64 RITMSVDTSKKHFSRLTSVTAADTAVYYCAR-----SDG-YTLDNMGGTLVTVSS 114  
Db 85 RVTISVDTSKKQLSLKLSVNAADTAVYYCARVITRASPGTDGRYGMVWGQITVTVSS 144  
  
Search completed: July 26, 2005, 09:26:18  
Job time : 72.6818 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: July 26, 2005, 08:50:20 ; Search time 85.3273 Seconds  
(without alignments)  
516.724 Million cell updates/sec

Title: US-10-027-725a-8  
Perfect score: 614  
Sequence: 1 LBSGPGLVKPSQTLISLCTV.....RSDGYTLDMWGQGLVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	100.0	114	5	ABG30446 Human IGE
2	608	99.0	114	5	ABG30447 Human IGE
3	546	88.9	114	5	ABG30445 Human IGE
4	511	83.2	128	8	ADP22124 Human ant
5	511	83.2	128	8	ADP22104 Human ant
6	511	83.2	128	8	ADP22096 Human ant
7	510.5	83.1	121	7	ADP03982 Murine-ex
8	510	83.1	118	7	ADP03968 Murine-ex
9	509.5	83.0	123	7	ADP03870 Murine-ex
10	507.5	82.7	125	7	ADP03871 Murine-ex
11	507	82.6	120	7	ADP03974 Murine-ex
12	507	82.6	120	7	ADP03873 Murine-ex
13	507	82.6	122	7	ADP03977 Murine-ex
14	507	82.6	473	4	AAB36206 Human imm
15	506	82.4	221	7	ADJ32126 Human int
16	505.5	82.3	121	7	ADP03981 Murine-ex
17	505	82.2	128	8	ADP22120 Human ant
18	504.5	82.2	117	7	ADCC99784 Anti-huma
19	504.5	82.2	117	7	ADDO5388 Anti-MUC1
20	504.5	82.2	117	7	ADFO9826 Human ant
21	503.5	82.0	119	7	ADP03970 Murine-ex
22	502.5	81.8	123	2	AAW78433 Antibody
23	502.5	81.8	123	5	ABB97976 Heavy cha
24	502.5	81.8	123	7	ADG88414 anti-Ob-R
25	502.5	81.8	123	7	ADP03872 Murine-ex

26	502	81.8	124	7	ADP03935	Adp03935 Murine-ex
27	501	81.6	252	5	ABP45318	Adp45318 Human Bly
28	501	81.6	252	7	ADG96145	Adg96145 Single ch
29	500.5	81.5	127	4	AAQ80217	Haq80217 Human aut
30	500	81.4	120	7	ADP03958	Adp03958 Murine-ex
31	500	81.4	120	7	ADP03969	Adp03969 Murine-ex
32	500	81.4	121	7	ADJ80377	Adj80377 Antibody
33	500	81.4	126	3	AAB30584	Abp30584 A human v
34	500	81.4	126	5	ABP54970	Abp54970 Anti-idio
35	500	81.4	251	5	ABG80712	Abg80712 Amyloid P
36	500	81.4	254	5	ABG80713	Abg80713 Amyloid P
37	500	81.4	253	5	ABG80714	Abg80714 Human Igg
38	499.5	81.4	120	4	AAB62775	Aab62775 Human HIV
39	499.5	81.4	123	7	AAY42965	Aay42965 Kabat Id
40	499.5	81.4	135	7	AAY42974	Aay42974 Kabat Id
41	499	81.3	116	7	ADP03957	Adp03957 Murine-ex
42	498.5	81.2	125	7	ADP03868	Adp03868 Murine-ex
43	498.5	81.2	125	7	ADP03876	Adp03876 Murine-ex
44	498	81.1	123	4	AAB62745	Aab62745 Human HIV
45	497.5	81.0	119	7	ADP03961	Adp03961 Murine-ex

## ALIGNMENTS

RESULT 1	
ABG30446	
ID	ABG30446 standard; protein: 114 AA.
XX	
AC	ABG30446;
DT	21-OCT-2002 (first entry)
XX	
DE	Human IGE Fab clone 60 heavy chain protein.
XX	
KW	Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
KM	timothy grass pollen allergen; passive immunotherapy.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	/note= "FRI region"
FT	/note= "FR1 region"
FT	Region
FT	/note= "CDR1 region"
FT	/note= "FR2 region"
FT	Region
FT	/note= "CDR2 protein"
FT	/note= "FR3 region"
FT	Region
FT	/note= "CDR2 region"
FT	Region
FT	/note= "FR4 region"
XX	
PN	MO200253595-A1.
XX	
PD	11-JUL-2002.
XX	
PP	27-DEC-2001; 2001WO-SE002908.
XX	
PR	29-DEC-2000; 2000SF-00004892.
XX	
PA	(PHAA ) PHARMACIA DIAGNOSTICS AB.
XX	
PI	Flicker S, Steinberger P, Kraft D, Valenta R;
XX	
DR	WPI: 2002-583604/62.
XX	
PT	N-PSDB; ABK89638.
PT	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising variable region of group 2 allergen specific-human IGE Fabs, useful for

PT diagnosing or passive immunotherapy of type I allergy, for environmental  
PT allergen detection.  
XX  
XX  
PS Disclosure; Page 37; 45pp; English.  
XX  
XX This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE Fabs and methods for their use. The proteins  
CC of the invention may have antiallergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE  
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific Fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The Fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific Fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergic patients  
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
CC Fab, clone 60 heavy chain protein of the invention  
XX  
SQ Sequence 114 AA;  
Query Match 100.0%; Score 614; DB 5; Length 114;  
Best Local Similarity 100.0%; Pred. No. 9.9e-45;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWVROPFGKGLWIGNIYHSGNTYNNPS 60  
1 LESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWVROPFGKGLWIGNIYHSGNTYNNPS 60  
Db 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWVROPFGKGLWIGNIYHSGNTYNNPS 60  
QY 61 LKSRITMSVDTSKNHFSLRLTSVTADTAVYYCARSDGYTLDMWGQGLTVTVSS 114  
61 LKSRITMSVDTSKNHFSLRLTSVTADTAVYYCARSDGYTLDMWGQGLTVTVSS 114  
Db 61 LKSRITMSVDTSKNHFSLRLTSVTADTAVYYCARSDGYTLDMWGQGLTVTVSS 114  
RESULT 2  
ABG30447 ID ABG30447 standard; protein; 114 AA.  
XX  
AC ABG30447;  
XX  
XX 21-OCT-2002 (first entry)  
DE Human IgE Fab clone 100 heavy chain protein.  
XX  
XX Human; Fab; antiallergic; vaccine; grass pollen; Phi p 2;  
KM timothy grass pollen allergen; passive immunotherapy.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH 1..26  
FT /note= "FR1 region"  
FT 27..33  
FT /note= "CDR1 region"  
FT 34..47  
FT /note= "FR2 region"  
FT 48..63  
FT /note= "CDR2 protein"  
FT 64..95  
FT /note= "FR3 region"  
FT 96..103  
FT /note= "CDR2 region"  
FT 104..114  
FT /note= "FR4 region"  
XX  
XX WO200253595-A1.  
XX  
XX 11-JUL-2002.  
XX  
XX 27-DEC-2001; 2001WO-SB002908.  
XX

PR 29-DEC-2000; 2000SE-00004892.  
XX  
XX (PHAA ) PHARMACIA DIAGNOSTICS AB.  
XX  
XX Flicker S, Steinberger P, Kraft D, Valenta R;  
PI WPI; 2002-583604/62.  
XX  
XX N-PSDB; ABK89639.  
DR  
XX  
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
PT diagnosing or passive immunotherapy of type I allergy, for environmental  
PT allergen detection.  
XX  
XX  
PS Disclosure; Page 38; 45pp; English.  
XX  
XX This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE Fabs and methods for their use. The proteins  
CC of the invention may have antiallergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE  
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific Fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The Fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific Fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergic patients  
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
CC Fab, clone 100 heavy chain protein of the invention  
XX  
SQ Sequence 114 AA;  
Query Match 99.0%; Score 608; DB 5; Length 114;  
Best Local Similarity 97.4%; Pred. No. 3.2e-44;  
Matches 111; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWVROPFGKGLWIGNIYHSGNTYNNPS 60  
1 LESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWVROPFGKGLWIGNIYHSGNTYNNPS 60  
Db 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWVROPFGKGLWIGNIYHSGNTYNNPS 60  
QY 61 LKSRITMSVDTSKNHFSLRLTSVTADTAVYYCARSDGYTLDMWGQGLTVTVSS 114  
61 LKSRITMSVDTSKNHFSLRLTSVTADTAVYYCARSDGYTLDMWGQGLTVTVSS 114  
Db 61 LKSRITMSVDTSKNHFSLRLTSVTADTAVYYCARSDGYTLDMWGQGLTVTVSS 114  
RESULT 3  
ABG30445 ID ABG30445 standard; protein; 114 AA.  
XX  
AC ABG30445;  
XX  
XX 21-OCT-2002 (first entry)  
DE Human IgE Fab clone 94 heavy chain protein.  
XX  
XX Human; Fab; antiallergic; vaccine; grass pollen; Phi p 2;  
KM timothy grass pollen allergen; passive immunotherapy.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH 1..26  
FT /note= "FR1 region"  
FT 27..33  
FT /note= "CDR1 region"  
FT 34..47  
FT /note= "FR2 region"  
FT 48..63  
FT /note= "CDR2 protein"  
FT 64..95  
FT /note= "FR3 region"  
XX  
XX



FT Region 96.103  
FT /note="CDR2 region"  
FT 104.114  
FT Region /note="FR4 region"  
XX  
XX WO200253595-A1.  
XX  
XX 11-JUL-2002.  
XX  
XX 27-DEC-2001; 2001WO-SE002908.  
XX  
XX 29-DEC-2000; 2000SE-00004892.  
XX  
XX (PHAA) PHARMACIA DIAGNOSTICS AB.  
XX  
XX Flicker S, Steindberger P, Kraft D, Valenta R;  
XX  
XX WPI; 2002-583604/62.  
XX  
XX N-PSDB; ABK89637.  
XX  
XX  
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
PT diagnosing or passive immunotherapy of type I allergy, for environmental  
PT allergen detection.  
XX  
XX  
XX Disclosure; Page 36; 45pp; English.  
XX  
XX This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE Fabs and methods for their use. The proteins  
CC of the invention may have antiallergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE  
CC antibodies to Phi P 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific Fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The Fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific Fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergic patients  
CC IgE antibodies to Phi P 2. The present sequence represents the human IgG  
CC Fab, clone 94 heavy chain protein of the invention  
XX  
XX Sequence 114 AA:  
SQ  
Query Match 88.9%; Score 546; DB 5; Length 114;  
Best Local Similarity 89.5%; Pred. No. 6.1e-39;  
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
QY 1 LESGPGVLPKPSQTLSTCTVSGSIRSGGYWVSWRPPGKGLWIGNIYHSGNTYVNS 60  
DB 1 LESGPGVLPKPSQTLSTCTVSGSIRSGGYWVSWRPPGKGLWIGNIYHSGNTYVNS 60  
QY 61 LKSRITMSVDSKQHFSLRTSTYAADPAVYVCARSDGYTDNNQGLTVVSS 114  
DB 61 LKSRITMSVDSKQHFSLRTSTYAADPAVYVCARSDGYTDNNQGLTVVSS 114  
ID ADP22124 standard; protein, 128 AA.  
XX  
XX ADP22124;  
XX  
XX 09-SEP-2004 (first entry)  
XX  
XX Human anti-TNFA antibody heavy chain variable region SEQ ID NO:30.  
XX  
XX human, monoclonal antibody; tumour necrosis factor-alpha, TNFA;  
XX anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
XX antibacterial; antiinflammatory; antiproliferative; antineoplastic;  
XX eating-disorder; immunomodulator; immunosuppressive; nephrotoxic;  
XX neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;  
XX

KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
KW metastatic cancer; kidney cancer; colon cancer; pancreatic cancer;  
KW prostate cancer; immuno-mediated inflammatory disease;  
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
KW septic shock; cachexia; anorexia; multiple sclerosis.  
XX  
XX Homo sapiens.  
XX  
XX WO2004050683-A2.  
XX  
XX 17-JUN-2004.  
XX  
XX 02-DEC-2003; 2003WO-US038281.  
XX  
XX 02-DEC-2002; 2002US-0430729P.  
XX  
XX (ABGE-) AGENIX INC.  
XX  
XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
PI Haak-Frendrich M, Rathnaswami P, Pigott C, Liang ML, Lee R;  
PI Manchulenko K, Feghioni R, Senaldi G, Qiaojuan JS;  
XX  
XX WPI; 2004-480601/45.  
XX  
XX N-PSDB; ADP22123.  
XX  
XX  
XX New recombinant human monoclonal antibody that specifically binds to  
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
PT arthritis.  
XX  
XX Example 10; SEQ ID NO 30; 213pp; English.  
XX  
XX The present invention describes a human monoclonal antibody (I) that  
CC specifically binds to tumour necrosis factor-alpha (TNF) and comprises:  
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
CC (M1) the level of TNF in a patient sample, comprising contacting with  
CC (I), and detecting the level of binding between the antibody and TNF in  
CC the sample; (2) a composition comprising the antibody or its functional  
CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
CC animal in need of treatment for the disease by administering the human  
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNF induced  
CC apoptosis in an animal by selecting an animal in need of treatment for  
CC TNF induced apoptosis by administering the human monoclonal antibody of  
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
CC antibacterial, antiinflammatory, antiproliferative, antineoplastic, eating-  
CC disorders, immunomodulator, immunosuppressive, nephrotoxic,  
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
CC as a TNF antagonist. The antibody (I) is useful in the preparation of  
CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
CC diseases such as rheumatoid arthritis, glomerulonephritis,  
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
CC multiple sclerosis. The present sequence represents a human anti-TNFA  
CC antibody heavy chain variable region, which is used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 128 AA:  
SQ  
Query Match 83.2%; Score 511; DB 8; Length 128;  
Best Local Similarity 78.9%; Pred. No. 6.5e-36;  
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;  
QY 2 ESGPGVLPKPSQTLSTCTVSGSIRSGGYWVSWRPPGKGLWIGNIYHSGNTYVNS 61  
ID ADP22124 standard; protein, 128 AA.  
XX  
XX ADP22124;  
XX  
XX 09-SEP-2004 (first entry)  
XX  
XX Human anti-TNFA antibody heavy chain variable region SEQ ID NO:30.  
XX  
XX human, monoclonal antibody; tumour necrosis factor-alpha, TNFA;  
XX anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
XX antibacterial; antiinflammatory; antiproliferative; antineoplastic;  
XX eating-disorder; immunomodulator; immunosuppressive; nephrotoxic;  
XX neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;  
XX

DB 6 ESRGLVKEPQTLSTCTVSGGSISSGGYWSWVRPGKLEWIGNIYSGTYNPSL 65  
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDG-----YTIDNNQGGTLVY 111  
DB 66 KSRVITISVDTSKNHFSLRLTSVTAADTAVVYCARSDG-----YTIDNNQGGTLVY 125  
QY 112 VSS 114  
DB 126 VSS 128

RESULT 5  
ADP22104  
ID ADP22104 standard; protein; 128 AA.  
AC ADP22104;  
XX 09-SEP-2004 (first entry)  
DT Human anti-TNFa antibody heavy chain variable region SEQ ID NO:10.  
XX  
DE human, monoclonal antibody; tumour necrosis factor-alpha; TNFa;  
XX anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;  
XX antibacterial; antiinflammatory; antipsoiatic; antirheumatic;  
XX eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
XX neuoprotective; vasotropic; antiapoptotic; TNFa antagonist;  
XX TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
XX bladder cancer; lung cancer; glioblastoma; stomach cancer;  
XX endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
XX prostate cancer; immun-mediated inflammatory disease;  
XX rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
XX restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
XX septic shock; cachexia; anorexia; multiple sclerosis.  
OS Homo sapiens.  
XX  
XX WO2004050683-A2.  
PN 17-JUN-2004.  
XX  
XX 02-DEC-2003; 2003WO-US038281.  
PF  
XX 02-DEC-2002; 2002US-0430729P.  
PR  
XX (ABGE-) ABGENIX INC.  
PA Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
PI Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;  
PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan US;  
XX WPI; 2004-480601/45.  
XX N-PSDB; ADP22103.  
DR  
XX  
PT New recombinant human monoclonal antibody that specifically binds to  
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
PT arthritis.  
PT  
XX Example 10; SEQ ID NO 10; 213pp; English.

CC The present invention describes a human monoclonal antibody (I) that  
CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:  
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
CC (M1) the level of TNFa in a patient sample, comprising contacting with  
CC (11), and detecting the level of binding between the antibody and TNFa in  
CC the sample; (2) a composition comprising the antibody or its functional  
CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
CC animal in need of treatment for the disease by administering the human  
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced

CC apoptosis in an animal by selecting an animal in need of treatment for  
CC TNFa induced apoptosis by administering the human monoclonal antibody of  
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
CC antibacterial, antiinflammatory, antipsoiatic, antirheumatic, eating-  
CC disorder, immunomodulator, immunosuppressive, nephrotropic,  
CC neuoprotective, vasotropic and antiapoptotic activities, and can be used  
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of  
CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
CC diseases such as rheumatoid arthritis, glomerulonephritis, Crohn's  
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
CC multiple sclerosis. The present sequence represents a human anti-TNFa  
CC antibody heavy chain variable region, which is used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 128 AA;  
Query Match 83.2%; Score 511; DB 8; Length 128;  
Best Local Similarity 78.9%; Pred. No. 6.5e-36;  
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;  
QY 2 ESRGLVKEPQTLSTCTVSGGSISSGGYWSWVRPGKLEWIGNIYSGTYNPSL 61  
DB 6 ESRGLVKEPQTLSTCTVSGGSISSGGYWSWVRPGKLEWIGNIYSGTYNPSL 65  
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDG-----YTIDNNQGGTLVY 111  
DB 66 KSRVITISVDTSKNHFSLRLTSVTAADTAVVYCARSDG-----YTIDNNQGGTLVY 125  
QY 112 VSS 114  
DB 126 VSS 128

RESULT 6  
ADP22096  
ID ADP22096 standard; protein; 128 AA.  
AC ADP22096;  
XX 09-SEP-2004 (first entry)  
DT Human anti-TNFa antibody heavy chain variable region SEQ ID NO:2.  
XX  
DE human, monoclonal antibody; tumour necrosis factor-alpha; TNFa;  
XX anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;  
XX antibacterial; antiinflammatory; antipsoiatic; antirheumatic;  
XX eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
XX neuoprotective; vasotropic; antiapoptotic; TNFa antagonist;  
XX TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
XX bladder cancer; lung cancer; glioblastoma; stomach cancer;  
XX endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
XX prostate cancer; immun-mediated inflammatory disease;  
XX rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
XX restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
XX septic shock; cachexia; anorexia; multiple sclerosis.  
OS Homo sapiens.  
XX  
XX WO2004050683-A2.  
PN 17-JUN-2004.  
XX  
XX 02-DEC-2003; 2003WO-US038281.  
PF  
XX 02-DEC-2002; 2002US-0430729P.  
PR  
XX (ABGE-) ABGENIX INC.  
PA Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
PI

PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenchu K, Fagioni R, Senaldi G, Qiaojuan JS;  
 XX WPI; 2004-480601/45.  
 DR N-PSDB; ADP22095.

PT New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor- $\alpha$ , useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.

XX Example 10; SEQ ID NO 2; 213pp; English.

XX The present invention describes a human monoclonal antibody (1) that  
 CC specifically binds to tumor necrosis factor- $\alpha$  (TNF $\alpha$ ) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNF $\alpha$  in a patient sample, comprising contacting with  
 CC (1), and detecting the level of binding between the antibody and TNF $\alpha$  in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (1); and (4) inhibiting (M3) TNF $\alpha$  induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNF $\alpha$  induced apoptosis by administering the human monoclonal antibody of  
 CC (1). (1) has anabolic, antiarteriosclerotic, antirheumatic, eating-  
 CC disorder, antiinflammatory, antiproliferative, antihemetic, eating-  
 CC neuroprotective, vasotropic and antiproliferative activities, and can be used  
 CC as a TNF $\alpha$  antagonist. The antibody (1) is useful in the preparation of a  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNF $\alpha$   
 CC antibody heavy chain variable region, which is used in the  
 CC exemplification of the present invention.

XX Sequence 128 AA;

Query Match 83.2%; Score 511; DB 8; Length 128;

Best Local Similarity 78.9%; Pred. No. 6.5e-36;  
 Matches 97; Conservative 7; Mismatches 3; Indels 10; Gaps 1;

QY 2 ESGGGLVKEPQSLTCTVSGGSIKSGGYMSWVROPKGLKLEWIGNIYHSGNTYNPSTL 61  
 DB 6 ESGGGLVKEPQSLTCTVSGGSIKSGGYMSWVROPKGLKLEWIGNIYHSGNTYNPSTL 65  
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYVCARSDG-----YTLDDNMGQGLTVT 111  
 DB 66 KSRITISVDTSKNHFSLRLTSVTAADTAIVYVCARSDG-----YTLDDNMGQGLTVT 125

QY 112 VSS 114  
 DB 126 VSS 128

RESULT 7  
 ADP03982  
 ID ADP03982 standard; protein, 121 AA.

AC ADP03982;

DT 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 152.

KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX Unidentified.

OS WO2003048328-A2.

XX 12-JUN-2003.

PF 02-DEC-2002; 2002WO-US038550.

PR 03-DEC-2001; 2001US-0337275P.

PA (ABGE-) ABGENIX INC.

PI Gudae J, Foltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.

PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Example 2; SEQ ID NO 152; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytotoxic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.

XX Sequence 121 AA;

Query Match 83.1%; Score 510.5; DB 7; Length 121;

Best Local Similarity 82.8%; Pred. No. 6.8e-36;  
 Matches 96; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 2 ESGGGLVKEPQSLTCTVSGGSIKSGGYMSWVROPKGLKLEWIGNIYHSGNTYNPSTL 61  
 DB 6 ESGGGLVKEPQSLTCTVSGGSIKSGGYMSWVROPKGLKLEWIGNIYHSGNTYNPSTL 65  
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYVCARSDG-----GYTLDDNMGQGLTVT 114  
 DB 66 KSRITISVDTSKNHFSLRLTSVTAADTAIVYVCARSDG-----GYTLDDNMGQGLTVT 121

RESULT 8  
 ADP03968  
 ID ADP03968 standard; protein, 118 AA.

AC ADP03968;

DT 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.

XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;

XX cytosolic; colorectal neoplasm; renal cell carcinoma;

XX cervical intraepithelial squamous neoplasia; oesophageal; breast cancer;  
 XX cervical intraepithelial glandular neoplasia; human; heavy chain variable domain.

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OS Unidentified.
XX
XX WO2003048328-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudae J, Foltz I, Handa M, Gallo M;
XX WPI, 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 138, 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytosstatic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.
XX
XX Sequence 118 AA.
SQ
XX
XX Query Match 83.1%; Score 510; DB 7; Length 118;
XX Best Local Similarity 85.0%; Pred. No. 7.3e-36;
XX Matches 96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
XX
XX QY 2 ESGPGLVKEPQTLSTCTVSGGSRGGYMSWVRPGKGLWIGNIHSGNTYNPSTL 61
XX DB 6 ESGPGLVKEPQTLSTCTVSGGSRGGYMSWVRPGKGLWIGNIHSGNTYNPSTL 65
XX
XX QY 62 KSRITMSVDPFSKQHFSLRITSVTAADTAAYVYCARSDGYTLDMWGQGLVTVSS 114
XX DB 66 KSRVITISVDPFSKQHFSLRITSVTAADTAAYVYCARSDGYTLDMWGQGLVTVSS 118
XX
XX RESULT 9
XX ADP03870
XX ID ADP03870 standard; protein; 123 AA.
XX
XX AC ADP03870;
XX
XX DT 29-JUL-2004 (first entry)
XX
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.
XX
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX cytosstatic; colorectal neoplasm; renal cell carcinoma;
XX cervical intraepithelial squamous neoplasia;
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
XX
XX OS WO2003048328-A2.
XX
XX PN 12-JUN-2003.
XX
XX PD
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PF 02-DEC-2002; 2002WO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudae J, Foltz I, Handa M, Gallo M;
XX WPI, 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Claim 1; SEQ ID NO 10; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytosstatic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.
XX
XX Sequence 123 AA.
SQ
XX
XX Query Match 83.0%; Score 509.5; DB 7; Length 123;
XX Best Local Similarity 82.2%; Pred. No. 8.4e-36;
XX Matches 97; Conservative 8; Mismatches 8; Indels 5; Gaps 1;
XX
XX QY 2 ESGPGLVKEPQTLSTCTVSGGSRGGYMSWVRPGKGLWIGNIHSGNTYNPSTL 61
XX DB 6 ESGPGLVKEPQTLSTCTVSGGSRGGYMSWVRPGKGLWIGNIHSGNTYNPSTL 65
XX
XX QY 62 KSRITMSVDPFSKQHFSLRITSVTAADTAAYVYCARSDGYTLDMWGQGLVTVSS 114
XX DB 66 KSRVITISVDPFSKQHFSLRITSVTAADTAAYVYCARSDGYTLDMWGQGLVTVSS 123
XX
XX RESULT 10
XX ADP03871
XX ID ADP03871 standard; protein; 125 AA.
XX
XX AC ADP03871;
XX
XX DT 29-JUL-2004 (first entry)
XX
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.
XX
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX cytosstatic; colorectal neoplasm; renal cell carcinoma;
XX cervical intraepithelial squamous neoplasia;
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
XX
XX OS WO2003048328-A2.
XX
XX PN 12-JUN-2003.
XX
XX PD 02-DEC-2002; 2002WO-US038550.
XX
XX PF 03-DEC-2001; 2001US-0337275P.
XX
XX PR (ABGE-) ABGENIX INC.
XX
XX PA
```

PI Gudas J, Foltz I, Handa M, Gallo M;  
 XX WPI; 2003-523295/49.  
 XX  
 PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 XX intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 PS Claim 1; SEQ ID NO 11; 89pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody (mab)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention  
 CC demonstrates cyrostatic activity and may be useful for treating a tumor,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 CC  
 CC Sequence 125 AA;  
 SQ  
 XX  
 Query Match 82.7%; Score 507.5; DB 7; Length 125;  
 Best Local Similarity 81.7%; Pred. No. 1.3e-35;  
 Matches 98; Conservative 7; Mismatches 8; Indels 7; Gaps 2;  
 QY 2 ESGPGLVKEPQTLSTLCTVSGSIRSGYYSWVRQPGKLEWIGNIYHSGNTYVPSL 61  
 DB 6 ESGPGLVKEPQTLSTLCTVSGSIRSGYYSWVRQPGKLEWIGNIYHSGNTYVPSL 65  
 QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYYCARSDGVT--LDNMCGTLVTYSS 114  
 DB 66 KSRITISVDTSKNHFSLRTSVTAADTAVYYCARSDGVT--LDNMCGTLVTYSS 125  
 DB  
 QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYYCARSDGVT--LDNMCGTLVTYSS 114  
 DB 66 KSRITISVDTSKNHFSLRTSVTAADTAVYYCARSDGVT--LDNMCGTLVTYSS 125  
 DB  
 RESULT 11  
 ADP03974 ID ADP03974 standard; protein; 120 AA.  
 XX  
 AC ADP03974;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.  
 XX  
 KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cyrostatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 OS Unidentified.  
 OS  
 PN WO2003048328-A2.  
 PN  
 PD 12-JUN-2003.  
 PD  
 PF 02-DEC-2002; 2002MO-US038550.  
 PF  
 PR 03-DEC-2001; 2001US-0337275P.  
 PR  
 PA (ABGE-) ABGENIX INC.  
 PA  
 PI Gudas J, Foltz I, Handa M, Gallo M;  
 XX WPI; 2003-523295/49.  
 XX  
 PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 PS Example 2; SEQ ID NO 144; 89pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody (mab)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention  
 CC demonstrates cyrostatic activity and may be useful for treating a tumor,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 CC  
 CC Sequence 120 AA;  
 SQ  
 XX  
 Query Match 82.6%; Score 507; DB 7; Length 120;  
 Best Local Similarity 83.6%; Pred. No. 1.3e-35;  
 Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;  
 QY 2 ESGPGLVKEPQTLSTLCTVSGSIRSGYYSWVRQPGKLEWIGNIYHSGNTYVPSL 61  
 DB 6 ESGPGLVKEPQTLSTLCTVSGSIRSGYYSWVRQPGKLEWIGNIYHSGNTYVPSL 65  
 QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYYCARSDGVT--LDNMCGTLVTYSS 114  
 DB 66 KSRITISVDTSKNHFSLRTSVTAADTAVYYCARSDGVT--LDNMCGTLVTYSS 120  
 DB  
 QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYYCARSDGVT--LDNMCGTLVTYSS 114  
 DB 66 KSRITISVDTSKNHFSLRTSVTAADTAVYYCARSDGVT--LDNMCGTLVTYSS 120  
 DB  
 RESULT 12  
 ADP03873 ID ADP03873 standard; protein; 120 AA.  
 XX  
 AC ADP03873;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.  
 XX  
 KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cyrostatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 OS Unidentified.  
 OS  
 PN WO2003048328-A2.  
 PN  
 PD 12-JUN-2003.  
 PD  
 PF 02-DEC-2002; 2002MO-US038550.  
 PF  
 PR 03-DEC-2001; 2001US-0337275P.  
 PR  
 PA (ABGE-) ABGENIX INC.  
 PA  
 PI Gudas J, Foltz I, Handa M, Gallo M;  
 XX WPI; 2003-523295/49.  
 XX  
 PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 PS Claim 1; SEQ ID NO 13; 89pp; English.  
 PS  
 CC The invention relates to a novel isolated monoclonal antibody (mab)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention  
CC demonstrates cytosolic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

SO Sequence 120 AA;

Query Match 82.6%; Score 507; DB 7; Length 120;  
Best Local Similarity 83.6%; Pred. No. 1.3e-35;  
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWROPGKGLWIGNIYHSGNTYVPSL 61  
Db 6 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWROPGKGLWIGNIYHSGNTYVPSL 65

Qy 62 KSRITMSVDTSKKNFSLRLTSVTAADTAVYYCARSDGYT---LDMWGQTLVTVSS 114  
Db 66 KSRVITISVDTSKKNQFSLKLSVTAADTAVYYCAR-DEQNTWYFPLWGRGLVTVSS 120

RESULT 13  
ADP03977  
ID ADP03977 standard; protein; 122 AA.  
XX  
AC ADP03977;  
DT 29-JUL-2004 (first entry)  
XX  
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.  
XX  
DE Monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX cytosolic; colorectal neoplasm; renal cell carcinoma;  
XX cervical intraepithelial squamous neoplasia;  
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
OS Unidentified.  
XX  
PN WO2003048328-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 02-DEC-2002; 2002MO-US038550.  
XX  
PR 03-DEC-2001; 2001US-0337275P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudae J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX  
DR WPI; 2003-523295/49.  
XX  
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.;  
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
PS Example 2; SEQ ID NO 147; 89pp; English.  
XX  
CC The invention relates to a novel isolated monoclonal antibody (mab)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytosolic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal

CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

SO Sequence 122 AA;

Query Match 82.6%; Score 507; DB 7; Length 122;  
Best Local Similarity 82.1%; Pred. No. 1.4e-35;  
Matches 96; Conservative 8; Mismatches 9; Indels 4; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWROPGKGLWIGNIYHSGNTYVPSL 61  
Db 6 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWROPGKGLWIGNIYHSGNTYVPSL 65

Qy 62 KSRITMSVDTSKKNFSLRLTSVTAADTAVYYCAR---SPGYTLDMWGQTLVTVSS 114  
Db 66 KSRVITISVDTSKKNQFSLKLSVTAADTAVYYCARYDYILTYGMDPWGQTLVTVSS 122

RESULT 14  
AAB36206  
ID AAB36206 standard; protein; 473 AA.  
XX  
AC AAB36206;  
DT 15-FEB-2001 (first entry)  
XX  
DE Human immune system associated protein HISAP-4.  
XX  
DE Human immune system associated protein; HISAP-4; immune disorder;  
XX infection; autoimmune disease; cancer.  
XX  
OS Homo sapiens.  
XX  
PN US6135941-A.  
XX  
PD 24-OCT-2000.  
XX  
PF 27-MAR-1998; 98US-00049672.  
XX  
PR 27-MAR-1998; 98US-00049672.  
XX  
PA (INCY-) INCYTE PHARM INC.  
XX  
PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;  
XX Hillman JL, Au-Young J;  
XX WPI; 2001-030926/04.  
XX  
DR N-FSDB; AAC66522.  
XX  
PT New human immune system associated proteins (HISAP) and polynucleotides  
XX encoding the HISAP, useful for diagnosing, treating or preventing immune  
XX or cell proliferative disorders or infections.  
XX  
PS Claim 1; Col 53-56; 54pp; English.  
XX  
CC The present invention provides the coding and protein sequences for a  
CC number of human immune system associated proteins (HISAPs). These can be  
CC used in the diagnosis and treatment of various autoimmune disorders,  
CC infections and cell proliferation diseases. The diseases include AIDS,  
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,  
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia  
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus  
CC erythematosus, arteriosclerosis, cirrhosis and cancer

SO Sequence 473 AA;

Query Match 82.6%; Score 507; DB 4; Length 473;  
Best Local Similarity 79.8%; Pred. No. 5.7e-35;  
Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;

Qy 2 ESGGGLVYKPSQTLTCTVSGSGSIRSGYVSWVROPKGLWIGNITVSGNTYVNSL 61  
 Db 25 ESGGGLVYKPSQTLTCTVSGSGSIRSGYVSWVROPKGLWIGNITVSGNTYVNSL 84  
 Qy 62 KSRITMSVDTSKNHSRLTSTVTAADTAIVVYCARSD-----GYLDMWGQTLVTVSS 114  
 Db 85 KSRVTVISVDTSKNSPILKLSSTVTAADTAIVVYCARSDVGLRGNGYGMVDWGQTLVTVSS 143

RESULT 15

ID ADJ32126 standard; protein; 221 AA.

ADJ32126;

22-APR-2004 (first entry)

DE Human interferon-gamma antibody heavy chain amino acid sequence SegID80.

KW antibody; antigen binding domain; interferon-gamma; INF-gamma;  
 KW antagonist antibody; antiinflammatory; immunosuppressive;  
 KW autoimmune disease; inflammatory condition; human; heavy chain.

OS Homo sapiens.

PN US2003099647-A1.

PD 29-MAY-2003.

PE 05-OCT-2001; 2001US-00972656.

PR 05-OCT-2001; 2001US-00972656.

PA (DESH/) DESHPANDE R V.

PA (TSAI/) TSAI M.

PI Deshpande RV, Tsai M;

DR WPI: 2003-696068/66.

DR N-PSDB; ADJ32125.

PT New antibody or antigen binding domain, or its fragment, variant or  
 PT derivative, which binds to an interferon-gamma protein, useful for  
 PT preparing a composition for preventing or treating inflammatory or  
 PT autoimmune disorders.

PS Claim 10; SEQ ID NO 80; 113pp; English.

CC This invention relates to a novel antibody or antigen binding domain, or  
 CC its fragment, variant or derivative, which binds to an interferon-gamma  
 CC (INF-gamma) protein, and is an antagonist antibody. The invention may be  
 CC useful for the development of compounds with an antiinflammatory or  
 CC immunosuppressive activity through action as interferon-gamma agonists. A  
 CC composition containing the antibody is useful for preventing or treating  
 CC an autoimmune disease and an inflammatory condition. The present sequence  
 CC is that of an antibody heavy chain of a human IFN-gamma antibody which  
 CC may be part of the invention.

SQ Sequence 221 AA;

Query Match 82.4%; Score 506; DB 7; Length 221;

Best Local Similarity 83.2%; Pred. No. 3.1e-35; Mismatches 12; Indels 0; Gaps 0;

Matches 94; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 2 ESGGGLVYKPSQTLTCTVSGSGSIRSGYVSWVROPKGLWIGNITVSGNTYVNSL 61

Db 6 ESGGGLVYKPSQTLTCTVSGSGSIRSGYVSWVROPKGLWIGNITVSGNTYVNSL 65

Qy 62 KSRITMSVDTSKNHSRLTSTVTAADTAIVVYCARSDGYLDMWGQTLVTVSS 114

Db 66 KSRVTVISVDTSKNSPILKLSSTVTAADTAIVVYCARSDGYLDMWGQTLVTVSS 118

Search completed: July 26, 2005, 09:19:18  
 Job time : 86.3273 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:07:26 ; Search time 14.6818-Seconds  
(without alignments)  
747.095 Million cell updates/sec

Title: US-10-027-725a-7  
Perfect score: 609  
Sequence: 1 IESGPGHVKPQTLSTLSCAV.....RLDGYTLDIWGQGLTVVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	479.5	78.7	116	2 S37456	Ig mu chain - huma
2	476.5	78.2	138	2 S78051	Ig heavy chain pre
3	475.5	78.1	125	2 S31514	Ig heavy chain - h
4	465	76.4	122	2 S69912	Ig V-D-J region (N
5	464.5	76.3	147	2 S13519	Ig heavy chain V r
6	460	75.5	130	2 S30534	Ig heavy chain V r
7	458.5	75.3	140	2 I37782	Ig variable region
8	453	74.4	99	2 S26801	Ig heavy chain V r
9	452.5	74.3	146	2 S09710	Ig heavy chain V r
10	451.5	74.1	121	2 S44113	Ig heavy chain V r
11	450.5	74.0	130	2 S31690	Ig heavy chain V r
12	450.5	74.0	127	2 S19668	Ig heavy chain V r
13	450.5	74.0	146	2 S09711	Ig heavy chain V r
14	449.5	73.8	155	2 S31512	Ig heavy chain - h
15	446.5	73.3	155	2 S31512	Ig heavy chain - h
16	444	72.9	137	2 S31676	Ig heavy chain V r
17	440	72.2	139	2 S31586	Ig heavy chain V r
18	439	72.1	145	2 S78055	Ig heavy chain pre
19	436	71.6	99	2 S26803	Ig heavy chain V r
20	435.5	71.5	123	2 S30530	Ig heavy chain V r
21	433	71.3	129	2 S44114	Ig heavy chain V r
22	433.5	71.2	117	2 S34964	Ig heavy chain pre
23	432.5	71.0	109	2 PH1673	Ig heavy chain V r
24	431	70.8	99	2 S26802	Ig heavy chain V r
25	430	70.6	97	2 PH0118	Ig heavy chain V-I
26	430	70.6	99	2 S26899	Ig heavy chain V r
27	427	70.1	110	2 S44110	Ig heavy chain V-D
28	426	70.0	139	2 A41287	Ig heavy chain pre
29	425.5	69.9	121	2 C55257	Ig gamma heavy cha

30	424	69.6	118	2 A26340	Ig heavy chain pre
31	423	69.5	118	2 S20780	Ig heavy chain V r
32	421.5	69.2	140	2 A49045	Ig heavy chain V r
33	419.5	68.9	129	1 D2HWA	Ig heavy chain V-I
34	419	68.8	135	2 S31604	Ig heavy chain V r
35	418.5	68.7	132	2 A38911	Ig heavy chain V r
36	418	68.6	99	2 S26807	Ig heavy chain V r
37	417	68.5	115	2 S57464	Ig heavy chain V-J
38	417	68.5	126	2 S47010	Ig heavy chain V4.
39	417	68.5	140	2 S78052	Ig heavy chain pre
40	416.5	68.4	140	2 A24770	hypothetical hbr1
41	415.5	68.2	143	2 B49028	Ig heavy chain V-I
42	415	68.1	99	2 S12418	Ig heavy chain V r
43	414.5	68.1	137	2 S31585	Ig heavy chain V r
44	414	68.0	120	2 PT0370	Ig mu chain precu
45	412.5	67.7	98	2 S26902	Ig heavy chain V r

## ALIGNMENTS

RESULT 1  
S37456  
Ig mu chain - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S37456  
R/McIntosh, R.S.; Tandon, N.; Weetman, A.P.  
submitted to the EMBL Data Library, September 1993  
A/Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from  
A/Reference number: S37453  
A/Accession: S37456  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-116 <NCI>  
A/Cross-references: EMBL:X75024; NID:9404313; PIDN:CAA52932.1; PID:9758095  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F/6-90/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 479.5; DB 2; Length 116;  
Best Local Similarity 76.1%; Pred. No. 6.9e-38;  
Matches 89; Conservative 14; Mismatches 5; Indels 9; Gaps 2;

Qy 6 GLVYPAQTLSTLSCAVSGGSTRSGGYWMTROHPKGLIEWIGTYHSGMTYVNSLSRSI 65  
Db 1 GLVYPAQTLSTLSCAVSGGSTRSGGYWMTROHPKGLIEWIGTYHSGMTYVNSLSRSV 60  
Qy 66 AMSVDTSSENKFSRLNSGVTADPTAVYYCARLDGYT-----LDIWGGTLTVVSS 114  
Db 61 TISVDTSKNQPSLKLSSVTADPTAVYYCAR-GGYSGYGYYYVNDVWGKRTTVVSS 116

RESULT 2  
S78051  
Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C/Accession: S78051; S23716  
R/Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A/Reference number: S78051  
A/Accession: S78051  
A/Molecule type: mRNA  
A/Residues: 1-135 <HAR>  
A/Cross-references: EMBL:X54437; NID:937814; PIDN:CAA38306.1; PID:9930117  
R/Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins  
Int. Immunol. 3, 865-875, 1991  
A/Title: Complete sequence of the genes encoding the VH and VL regions of low- and h  
patient.  
A/Reference number: S23716; MUID:92031262; PMID:1718404  
A/Accession: S23716  
A/Molecule type: mRNA





RESULT 11  
S31690  
Ig heavy chain V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31690  
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tommelle, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31690  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-130 <CUI>  
A/Cross-references: EMBL:Z14199; NID:930984; PIDN:CAA78568.1; PID:g30985  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 451.5; DB 2; Length 130;  
Best Local Similarity 72.1%; Pred. No. 3.2e-35;  
Matches 88; Conservative 11; Mismatches 12; Indels 11; Gaps 2;

QY 2 ESGGGLVKAPOQTSLSCAVSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYNPSTL 61  
Db 11 ESGGGLVKAPEETSLTCTVSGGSIS--YWSWSRQPPGKLEWIGYIYHSGNTYNPSTL 68  
QY 62 KSRIAMSVDTSENKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 112  
Db 69 KSRVTISVDTSKNQFSLKLSVTADTAAYVYCARGSVVLWFGELLYFPDVGQGLTVTV 128  
QY 113 SS 114  
Db 129 SS 130

RESULT 12  
S19668  
Ig heavy chain V region (VH4DUH6) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 12-Apr-1996 #text\_change 20-Jun-2000  
C/Accession: S19668; S24445  
R/Marko, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991  
A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage  
A/Reference number: S19663; MUID:92085276; PMID:1748994  
A/Accession: S19668  
A/Molecule type: mRNA  
A/Residues: 1-127 <MAR>  
A/Cross-references: EMBL:X61648  
R/Jones, P.T.  
submitted to the EMBL Data Library, October 1991  
A/Reference number: S24442  
A/Accession: S24445  
A/Molecule type: mRNA  
A/Residues: 1-118,'E',120-121,'T',123-126,'F',<JON>  
A/Cross-references: EMBL:X61648; NID:937722; PIDN:CAA43829.1; PID:g3135380  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 450.5; DB 2; Length 127;  
Best Local Similarity 69.7%; Pred. No. 3.9e-35;  
Matches 85; Conservative 15; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGGGLVKAPOQTSLSCAVSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYNPSTL 61  
Db 6 QSSGGLVKAPEETSLTCTVSGGSIS--YWSWSRQPPGKLEWIGYIYHSGNTYNPSTL 65  
QY 62 KSRIAMSVDTSENKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 112  
Db 66 KSRVTISVDTSKNQFSLKLSVTADTAAYVYCARGSVVLWFGELLYFPDVGQGLTVTV 125

QY 113 SS 114  
Db 126 SS 127  
RESULT 13  
S09711  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C/Accession: S09711  
R/Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A/Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of  
A/Reference number: S09710; MUID:90262535; PMID:2111699  
A/Accession: S09711  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-146 <HUG>  
A/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F;34-118/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 450.5; DB 2; Length 146;  
Best Local Similarity 68.0%; Pred. No. 4.5e-35;  
Matches 83; Conservative 17; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGGGLVKAPOQTSLSCAVSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYNPSTL 61  
Db 25 ESGGGLVKAPEETSLTCTVSGGSVSSGLYWSMIROHPGKLEWIGYIYHSGNTYNPSTL 84  
QY 62 KSRIAMSVDTSENKFSRLNSVTADTAAYVYCARLDG-----DGYTLDIWGQGLTVTV 112  
Db 85 RSRVTISVDTSKNQFSLKLSVTADTAAYVYCARVLVSRISQSYMDVWGQGLTVTV 144  
QY 113 SS 114  
Db 145 SS 146

RESULT 14  
S31511  
Ig heavy chain - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S31511  
R/Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto-  
A/Reference number: S31509  
A/Accession: S31511  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-155 <CHA>  
A/Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 73.8%; Score 449.5; DB 2; Length 155;  
Best Local Similarity 70.8%; Pred. No. 5.9e-35;  
Matches 85; Conservative 15; Mismatches 11; Indels 9; Gaps 2;

QY 2 ESGGGLVKAPOQTSLSCAVSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYNPSTL 61  
Db 38 ESGGGLVKAPEETSLTCTVSGGSIS--YWSWSRQPPGKLEWIGYIYHSGNTYNPSTL 95  
QY 62 KSRIAMSVDTSENKFSRLNSVTADTAAYVYCARLDG-----LDGYTLDIWGQGLTVTV 114  
Db 96 KSRVTISVDTSKNQFSLKLSVTADTAAYVYCARGSVSSGLYMDVWGQGLTVTV 155

RESULT 15



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OM protein - protein search, using SW model

Run on: July 26, 2005, 08:52:21 ; Search time 71.6818 Seconds  
(without alignments)  
814.391 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609  
Sequence: 1 LESGPGIVKPAQTLISLSCAV.....RLDGYTLIDWCGGLTVVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	483.5	79.4	476 2	O6GMX1 homo sapien
2	473	77.7	478 2	O7Z379 homo sapien
3	451	74.1	150 2	O9S973 homo sapien
4	449	73.7	477 2	O6GMX7 homo sapien
5	446.5	73.3	119 2	O9UL73 homo sapien
6	444	72.9	465 2	O6GMX6 homo sapien
7	440	72.2	576 2	O6P418 homo sapien
8	432	70.9	496 2	O96KX8 homo sapien
9	430.5	70.7	492 2	O7Z374 homo sapien
10	430	70.6	620 2	O96EY0 homo sapien
11	419.5	68.9	129 1	HV2F_HUMAN
12	412.5	67.7	478 2	O6NTH3 homo sapien
13	409.5	67.2	595 2	O6MIX4 homo sapien
14	409.5	67.2	597 2	O6GMX5 homo sapien
15	409.5	67.2	597 2	O9BUI0 homo sapien
16	409.5	67.2	625 2	O96AA6 homo sapien
17	408	67.0	139 2	O6GSX2 homo sapien
18	405.5	66.6	597 2	O9BOB8 homo sapien
19	405	66.6	130 2	O8I2D7 homo sapien
20	405	66.5	146 1	HV2I_HUMAN
21	388	63.7	473 2	O8TC63 homo sapien
22	383	62.9	136 2	O6LBO5 mus musculu
23	377.5	62.0	479 2	O9M22 mus musculu
24	374.5	61.5	137 1	HV46_MOUSE
25	374	61.4	116 2	O7Z3Y6 mus musculu
26	370.5	60.8	262 2	O6SZ11 mus musculu
27	369.5	60.7	117 1	HV2G_HUMAN
28	362	59.4	122 2	O9UL75 homo sapien
29	361.5	59.4	113 1	HV47_MOUSE
30	357.5	58.7	476 2	O6MZX7 mus musculu
31	342.5	56.2	116 1	HV61_MOUSE

32	341.5	56.1	116 1	HV60_MOUSE	P18531 mus musculu
33	334	54.8	117 1	HV62_MOUSE	P18533 mus musculu
34	326	53.5	118 2	O81I05	O81I05 mus musculu
35	323	53.0	121 2	O99NG4	O99NG4 mus musculu
36	321.5	52.8	144 1	HV43_MOUSE	P01819 mus musculu
37	316.5	52.0	121 2	O9US6	O9US6 homo sapien
38	315	51.7	482 2	O91X92	O91X92 mus musculu
39	312.5	51.3	118 2	O9UL74	O9UL74 homo sapien
40	304.5	50.0	466 2	O6IN78	O6IN78 homo sapien
41	304	49.9	135 1	HV02_XENLA	P20957 xenopus lae
42	304	49.9	473 2	O6MZ7	O6MZ7 homo sapien
43	302.5	49.7	240 2	O6SZC9	O6SZC9 homo sapien
44	301	49.4	606 2	O6GM72	O6GM72 homo sapien
45	300	49.3	120 1	HV2B_HUMAN	P01815 homo sapien

## ALIGNMENTS

RESULT 1  
O6GMX1 PRELIMINARY; PRT; 476 AA.  
ID O6GMX1  
AC O6GMX1  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins L., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heath F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Umed T.B., Toshitsuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Kravinsky M.I., Skolnik U., Smalton D.E., Schermer A., Schein J.E.,  
RA Jones S.J., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.,  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073773; AAH73773.1, -  
DR InterPro; IPR003599; IG-like.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; CI-set; 3.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

KM Hypoetical protein.  
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DD3D CRC64;  
Query Match 79.4%; Score 483.5; DB 2; Length 476;  
Best Local Similarity 72.6%; Pred. No. 8,76-43;  
Matches 90; Conservative 16; Mismatches 5; Indels 13; Gaps 2;  
QY 2 ESGRGLVKAPOTLSTLSCAVSGSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYVPSL 61  
DB 25 ESGRGLVKAPOTLSTLCTVSGSGSISSDYYWMIROHPGKLEWIGYIYHSGNTYVPSL 84  
QY 62 KSRITMSVDTSENKFSRLNSVTADTAIVYCARLDGY--TLDIWGQGLTVVSS 110  
DB 85 KSRITMSVDTSENKFSRLNSVTADTAIVYCARLDGY--TLDIWGQGLTVVSS 142  
QY 111 TVSS 114  
DB 143 TVSS 146  
RESULT 2  
QY 072379 PRELIMINARY; PRT; 478 AA.  
AC 072379;  
DT 01-OCT-2003 (TReMBLrel. 25, Created)  
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Hypoetical protein DKFZp686K04218 (Fragment).  
GN Name=DKFZp686K04218;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP TISSUE=Human rectum tumor;  
RA Bloecher H., Boecher M., Mewes H.W., Weill B., Amlid C., Oesanger A.,  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538066; CAD97996.1; -.  
DR HSSP; P01820; 1G7J.  
DR InterPro; IPR007110; IG-1ike.  
DR InterPro; IPR003597; IG-1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-sec; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KM Hypoetical protein.  
FT NON TER 1  
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;  
Query Match 77.7%; Score 473; DB 2; Length 478;  
Best Local Similarity 75.7%; Pred. No. 1,1e-41;  
Matches 87; Conservative 17; Mismatches 9; Indels 2; Gaps 1;  
QY 2 ESGRGLVKAPOTLSTLSCAVSGSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYVPSL 61  
DB 24 ESGRGLVKAPOTLSTLCTVSGSGSISSDYYWMIROHPGKLEWIGYIYHSGNTYVPSL 83  
QY 62 KSRITMSVDTSENKFSRLNSVTADTAIVYCARLDGY--TLDIWGQGLTVVSS 114  
DB 84 KSRITMSVDTSENKFSRLNSVTADTAIVYCARLDGY--TLDIWGQGLTVVSS 138  
RESULT 3  
QY 095973 PRELIMINARY; PRT; 150 AA.  
AC 095973;  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Vh4 heavy chain variable region precursor (Fragment).  
GN Name=IGM;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP TISSUE=Human rectum tumor;  
RA Bloecher H., Boecher M., Mewes H.W., Weill B., Amlid C., Oesanger A.,  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF103795; AAC79084.1; -.  
DR PIR; S31673; S31673.  
DR PIR; S78056; S78056.  
DR HSSP; P01820; 1G7J.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003596; IG\_V.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KM Signal.  
FT SIGNAL 1 19 Potential.  
FT CHAIN 20 >150 Vh4 heavy chain variable region.  
FT NON TER 150  
SQ SEQUENCE 150 AA; 16315 MW; 85664B04938AA7C9 CRC64;  
Query Match 74.1%; Score 451; DB 2; Length 150;  
Best Local Similarity 74.3%; Pred. No. 7e-40;  
Matches 84; Conservative 12; Mismatches 17; Indels 0; Gaps 0;  
QY 2 ESGRGLVKAPOTLSTLSCAVSGSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYVPSL 61  
DB 25 ESGRGLVKAPOTLSTLCTVSGSGSISSDYYWMIROHPGKLEWIGYIYHSGNTYVPSL 84  
QY 62 KSRITMSVDTSENKFSRLNSVTADTAIVYCARLDGY--TLDIWGQGLTVVSS 114  
DB 85 KSRITMSVDTSENKFSRLNSVTADTAIVYCARLDGY--TLDIWGQGLTVVSS 137  
RESULT 4  
QY 06GMX7 PRELIMINARY; PRT; 477 AA.  
AC 06GMX7;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Hypoetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP TISSUE=Human rectum tumor;  
RA Bloecher H., Boecher M., Mewes H.W., Weill B., Amlid C., Oesanger A.,  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538066; CAD97996.1; -.  
DR HSSP; P01820; 1G7J.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003597; IG-1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-sec; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KM Hypoetical protein.  
FT NON TER 1  
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;  
Query Match 77.7%; Score 473; DB 2; Length 478;  
Best Local Similarity 75.7%; Pred. No. 1,1e-41;  
Matches 87; Conservative 17; Mismatches 9; Indels 2; Gaps 1;  
QY 2 ESGRGLVKAPOTLSTLSCAVSGSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYVPSL 61  
DB 24 ESGRGLVKAPOTLSTLCTVSGSGSISSDYYWMIROHPGKLEWIGYIYHSGNTYVPSL 83  
QY 62 KSRITMSVDTSENKFSRLNSVTADTAIVYCARLDGY--TLDIWGQGLTVVSS 114  
DB 84 KSRITMSVDTSENKFSRLNSVTADTAIVYCARLDGY--TLDIWGQGLTVVSS 138  
RESULT 5  
QY 095973 PRELIMINARY; PRT; 150 AA.  
AC 095973;  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)



RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073765; AAH73765.1; -  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; CI-set; 2.  
 DR Pfam; PF00047; IG; 3.  
 DR SMART; SM00409; IG; 4.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CF85 CRC64;  
 Query Match 73.7%; Score 449; DB 2; Length 477;  
 Best Local Similarity 75.7%; Pred. No. 4.1e-39;  
 Matches 87; Conservative 10; Mismatches 14; Indels 4; Gaps 2;  
 Oy 2 ESGGGLVPAQTLSLSCAVSGSGSIRSGGYWSWIRORPGKLEWIGYIYHSGNTYVPSL 61  
 Db 25 ESGGGLVPAQTLSLSCAVSGSGSIRSGGYWSWIRORPGKLEWIGYIYHSGNTYVPSL 82  
 Oy 62 KSRIAMVDTSNFKSLRLNSVTADTAAYVYCARLDG--YTLDIMOGGTLVTYSS 114  
 Db 83 KSRVTLSDTSKQPSLRINSVTADTAAYVYCARLDG--YTLDIMOGGTLVTYSS 137  
 RESULT 5  
 ID 09UL73 PRELIMINARY; PRT; 119 AA.  
 AC 09UL73;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98271139; PubMed=9614934; DOI=10.1006/cln.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Betney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035041; AAD56277.1; -  
 DR PIR; PH0876; PH0876.  
 DR PIR; S12416; S12416.  
 DR HSP; P01820; IGTJ.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EAOBE CRC64;  
 Query Match 73.3%; Score 446.5; DB 2; Length 119;  
 Best Local Similarity 74.1%; Pred. No. 1.6e-39;  
 Matches 86; Conservative 12; Mismatches 13; Indels 5; Gaps 2;  
 Oy 2 ESGGGLVPAQTLSLSCAVSGSGSIRSGGYWSWIRORPGKLEWIGYIYHSGNTYVPSL 61  
 Db 25 ESGGGLVPAQTLSLSCAVSGSGSIRSGGYWSWIRORPGKLEWIGYIYHSGNTYVPSL 82

Db 6 ESGGGLVPAQTLSLSCAVSGSGSIRSGGYWSWIRORPGKLEWIGYIYHSGNTYVPSL 63  
 Oy 62 KSRIAMVDTSNFKSLRLNSVTADTAAYVYCARLDG--YTLDIMOGGTLVTYSS 114  
 Db 64 KSRVTLSDTSKQPSLRINSVTADTAAYVYCARLDG--YTLDIMOGGTLVTYSS 119  
 RESULT 6  
 ID 06GMX6 PRELIMINARY; PRT; 465 AA.  
 AC 06GMX6;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,  
 RA Diatchenko L., Marins K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshibyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bostak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez M.I., Skalela U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.T., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073766; AAH73766.1; -  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; CI-set; 3.  
 DR Pfam; PF00047; IG; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386B CRC64;  
 Query Match 72.9%; Score 444; DB 2; Length 465;  
 Best Local Similarity 77.0%; Pred. No. 1.3e-38;  
 Matches 87; Conservative 9; Mismatches 15; Indels 2; Gaps 1;  
 Oy 2 ESGGGLVPAQTLSLSCAVSGSGSIRSGGYWSWIRORPGKLEWIGYIYHSGNTYVPSL 61  
 Db 25 ESGGGLVPAQTLSLSCAVSGSGSIRSGGYWSWIRORPGKLEWIGYIYHSGNTYVPSL 82  
 Oy 62 KSRIAMVDTSNFKSLRLNSVTADTAAYVYCARLDG--YTLDIMOGGTLVTYSS 114

Db 83 KSRVTISVDSKNOFSLKSLSSVTADTAAYVYCAAGRTTYPDWGGGLTVVSS 135

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RESULT 7
ID 06P418 PRELIMINARY; PRT; 576 AA.
AC 06P418;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG protein.
GN Name=IGHG;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Krzywnski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR HSSP; P01820; 1A7N.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MM; FBB97C949D720F1B CRC64;

Query Match 72.2%; Score 440; DB 2; Length 576;
Best Local Similarity 73.3%; Pred. No. 4.5e-38;
Matches 85; Conservative 13; Mismatches 14; Indels 4; Gaps 2;

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RESULT 8
ID 096KX8 PRELIMINARY; PRT; 496 AA.
AC 096KX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MCC27165 protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1; -.
DR HSSP; P01876; 1O00.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 496 AA; 53391 MM; D3f6929849040D69 CRC64;

Query Match 70.3%; Score 432; DB 2; Length 496;
Best Local Similarity 69.2%; Pred. No. 2.7e-37;
Matches 83; Conservative 13; Mismatches 16; Indels 8; Gaps 2;

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DT 01-OCT-2003 (TrEMBLrel. 25, last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)  
 DE Hypothetical protein DKFZp686C02218 (Fragment).  
 GN Name=DKFZp686C02218;  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human rectum tumor;  
 RA Bioecker H., Boecker W., Mewes H.W., Weil B., Amid C., Oeanger A.,  
 RA Fobo G., Han M., Wiemann S.,  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX538077; CAD98001.1;  
 DR HSSP; P01820; IG7J.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003597; IG\_cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; Cl-sect; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 FT NCN TER 1 1  
 SQ SEQUENCE 492 AA; 5376 MW; 1E7A15760F0CA74B CRC64;

Query Match 70.7%; Score 430.5; DB 2; Length 492;  
 Best Local Similarity 71.6%; Pred. No. 3.9e-37;  
 Matches 83; Conservative 13; Mismatches 17; Indels 3; Gaps 2;

QY 2 ESGPGIVKPAQTSLSCAVSGGSIIRSGGYMSWIRHPGKLEWIGYIYSGNTYNSPL 61  
 DB 37 ESGGIVKPESTSLTCTVSGGSVSNRYMGWIRPQKLEWIGIYIYSGNTYNSPL 96  
 QY 62 KSRIAMSVDTSEKFSRLNSVTAPADYAVYCA--YTDIDWGGTLYTVSS 114  
 DB 97 KSRITIVDTSKHFSRLNSVTAPADYAVYCAVHVGPGMFPDQGLTVTVSS 152

RESULT 10  
 Q96EYO PRELIMINARY; PRT; 620 AA.  
 AC Q96EYO;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 19, last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)  
 DE IGHM protein.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 DE MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Krausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Butler K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallov D.E., Scherch A., Schein J.E.,

RA Jones S.J., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.,  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC011857; AAH11857.2;  
 DR PIR; S15590; S15590.  
 DR HSSP; P01820; IG7J.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003597; IG\_cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; Cl-sect; 4.  
 DR SMART; SM00409; IGV; 2.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6B8FF27B CRC64;

Query Match 70.6%; Score 430; DB 2; Length 620;  
 Best Local Similarity 74.4%; Pred. No. 5.7e-37;  
 Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

QY 2 ESGPGIVKPAQTSLSCAVSGGSIIRSGGYMSWIRHPGKLEWIGYIYSGNTYNSPL 61  
 DB 32 ESGGIVKPESTSLTCTVSGGSISS--YVSWIRPQKLEWIGIYIYSGNTYNSPL 89  
 QY 62 KSRIAMSVDTSEKFSRLNSVTAPADYAVYCA---RLDGYLIDWGGTLYTVSS 114  
 DB 90 KSRIVMSVDTSEKFSRLNSVTAPADYAVYCA--PQWELPTVGLFVWGGTLYTVSS 146

RESULT 11  
 HV2P\_HUMAN STANDARD; PRT; 129 AA.  
 ID HV2P\_HUMAN  
 AC P01824;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, last sequence update)  
 DT 05-JUL-2004 (Rel. 44, last annotation update)  
 DE Ig heavy chain V-II region WH.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=8222235; PubMed=6806818;  
 RA Takahashi N., Tetaert D., Debut B., Lin L.-C., Putnam F.W.,  
 RT "Complete amino acid sequence of the delta heavy chain of human  
 RT immunoglobulin D."  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).  
 CC -1- MISCELLANEOUS: This chain was isolated from an Igd myeloma  
 CC protein.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC PIR; A02099; D2HUMA.  
 DR HSSP; P01820; IG7J.  
 DR GlycoSiteDB; P01824;  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; F:immune response; NAS.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF0047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 113  
 IG-like.

FT	NON TERM	129	129	MM;	DS53D47ABE51319	CRC64;
SO	SEQUENCE	129	AA;	14117	MW;	
	Query Match			68.9%;	Score 419.5;	DB 1;
	Best Local Similarity			62.7%;	Pred. No. 1.3e-36;	
	Matches	79;	Conservative	16;	Mismatches	16;
					Indels	15;
					Gaps	2
QY	2	ESGGLVNPACTLISLSCAVSGSIRISGGYMSWIRHQHGKLEWIGIYHSANTYNNSL	61			
DB	6	ESGGLVNPACTLISLSCAVSGSIRISGGYMSWIRHQHGKLEWIGIYHSANTYNNSL	65			
QY	62	KSRIAMSVDTSENNKSLRLNSVTADPTAVVYCAR-----LDGTLTDMGGCT	108			
DB	66	KGRVTISVDITSRNPSLNLRLMSADTAMTYCARGNPPPYDITGSGDDG--IDWVGCT	123			
QY	109	LVTVSS 114				
DB	124	TWVSS 129				
RESULT 12						
Q6NYH3						
AC	Q6NYH3	PRELIMINARY;	PRT;	478	AA.	
DT	05-JUN-2004	(TREMBLrel. 27, Created)				
DT	05-JUN-2004	(TREMBLrel. 27, Last sequence update)				
DT	05-JUN-2004	(TREMBLrel. 27, Last annotation update)				
DE	Hypothetical protein.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Blood;					
RX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;					
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,					
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,					
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,					
RA	Datchenko L., Matusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA	Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA	Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,					
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,					
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultj S.W.,					
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA	Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,					
RA	Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,					
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,					
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,					
RA	Krzywinski M.I., Skalski U., Smailus D.E., Scherch A., Schein J.E.,					
RT	James S.J., Mair M.A.;					
RT	"Generation and initial analysis of more than 15,000 full-length human					
RT	and mouse cDNA sequences."					
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).					
RL	[2]					
RN	SEQUENCE FROM N.A.					
RC	TISSUE=Blood;					
RA	Strausberg R.;					
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; BC066594; AAH6594.1; -					
DR	HSSP; P01820; IATN					
DR	InterPro; IPR003599; IG_					
DR	InterPro; IPR007110; IG_					
DR	InterPro; IPR003597; IG_					
DR	InterPro; IPR003006; IG_MHC.					
DR	InterPro; IPR003596; IG_V.					
DR	Pfam; PF07654; Cl-set; 2.					
DR	SMART; SM00409; IG; 4.					
DR	SMART; SM00407; IGC1; 3.					
DR	SMART; SM00406; IGV; 1.					
DR	PROSITE; PS50835; IG LIKE; 4.					

Query Match	67.7%	Score 412.5	DB 2	Length 478
Best Local Similarity	66.9%	Pred. No. 3.1e-35		
Matches 79	Conservative 17	Mismatches 13	Indels 9	Gaps 3
Qy	2	ESGGLVKEPQDTLSLCAVSGGSIIRSGGYWMSWIRHFGKLEIGIYHSNTYNPSTL	61	
Db	25	ESGGLVKEPSETLSLTCVSGVSGDIAS--YWSMWRKSPQCGMIEWIGYIFHSGLTYNPSTL	82	
Qy	62	KSRIAMSVDSSENFSLRLNSYTAADPAVYVCARLDY-----TLIDWGGTLYTVSS	114	
Db	83	ESRYTAVSDVSFKQFQSMKLTSTVTAADPAIYYCAR--GYGSKSRFYDLMGKGVPTVSS	138	
RESULT 13				
Q8WUX4				
Q8WUX4	PRELIMINARY	PRT	595 AA.	
AC	Q8WUX4			
DT	01-MAR-2002 (TRENBLREL, 20, Created)			
DT	01-MAR-2004 (TRENBLREL, 26, Last sequence update)			
DT	01-MAR-2004 (TRENBLREL, 26, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_Taxid=9606;			
NP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymph;			
RA	MEBLINB=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grose L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heien F.,			
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownestein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pang C.,			
RA	Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunnarane P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahney J., Heltón E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko J., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences";			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymph;			
RA	Strausberg R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC019235; AAH19235.2; -.			
DR	PIR; G34964; G34964.			
DR	HSSP; P01861; 1AD0.			
DR	Pfam; PF07654; C1-sect; 4.			
DR	SMART; SMO0409; IG; 2.			
DR	SMART; SMO0407; IGcl; 4.			
DR	SMART; SMO0406; IGV; 1.			
DR	PROSITE; PS50835; IG-LIKE; 5.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_3.			
KW	Hypothetical protein.			
SO	SEQUENCE 595 AA; 65290 MM; OD4B50776545714E CRC64;			
Query Match	67.2%	Score 409.5	DB 2	Length 595
Best Local Similarity	66.7%	Pred. No. 8.3e-35		
Matches 80	Conservative 14	Mismatches 15	Indels 11	Gaps 3

QY 4 GPGVIVKPAQQTLSLCAVSGGSIIRSGGYYWMSYIRPHPGKGLMIYVYIYHSGNTYVNPISLKS 63  
 DB 34 GAGLKLKSRSETLSLTCGYGGSF--SGYVMSYIRPPKGLMIYVYIYHSGNTYVNPISLKS 91  
 QY 64 RIANSVDTISENKFSLRINSVTYADTAVYCARL-----DG-YTLDIWGGTLTVSS 114  
 DB 92 RVTISVDTSKQSLSLKTSVVAADTAVYCARVITRASPGRDGRYGMVWGQGTTVYSS 151  
 RESULT 14  
 Q6GMX5 PRELIMINARY; PRT; 597 AA.  
 AC O6GMX5;  
 DT 05-JUN-2004 (TREMblrel. 27, Created)  
 DT 05-JUN-2004 (TREMblrel. 27, Last sequence update)  
 DT 05-JUN-2004 (TREMblrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rabin G.M., Hong L.,  
 RA Stadleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Ueiri T.B., Toshilyski S., Carninci P., Prange C.J.,  
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatane P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.K., Sklirwood J., Schmutz J., Myers L.J., Butterfield Y.S.,  
 RA Krzywnicki M.I., Sklirwood J., Smalish D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, BC073767; AAH73767.1; --  
 DR InterPro: IPR003599; IG;  
 DR InterPro: IPR007110; IG-1like.  
 DR InterPro: IPR003097; IG\_C1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF07654; C1-set; 4.  
 DR Pfam: PF00047; Ig; 4.  
 DR SMART: SM00409; IG; 2.  
 DR SMART: SM00407; IG; 4.  
 DR SMART: SM00406; IG; 1.  
 DR PROSITE: PS00835; IG\_LIKE; 5.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AEDB5230 CRC64;

Db	Query Match	Similarity	Score	DB 2	Length	597
Db	Best Local	Similarity	66.7%	Pred. No.	8.3e-35	
	Matches	80	Conservative	14	Mismatches	15
				Indels	11	Gaps
						3
Qy	4	GGGIVKPAQCTLSLSCAVSGGIRSGGYWMSIRHPPKGLGEMIGYIYHSGTYYNPSLSK	63			
Db	27	GAGLKLKSESLSLTCGYGGSF--SGYYWSIRPPKGLGEMIGYIYHSGTYYNPSLSK	84			
Qy	64	RIAMSVDTSENKFSRLINSVTAADTAVYYCARL-----DG-YTIDIMQGGLTYTVSS	114			
Db	85	RVITISVDTSKKQSLKLSVVAADTAVYYCARVITRASPGTDGRYGMGVGQGLTYTVSS	144			

Thu Jul 28 05:42:30 2005

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Page 8

Search completed: July 26, 2005, 09:26:17  
Job time : 73.6818 secs

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PT diagnosing or passive immunotherapy of type I allergy, for environmental  
PT allergen detection.  
XX  
XX  
PS Disclosure; Page 36; 45pp; English.  
XX  
CC This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE Fabs and methods for their use. The proteins  
CC of the invention may have antiallergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE  
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific Fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The Fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific Fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergenic patients  
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
CC Fab, clone 94 heavy chain protein of the invention  
XX  
SQ Sequence 114 AA;  
XX  
Query Match 100.0%; Score 609; DB 5; Length 114;  
Best Local Similarity 100.0%; Pred. No. 3.1e-48; Indels 0; Gaps 0;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LESGPGLVKPAQTLISLCAVSGSIRSGYVMSWIRQHPGKLEWIGYIYHSGNTYVNS 60  
1 LESGPGLVKPAQTLISLCAVSGSIRSGYVMSWIRQHPGKLEWIGYIYHSGNTYVNS 60  
Db 1 LESGPGLVKPAQTLISLCAVSGSIRSGYVMSWIRQHPGKLEWIGYIYHSGNTYVNS 60  
QY 61 LKSRIMSVDTSEKFSRLNSVTAAADTAVYYCARLDGTYLDWGQGLTVTVSS 114  
61 LKSRIMSVDTSEKFSRLNSVTAAADTAVYYCARLDGTYLDWGQGLTVTVSS 114  
Db 61 LKSRIMSVDTSEKFSRLNSVTAAADTAVYYCARLDGTYLDWGQGLTVTVSS 114  
RESULT 2  
ID ABG30447 standard; protein; 114 AA.  
XX  
AC ABG30447;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human IgE Fab clone 100 heavy chain protein.  
XX  
KM Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;  
KM timothy grass pollen allergen; passive immunotherapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH Region 1..26  
FT /note= "FR1 region"  
FT Region 27..33  
FT /note= "CDR1 region"  
FT Region 34..47  
FT /note= "FR2 region"  
FT Region 48..63  
FT /note= "CDR2 protein"  
FT Region 64..95  
FT /note= "FR3 region"  
FT Region 96..103  
FT /note= "CDR2 region"  
FT Region 104..114  
FT /note= "FR4 region"  
XX  
XX WO200253595-A1.  
XX  
XX 11-JUL-2002.  
XX  
XX 27-DEC-2001; 2001WO-SE002908.  
XX

PR 29-DEC-2000; 2000SE-00004892.  
XX  
XX (PHAA ) PHARMACIA DIAGNOSTICS AB.  
XX  
XX Flicker S, Steinberger P, Kraft D, Valenta R;  
PI WPI; 2002-583604/62.  
XX  
XX N-PSDB; ABK89639.  
DR  
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
XX variable region of group 2 allergen specific-human IgE Fabs; useful for  
PT diagnosing or passive immunotherapy of type I allergy, for environmental  
PT allergen detection.  
XX  
XX Disclosure; Page 38; 45pp; English.  
XX  
PS This invention relates to the DNA and protein sequences of group 2  
XX allergen-specific human IgE Fabs and methods for their use. The proteins  
XX of the invention may have antiallergic activities and may be used as a  
XX vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE  
XX antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
XX 2 allergen-specific Fabs of the invention may be useful for environmental  
XX allergen detection and for standardisation of allergen extracts. The Fabs  
XX - or a vaccine against a type I allergy is useful for passive  
XX immunotherapy of type I allergy, it is also useful for diagnosing a type  
XX I allergy. The allergen-specific Fabs of the invention are useful for  
XX inter alia, diagnosis, therapy and prevention of type I allergy. They are  
XX also useful for identification of group 2 allergen-containing pollen and  
XX may be used for blocking the binding of grass pollen allergenic patients  
XX IgE antibodies to Phi p 2. The present sequence represents the human IgG  
XX Fab, clone 100 heavy chain protein of the invention  
XX  
SQ Sequence 114 AA;  
XX  
Query Match 89.8%; Score 547; DB 5; Length 114;  
Best Local Similarity 89.5%; Pred. No. 1.5e-42; Indels 0; Gaps 0;  
Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
QY 1 LESGPGLVKPAQTLISLCAVSGSIRSGYVMSWIRQHPGKLEWIGYIYHSGNTYVNS 60  
1 LESGPGLVKPAQTLISLCAVSGSIRSGYVMSWIRQHPGKLEWIGYIYHSGNTYVNS 60  
Db 1 LESGPGLVKPAQTLISLCAVSGSIRSGYVMSWIRQHPGKLEWIGYIYHSGNTYVNS 60  
QY 61 LKSRIMSVDTSEKFSRLNSVTAAADTAVYYCARLDGTYLDWGQGLTVTVSS 114  
61 LKSRIMSVDTSEKFSRLNSVTAAADTAVYYCARLDGTYLDWGQGLTVTVSS 114  
Db 61 LKSRIMSVDTSEKFSRLNSVTAAADTAVYYCARLDGTYLDWGQGLTVTVSS 114  
RESULT 3  
ID ABG30446 standard; protein; 114 AA.  
XX  
AC ABG30446;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human IgE Fab clone 60 heavy chain protein.  
XX  
KM Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;  
KM timothy grass pollen allergen; passive immunotherapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH Region 1..26  
FT /note= "FR1 region"  
FT Region 27..33  
FT /note= "CDR1 region"  
FT Region 34..47  
FT /note= "FR2 region"  
FT Region 48..63  
FT /note= "CDR2 protein"  
FT Region 64..95  
FT /note= "FR3 region"  
XX  
XX



FT Region 96..103  
 FT /note= "CDR2 region"  
 FT Region 104..114  
 FT /note= "FR4 region"  
 XX  
 PN WO200253595-A1.  
 XX  
 XX 11-JUL-2002.  
 XX  
 PD 27-DEC-2001; 2001WO-SE002908.  
 XX  
 PF 27-DEC-2001; 2001WO-SE002908.  
 XX  
 PR 29-DEC-2000; 2000SE-00004892.  
 XX  
 PA (PRAA) PHARMACIA DIAGNOSTICS AB.  
 XX  
 PI Flicker S, Steinberger P, Kraft D, Valenta R;  
 DR WPI; 2002-583604/62.  
 DR N-PSDB; ABK89638.  
 XX  
 PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.  
 XX  
 PS Disclosure; Page 37; 45pp; English.  
 XX  
 CC This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have anti-allergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE  
 CC antibodies to Phl p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific Fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The Fabs  
 CC - or a vaccine against a type I allergy is useful for diagnosing a type  
 CC I allergy. The allergen-specific Fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC IgE antibodies to Phl p 2. The present sequence represents the human IgG  
 CC Fab, clone 60 heavy chain protein of the invention  
 XX  
 SQ Sequence 114 AA;  
 QY  
 Query Match 89.7%; Score 546; DB 5; Length 114;  
 Best Local Similarity 89.5%; Pred. No. 1.9e-42;  
 Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 Db 1 LESGPGLVKPAQOTLSLSCAVSGSIRSGGYWMTWIRHKGKLEWIGYIHSGNTYNSL 60  
 1 LESGPGLVKPSQOTLSLTVSGSIRSGGYWMTWIRHKGKLEWIGYIHSGNTYNSL 60  
 QY 61 LKSRIVMSVDTSENKFSRLNSVTADTAIVYCARLDGYTLDIWQGTIVTVSS 114  
 61 LKSRITMSVDTISKNHFSRLRTSVTAADTAIVYCARSDERTIDNMGQGLTVTVSS 114  
 Db  
 RESULT 4  
 ID ADP03977 standard; protein; 122 AA.  
 XX  
 AC ADP03977;  
 XX  
 DT 29-JUN-2004 (first entry)  
 XX  
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.  
 XX  
 KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosol; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX  
 OS unidentified.  
 XX  
 XX WO2003048328-A2.  
 PN  
 XX 12-JUN-2003.  
 PD  
 PF 02-DEC-2002; 2002WO-US038550.  
 XX  
 PR 03-DEC-2001; 2001US-0337275P.  
 XX  
 PA (ABGE-) AGENIX INC.  
 XX  
 PI Gudas J, Foltz I, Handa M, Gallo M;  
 DR WPI; 2003-523295/49.  
 XX  
 DR New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 PS Example 2; SEQ ID NO 147; 89pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 XX  
 SQ Sequence 122 AA;  
 QY  
 Query Match 85.2%; Score 519; DB 7; Length 122;  
 Best Local Similarity 81.2%; Pred. No. 6.1e-40;  
 Matches 95; Conservative 12; Mismatches 6; Indels 4; Gaps 1;  
 Db 2 ESGPGLVKPAQOTLSLSCAVSGSIRSGGYWMTWIRHKGKLEWIGYIHSGNTYNSL 61  
 6 ESGPGLVKPSQOTLSLTVSGSIRSGGYWMTWIRHKGKLEWIGYIHSGNTYNSL 65  
 QY 62 KSRIVMSVDTSENKFSRLNSVTADTAIVYCARLDGYTLDIWQGTIVTVSS 114  
 66 KSRVTISVDTISKNHFSRLRTSVTAADTAIVYCARVYDILITGMDVWQGTIVTVSS 122  
 Db  
 RESULT 5  
 ID ADP03982 standard; protein; 121 AA.  
 XX  
 AC ADP03982;  
 XX  
 DT 29-JUN-2004 (first entry)  
 XX  
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 152.  
 XX  
 KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosol; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 OS unidentified.  
 XX  
 XX WO2003048328-A2.  
 PN  
 XX 12-JUN-2003.  
 PD

XX 02-DEC-2002; 2002WO-US038550.  
XX  
XX 03-DEC-2001; 2001US-0337275P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Gudas J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
XX Example 2; SEQ ID NO 152; 89pp; English.  
XX  
XX The invention relates to a novel isolated monoclonal antibody (mab)  
XX comprising a heavy chain polypeptide and light chain polypeptide having a  
XX sequence chosen from one of 53 fully defined amino acid sequences given  
XX in the specification, where the antibody specifically binds carbonic  
XX anhydrase IX (CA IX) tumor antigen. The antibody of the invention  
XX demonstrates cytostatic activity and may be useful for treating a tumor,  
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal  
XX tumour or breast cancer, possibly via gene therapy. The current sequence  
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
XX (heavy chain variable domain) protein of the invention. The protein was  
XX generated via the introduction of the human CA IX protein into a  
XX transgenic mouse strain.  
XX  
XX Sequence 121 AA;  
XX  
XX Query Match 85.1%; Score 518.5; DB 7; Length 121;  
XX Best Local Similarity 81.9%; Pred. No. 6.7e-40;  
XX Matches 95; Conservative 11; Mismatches 7; Indels 3; Gaps 1;  
XX  
XX 2 ESGGGLVKAQVTLSCAVSGGSTRSGGYWMTWRHFGKLEWIGYIHSGNTYNNPSL 61  
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
XX 6 ESGGGLVKAQVTLSCAVSGGSTRSGGYWMTWRHFGKLEWIGYIHSGNTYNNPSL 65  
XX  
XX 62 KSRIAMVDSENFESRLNSVTADPAVYYCARLDD---GYTLIDWGQGLTVYSS 114  
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
XX 66 KSRIAMVDSENFESRLNSVTADPAVYYCARLDD---GYTLIDWGQGLTVYSS 121  
XX  
XX RESULT 6  
XX ADP03871  
XX ID ADP03871 standard; protein; 125 AA.  
XX  
XX ADP03871;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.  
XX  
XX monoclonaal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX cytosstatic; colorectal neoplasm; renal cell carcinoma;  
XX cervical intraepithelial squamous neoplasia;  
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
XX Unidentified.  
XX  
XX OS  
XX WO2003048328-A2.  
XX  
XX PD 12-JUN-2003.  
XX  
XX 02-DEC-2002; 2002WO-US038550.  
XX  
XX PF 03-DEC-2001; 2001US-0337275P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX PA

XX Gudas J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
XX Claim 1; SEQ ID NO 11; 89pp; English.  
XX  
XX The invention relates to a novel isolated monoclonal antibody (mab)  
XX comprising a heavy chain polypeptide and light chain polypeptide having a  
XX sequence chosen from one of 53 fully defined amino acid sequences given  
XX in the specification, where the antibody specifically binds carbonic  
XX anhydrase IX (CA IX) tumor antigen. The antibody of the invention  
XX demonstrates cytostatic activity and may be useful for treating a tumor,  
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal  
XX tumour or breast cancer, possibly via gene therapy. The current sequence  
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
XX (heavy chain variable domain) protein of the invention. The protein was  
XX generated via the introduction of the human CA IX protein into a  
XX transgenic mouse strain.  
XX  
XX Sequence 125 AA;  
XX  
XX Query Match 85.0%; Score 517.5; DB 7; Length 125;  
XX Best Local Similarity 81.7%; Pred. No. 8.6e-40;  
XX Matches 98; Conservative 9; Mismatches 6; Indels 7; Gaps 2;  
XX  
XX 2 ESGGGLVKAQVTLSCAVSGGSTRSGGYWMTWRHFGKLEWIGYIHSGNTYNNPSL 61  
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
XX 6 ESGGGLVKAQVTLSCAVSGGSTRSGGYWMTWRHFGKLEWIGYIHSGNTYNNPSL 65  
XX  
XX 62 KSRIAMVDSENFESRLNSVTADPAVYYCARLDD---IDGY--TLDIWGQGLTVYSS 114  
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
XX 66 KSRIAMVDSENFESRLNSVTADPAVYYCARLDD---IDGY--TLDIWGQGLTVYSS 125  
XX  
XX RESULT 7  
XX ADP03981  
XX ID ADP03981 standard; protein; 121 AA.  
XX  
XX ADP03981;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 151.  
XX  
XX monoclonaal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX cytosstatic; colorectal neoplasm; renal cell carcinoma;  
XX cervical intraepithelial squamous neoplasia;  
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
XX Unidentified.  
XX  
XX OS  
XX WO2003048328-A2.  
XX  
XX PD 12-JUN-2003.  
XX  
XX 02-DEC-2002; 2002WO-US038550.  
XX  
XX PF 03-DEC-2001; 2001US-0337275P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Gudas J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX

[illegible]

CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
SQ Sequence 120 AA;  
Query Match 84.1%; Score 512; DB 7; Length 120;  
Best Local Similarity 81.9%; Pred. No. 2,6e-39;  
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;  
QY 2 ESGPGLVKAQTLTSLSCAVSGGSIIRSGGYWMIIRHPGKLEWIGYIYHSGNTYNPSTL 61  
DB 6 ESGPGLVKAQTLTSLTCTVSGGSIIRSGGYWMIIRHPGKLEWIGYIYHSGNTYNPSTL 65  
QY 62 KSRVITISVDTSSENFSLRLNSVTAAADTAAYVYCAR-DGYNWYFPLMGRGLVTYSS 114  
DB 66 KSRVITISVDTSSENFSLRLNSVTAAADTAAYVYCAR-DGYNWYFPLMGRGLVTYSS 120  
RESULT 10  
ADP03873  
ID ADP03873 standard; protein; 120 AA.  
XX  
AC ADP03873;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.  
XX  
OS monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KM cytosolic; colorectal neoplasm; renal cell carcinoma;  
KM cervical intraepithelial squamous neoplasia;  
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KM gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
OS Unidentified.  
XX  
OS WO2003048328-A2.  
XX  
PN 12-JUN-2003.  
XX  
PD 02-DEC-2002; 2002WO-US038550.  
XX  
PF 03-DEC-2001; 2001US-0337275P.  
XX  
PR (ABGE-) ABGENIX INC.  
XX  
PA Gudus J, Foltz I, Handa M, Gallo M;  
XX  
PI WPI; 2003-523295/49.  
XX  
DR WPI; 2003-523295/49.  
XX  
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
PS Claim 1; SEQ ID NO 13; 89pp; English.  
XX  
CC The invention relates to a novel isolated monoclonal antibody (mab)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

XX  
SQ Sequence 120 AA;  
Query Match 84.1%; Score 512; DB 7; Length 120;  
Best Local Similarity 81.9%; Pred. No. 2,6e-39;  
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;  
QY 2 ESGPGLVKAQTLTSLSCAVSGGSIIRSGGYWMIIRHPGKLEWIGYIYHSGNTYNPSTL 61  
DB 6 ESGPGLVKAQTLTSLTCTVSGGSIIRSGGYWMIIRHPGKLEWIGYIYHSGNTYNPSTL 65  
QY 62 KSRVITISVDTSSENFSLRLNSVTAAADTAAYVYCAR-DGYNWYFPLMGRGLVTYSS 114  
DB 66 KSRVITISVDTSSENFSLRLNSVTAAADTAAYVYCAR-DGYNWYFPLMGRGLVTYSS 120  
RESULT 11  
ADP03872  
ID ADP03872 standard; protein; 123 AA.  
XX  
AC ADP03872;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 12.  
XX  
OS monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
KM cytosolic; colorectal neoplasm; renal cell carcinoma;  
KM cervical intraepithelial squamous neoplasia;  
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
KM gene therapy; murine; mouse; human; heavy chain variable domain.  
XX  
OS Unidentified.  
XX  
OS WO2003048328-A2.  
XX  
PN 12-JUN-2003.  
XX  
PD 02-DEC-2002; 2002WO-US038550.  
XX  
PF 03-DEC-2001; 2001US-0337275P.  
XX  
PR (ABGE-) ABGENIX INC.  
XX  
PA Gudus J, Foltz I, Handa M, Gallo M;  
XX  
PI WPI; 2003-523295/49.  
XX  
DR WPI; 2003-523295/49.  
XX  
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX  
PS Claim 1; SEQ ID NO 12; 89pp; English.  
XX  
CC The invention relates to a novel isolated monoclonal antibody (mab)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.  
XX  
SQ Sequence 123 AA;  
Query Match 83.7%; Score 509.5; DB 7; Length 123;  
Best Local Similarity 78.8%; Pred. No. 4,6e-39;  
Matches 93; Conservative 13; Mismatches 7; Indels 5; Gaps 1;

[illegible]

```

RESULT 12
ADP03870
ID      ADP03870 standard; protein; 123 AA

```

DT	29-JUL-2004	(first entry)
XX	Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10	
DE		
KW	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;	
KW	cervical intraepithelial squamous neoplasia; renal cell carcinoma;	
KW	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer	
KM	gene therapy; murine; mouse; human; heavy chain variable domain.	
XX		
UN	Unidentified.	

XX	12-JUN-2003.
PD	
XX	
PF	02-DEC-2002; 2002WO-US038550
XX	
PR	03-DEC-2001; 2001US-0337275P

PA (ABGE-) ABGENIX INC.  
XX  
XX Gudus J, Foltz I, Handa M, Gallo M,  
PI  
XX  
DR WPI; 2003-523295/49.

PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
PT intraepithelial squamous and glandular neoplasia or esophageal tumors  
XX  
PS Claim 1; SEQ ID NO 10; 89pp; English.

CC The invention relates to a novel isolated monoclonal antibody (mbb)  
CC comprising a heavy chain polypeptide and light chain polypeptide having a  
CC sequence chosen from one of 53 fully defined amino acid sequences given  
CC in the specification, where the antibody specifically binds carbonic  
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
CC demonstrates cytostatic activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

Query Match	83.5%;	Score 508.5;	DB 7;	Length 123;
Best Local Similarity	80.5%;	Pred. No. 5.6e-39;		
Matches 95; Conservative	10;	Mismatches 8;	Indels 5;	Gaps 1;

```
Oy      2  ESGPGLVPAQTLTSLSCAVSGGSIRSGGYWMSWIRQHPGKLEIEMIGIYIHSGNTYYNPSL 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      6  ESGPGLVKPSQTLSTLTCTVSSGGSISSGGYWMSWIRQHPGKLEIEMIGIYIYSGSTYYNPSL 65
```

QY 62 KSRIAMSVDTS ENKFSLR LNSVTADTAVVYCARL-----DGYTLDIWGQTLTVSS 114

Db 66 KSRVTSVDTSKNQFSLKLSVTADTAVYVCARAKRYGSSSYLDYVQGGTLVTWSS 123

RESULT 13  
ADP03879  
ID ADP03879 standard; protein; 123 AA

DT 29-JUL-2004 (first entry)

DE	Murine-expressed anti-human CA IX monoclonal antibody VH protein-SEQ 19.
XX	
KM	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM	cytostatic; colorectal neoplasms; renal cell carcinoma;
KM	cervical intraepithelial squamous neoplasia;
KM	cervical intraepithelial glandular neoplasia;
KM	gene therapy; murine; mouse; human; heavy chain variable domain.

OS	Unidentified.
XX	
PN	WO2003048328-A2.
XX	
PD	12-JUN-2003.

PF	02-DEC-2002; 2002WO-US038550.
XX	
PR	03-DEC-2001; 2001US-0337275P.

PA (ABGE-) ABGENIX INC.

PI Gudas J, Foltz I, Handa M, Gallo M,  
XX  
DR WPI; 2003-523295/49.

**Claim 1:** SEQ ID NO 19; 89PD; English.

The invention relates to a novel isolated monoclonal antibody (mab) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia, oesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a transgenic mouse strain.

Query Match	83.5%	Score 508.5	DB 7	Length 123
Best Local Similarity	80.5%	Pred. No. 5.6e-39		
Matches 95; Conservative	10;	Mismatches 8;	Indels 5;	Gaps 1.

Db 6 ESGPGVKPSQTLSLTCTVSGGSINSGGYMSWIRQHPKGLIEWIGIYYSGSTYNNPSL 65

QY 62 KSRINASVDTSENKFSRLNLSVTADTAVYYCAR----LDGYTLIDWGQGLVTVSS 114

Db 66 KSRVITISVDTS<sup>1</sup>ENQ<sup>1</sup>FS<sup>1</sup>LKLS<sup>1</sup>SVTAD<sup>1</sup>TA<sup>1</sup>VY<sup>1</sup>CARER<sup>1</sup>VTDY<sup>1</sup>Y<sup>1</sup>Y<sup>1</sup>Y<sup>1</sup>Y<sup>1</sup>Y<sup>1</sup>GLD<sup>1</sup>VMG<sup>1</sup>G<sup>1</sup>TT<sup>1</sup>VT<sup>1</sup>VS 123

RESULT 14  
ADP03878

```
ID ADP03878 standard; proctein; 123 AA.
AC
XX ADP03878;
XX
XX 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 18.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM cytosolic; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
OS
XX WO2003048328-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudas J, Foltz I, Handa M, Gallo M;
XX
XX WPI; 2003-523295/49.
XX
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX
XX Claim 1; SEQ ID NO 18; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytosolic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
XX
XX Sequence 123 AA;
SQ
XX
XX Query Match 83.5%; Score 508.5; DB 7; Length 123;
XX Best Local Similarity 80.5%; Pred. No. 5.6e-39;
XX Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;
XX
XX
XX 2 ESGPGLVKAQTLISCAVSGSIRSGYVSWIRQHPGKLEWIGYIYHSGNTYVNSL 61
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 6 ESGPGLVKAQTLISCAVSGSIRSGYVSWIRQHPGKLEWIGYIYHSGNTYVNSL 65
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 62 KSRIAMVDTSSENKFSRLNSVTADTAIVYCAR----LDGYTLDIWGQGLTVVSS 114
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 66 KSRVYISVDTSSENKFSRLNSVTADTAIVYCARERTVDYVYGGGLTVVSS 123
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX
XX RESULT 15
XX ID ADP03868 standard; proctein; 125 AA.
XX
XX ADP03868;
XX
XX
XX 29-JUL-2004 (first entry)
XX
```

```
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 8.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM cytosolic; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
OS
XX WO2003048328-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudas J, Foltz I, Handa M, Gallo M;
XX
XX WPI; 2003-523295/49.
XX
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX
XX Claim 1; SEQ ID NO 8; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytosolic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
XX
XX Sequence 125 AA;
SQ
XX
XX Query Match 83.5%; Score 508.5; DB 7; Length 125;
XX Best Local Similarity 79.2%; Pred. No. 5.7e-39;
XX Matches 95; Conservative 12; Mismatches 6; Indels 7; Gaps 2;
XX
XX
XX 2 ESGPGLVKAQTLISCAVSGSIRSGYVSWIRQHPGKLEWIGYIYHSGNTYVNSL 61
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 6 ESGPGLVKAQTLISCAVSGSIRSGYVSWIRQHPGKLEWIGYIYHSGNTYVNSL 65
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 62 KSRIAMVDTSSENKFSRLNSVTADTAIVYCAR----LDGY--TLDIWGQGLTVVSS 114
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 66 KSRVYISVDTSSENKFSRLNSVTADTAIVYCARERTVDYVYGGGLTVVSS 125
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX
XX Search completed: July 26, 2005, 09:19:17
XX Job time : 87.3273 secs
XX
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## OM protein - protein search, using sw model

Run on: July 26, 2005, 09:26:32 ; Search time 72.5455 Seconds

(without alignments)  
611.274 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609  
Sequence: 1 LESGGLVXPAQTLSLSCAV.....RLDGYTLIDWGGTLVTVSS 114Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications MA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09C\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US10F\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	609	100.0	114	US-10-027-725A-7	Sequence 7, Appl1
2	556	91.3	114	US-10-027-725A-9	Sequence 9, Appl1
3	546	89.7	114	US-10-027-725A-8	Sequence 8, Appl1
4	519	82.2	122	US-10-309-762-147	Sequence 147, Appl1
5	518.5	85.1	121	US-10-309-762-152	Sequence 152, Appl1
6	517.5	85.0	125	US-10-309-762-111	Sequence 11, Appl1
7	514.5	84.5	121	US-10-309-762-151	Sequence 151, Appl1
8	512	84.1	118	US-10-309-762-138	Sequence 138, Appl1
9	512	84.1	120	US-10-309-762-13	Sequence 13, Appl1
10	512	84.1	120	US-10-309-762-144	Sequence 144, Appl1
11	509.5	83.7	123	US-10-309-762-12	Sequence 12, Appl1

	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45																																																																																																																																																																																
US-10-027-725A-7	508.5	83.5	123	15	US-10-309-762-10	Sequence 10, Appl1	508.5	83.5	123	15	US-10-309-762-18	Sequence 18, Appl1	508.5	83.5	123	15	US-10-309-762-19	Sequence 19, Appl1	508.5	83.5	123	15	US-10-309-762-8	Sequence 8, Appl1	508.5	83.5	125	15	US-10-309-762-8	Sequence 8, Appl1	508.5	83.5	125	15	US-10-309-762-16	Sequence 16, Appl1	508.5	83.5	144	17	US-10-893-576-35	Sequence 35, Appl1	506.5	83.2	119	15	US-10-309-762-131	Sequence 131, Appl1	505.5	82.9	119	15	US-10-309-762-140	Sequence 140, Appl1	505	82.9	252	10	US-09-880-748-1994	Sequence 1994, Appl1	505	82.9	252	15	US-10-293-418-1994	Sequence 1994, Appl1	504.5	82.8	125	15	US-10-309-762-153	Sequence 153, Appl1	504.5	82.8	480	17	US-10-910-901-6	Sequence 6, Appl1	504	82.8	120	15	US-10-309-762-139	Sequence 139, Appl1	503.5	82.7	127	15	US-10-309-762-14	Sequence 14, Appl1	503	82.6	124	15	US-10-309-762-75	Sequence 75, Appl1	503	82.6	143	15	US-10-309-762-96	Sequence 96, Appl1	501.5	82.3	117	14	US-10-330-613-13	Sequence 13, Appl1	501.5	82.3	117	14	US-10-330-530-13	Sequence 13, Appl1	501.5	82.3	117	16	US-10-660-357-13	Sequence 22, Appl1	501	82.3	149	17	US-10-910-901-22	Sequence 190, Appl1	500.5	82.2	123	17	US-10-893-576-190	Sequence 75, Appl1	500.5	82.2	251	14	US-10-120-414-75	Sequence 75, Appl1	500	82.1	125	17	US-10-805-177-53	Sequence 53, Appl1	498.5	81.9	253	10	US-09-880-748-1619	Sequence 1619, Appl1	498.5	81.9	253	15	US-10-293-418-1619	Sequence 1619, Appl1	497.5	81.7	148	17	US-10-693-576-31	Sequence 31, Appl1	497	81.6	110	15	US-10-309-762-74	Sequence 74, Appl1	497	81.6	121	15	US-10-308-817-137	Sequence 137, Appl1	497	81.6	121	15	US-10-453-698-137	Sequence 137, Appl1	497	81.6	121	15	US-10-727-155-2	Sequence 2, Appl1	497	81.6	128	17	US-10-727-155-30	Sequence 30, Appl1	497	81.6	128	17	US-10-727-155-30	Sequence 30, Appl1	496.5	81.5	123	15	US-10-309-762-17	Sequence 17, Appl1	496.5	81.5	123	15	US-10-644-277-62	Sequence 62, Appl1

## ALIGNMENTS

RESULT 1  
US-10-027-725A-7  
; Sequence 7, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027.725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-027-725A-7

Query Match 100.0%; Score 609; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 5.7e-49;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESGGLVXPAQTLSLSCAVSGGSTRSGGYWIRQHPGKLEWIGYIHSGNTYNS 60  
DB 1 LESGGLVXPAQTLSLSCAVSGGSTRSGGYWIRQHPGKLEWIGYIHSGNTYNS 60  
QY 61 LKSRIVSVDSSEKFSRLNSVTAAADAVYYCARLDGYTLIDWGGTLVTVSS 114  
DB 61 LKSRIVSVDSSEKFSRLNSVTAAADAVYYCARLDGYTLIDWGGTLVTVSS 114

RESULT 2



```

US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-9

```

```

Query Match          91.3%; Score 556; DB 14; Length 114;
Best Local Similarity 90.4%; Pred. No. 4,8e-44;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 1 LESGPGLVKPAQTSLSCAVSGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 LKSRVITSVDTSENKFSRLNSVTADTAAYVYCARLDYTDIWDGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LKSRVITSVDTSENKFSRLNSVTADTAAYVYCARLDYTDIWDGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 3
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-8

```

```

Query Match          89.7%; Score 546; DB 14; Length 114;
Best Local Similarity 89.5%; Pred. No. 4.1e-43;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

```

```

Qy 1 LESGPGLVKPAQTSLSCAVSGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 LKSRVITSVDTSENKFSRLNSVTADTAAYVYCARLDYTDIWDGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LKSRVITSVDTSENKFSRLNSVTADTAAYVYCARLDYTDIWDGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 4
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa

```

```

; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-147

```

```

Query Match          85.2%; Score 519; DB 15; Length 122;
Best Local Similarity 81.2%; Pred. No. 1.4e-40;
Matches 95; Conservative 12; Mismatches 6; Indels 4; Gaps 1;

```

```

Qy 2 ESGPGLVPAQTSLSCAVSGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVPSQTLSTCTVSGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 62 KSRVITSVDTSENKFSRLNSVTADTAAYVYCARLDYTDIWDGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVITSVDTSENKFSRLNSVTADTAAYVYCARLDYTDIWDGQGLTVTVSS 122
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 5
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-152

```

```

Query Match          85.1%; Score 518.5; DB 15; Length 121;
Best Local Similarity 81.9%; Pred. No. 1.6e-40;
Matches 95; Conservative 11; Mismatches 7; Indels 3; Gaps 1;

```

```

Qy 2 ESGPGLVPAQTSLSCAVSGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVPSQTLSTCTVSGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 62 KSRVITSVDTSENKFSRLNSVTADTAAYVYCARLDYTDIWDGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVITSVDTSENKFSRLNSVTADTAAYVYCARLDYTDIWDGQGLTVTVSS 121
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 6
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian

```



```
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: AGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-11
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```
Query Match 85.0%; Score 517.5; DB 15; Length 125;
Best Local Similarity 81.7%; Pred. No. 2e-40;
Matches 98; Conservative 9; Mismatches 6; Indels 7; Gaps 2;
```

```
OY 2 ESGGGLVPAQTSLSCAVSGSIRSGGYWSWIRHFGKGLWIGIYHSNTYNSPL 61
DB 6 ESGGGLVPSQTLSTCTVSGSISSGGYWSWIRHFGKGLWIGIYHSNTYNSPL 65
OY 62 KSRIVSVDTSENKFSRLNSVTADTAIVYCARL---LDGY--TLDIMOGGTLVTVSS 114
DB 66 KSRITISVDTSKNQFSLKLSSTVTAADTAIVYCAATYIDFLGTGPDADPDIMOGGTLVTVSS 125
```

```
RESULT 7
US-10-309-762-151
```

```
Sequence 151, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: AGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 151
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-151
```

```
Query Match 84.5%; Score 514.5; DB 15; Length 121;
Best Local Similarity 81.0%; Pred. No. 3.7e-40;
Matches 94; Conservative 13; Mismatches 6; Indels 3; Gaps 1;
```

```
OY 2 ESGGGLVPAQTSLSCAVSGSIRSGGYWSWIRHFGKGLWIGIYHSNTYNSPL 61
DB 6 ESGGGLVPSQTLSTCTVSGSISSGGYWSWIRHFGKGLWIGIYHSNTYNSPL 65
OY 62 KSRIVSVDTSENKFSRLNSVTADTAIVYCARL---DGYTLDIMOGGTLVTVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAIVYCARVLMFGYGMVDVGGGTLVTVSS 121
```

```
RESULT 8
US-10-309-762-138
Sequence 138, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
```

```
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: AGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 138
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-138
```

```
Query Match 84.1%; Score 512; DB 15; Length 118;
Best Local Similarity 83.2%; Pred. No. 6.1e-40;
Matches 94; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
```

```
OY 2 ESGGGLVPAQTSLSCAVSGSIRSGGYWSWIRHFGKGLWIGIYHSNTYNSPL 61
DB 6 ESGGGLVPSQTLSTCTVSGSISSGGYWSWIRHFGKGLWIGIYHSNTYNSPL 65
OY 62 KSRIVSVDTSENKFSRLNSVTADTAIVYCARL---LDGY--TLDIMOGGTLVTVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAIVYCAATYIDFLGTGPDADPDIMOGGTLVTVSS 118
```

```
RESULT 9
```

```
US-10-309-762-13
Sequence 13, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: AGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-13
```

```
Query Match 84.1%; Score 512; DB 15; Length 120;
Best Local Similarity 81.9%; Pred. No. 6.2e-40;
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;
```

```
OY 2 ESGGGLVPAQTSLSCAVSGSIRSGGYWSWIRHFGKGLWIGIYHSNTYNSPL 61
DB 6 ESGGGLVPSQTLSTCTVSGSISSGGYWSWIRHFGKGLWIGIYHSNTYNSPL 65
OY 62 KSRIVSVDTSENKFSRLNSVTADTAIVYCARL---LDGY--TLDIMOGGTLVTVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAIVYCARL---LDGY--TLDIMOGGTLVTVSS 120
```

```
RESULT 10
US-10-309-762-144
Sequence 144, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
```

```

; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-144
```

```

Query Match      84.1%; Score 512; DB 15; Length 120;
Best Local Similarity 81.9%; Pred. No. 6.2e-40;
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;
```

```

Qy      2  EESGGLVKKPAQTLISLCAVSGGSIIRSGGYWMTIRQHPGKLEWIGIYHSGMTYVNSPL 61
Db      6  EESGGLVKKPQTLISLCTVSGGSIISGGYWSMIRQHPGKLEWIGIYHSGMTYVNSPL 65

Qy      62  KSRIVSVDTSENKFSRLNSVTAAADTAAYVYCARLDTGVT--LDIWGGTLVTVSS 114
Db      66  KSRVTVSVDTSENKFSRLNSVTAAADTAAYVYCAR--DGVNVMYFDLWGGTLVTVSS 120
```

```

RESULT 11
US-10-309-762-12
; Sequence 12, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-12
```

```

Query Match      83.7%; Score 509.5; DB 15; Length 123;
Best Local Similarity 78.8%; Pred. No. 1.1e-39;
Matches 93; Conservative 13; Mismatches 7; Indels 5; Gaps 1;
```

```

Qy      2  EESGGLVKKPAQTLISLCAVSGGSIIRSGGYWMTIRQHPGKLEWIGIYHSGMTYVNSPL 61
Db      6  EESGGLVKKPQTLISLCTVSGGSIISGGYWSMIRQHPGKLEWIGIYHSGMTYVNSPL 65

Qy      62  KSRIVSVDTSENKFSRLNSVTAAADTAAYVYCARL-----DGYTLDIWGGTLVTVSS 114
Db      66  KSRVTVSVDTSENKFSRLNSVTAAADTAAYVYCARVLMFGEDYGVDMWGGTLVTVSS 123
```

```

RESULT 12
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10
```

```

Query Match      83.5%; Score 508.5; DB 15; Length 123;
Best Local Similarity 80.5%; Pred. No. 1.3e-39;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;
```

```

Qy      2  EESGGLVKKPAQTLISLCAVSGGSIIRSGGYWMTIRQHPGKLEWIGIYHSGMTYVNSPL 61
Db      6  EESGGLVKKPQTLISLCTVSGGSIISGGYWSMIRQHPGKLEWIGIYHSGMTYVNSPL 65

Qy      62  KSRIVSVDTSENKFSRLNSVTAAADTAAYVYCARL-----DGYTLDIWGGTLVTVSS 114
Db      66  KSRVTVSVDTSENKFSRLNSVTAAADTAAYVYCARAGRTYSSGSLDVMWGGTLVTVSS 123
```

```

RESULT 13
US-10-309-762-18
; Sequence 18, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-18
```

```

Query Match      83.5%; Score 508.5; DB 15; Length 123;
Best Local Similarity 80.5%; Pred. No. 1.3e-39;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;
```

```

Qy      2  EESGGLVKKPAQTLISLCAVSGGSIIRSGGYWMTIRQHPGKLEWIGIYHSGMTYVNSPL 61
Db      6  EESGGLVKKPQTLISLCTVSGGSIISGGYWSMIRQHPGKLEWIGIYHSGMTYVNSPL 65

Qy      62  KSRIVSVDTSENKFSRLNSVTAAADTAAYVYCAR-----LDGYTLDIWGGTLVTVSS 114
Db      66  KSRVTVSVDTSENKFSRLNSVTAAADTAAYVYCARERTVDYVYGLDVMWGGTLVTVSS 123
```

```

RESULT 14
US-10-309-762-19
; Sequence 19, Application US/10309762
```

```
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-19
```

```
Query Match      83.5%; Score 508.5; DB 15; Length 123;
Best Local Similarity 80.5%; Pred. No. 1.3e-39;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;
```

```
QY      2  ESGGLVPAQTLISCAVSGSIRSGYWSWIRHPKGLWIGYIYHSGNTYVNSL 61
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      6  ESGGLVPAQTLISCAVSGSIRSGYWSWIRHPKGLWIGYIYHSGNTYVNSL 65
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      62  KSRVYISVDTSENQFSLKLSVTADTAIVYCAR----LDGYTLDIWGGLTVVSS 114
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      66  KSRVYISVDTSENQFSLKLSVTADTAIVYCARERTDYVYGLDVGCGTIVTVSS 123
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 15
US-10-309-762-8
; Sequence 8, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-8
```

```
Query Match      83.5%; Score 508.5; DB 15; Length 125;
Best Local Similarity 79.2%; Pred. No. 1.4e-39;
Matches 95; Conservative 12; Mismatches 6; Indels 7; Gaps 2;
```

```
QY      2  ESGGLVPAQTLISCAVSGSIRSGYWSWIRHPKGLWIGYIYHSGNTYVNSL 61
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      6  ESGGLVPAQTLISCAVSGSIRSGYWSWIRHPKGLWIGYIYHSGNTYVNSL 65
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      62  KSRVYISVDTSENQFSLKLSVTADTAIVYCAR----LDGY--TLDIWGGLTVVSS 114
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      66  KSRVYISVDTSENQFSLKLSVTADTAIVYCARERTDYVYGLDVGCGTIVTVSS 125
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Search completed: July 26, 2005, 10:05:18  
Job time : 73.7121 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:42:26 ; Search time 88.6545 Seconds

(without alignments)  
5869.253 Million cell updates/sec

Title: US-10-027-725A-6

Perfect score: 318  
Sequence: 1 gagctcagcagctctcctc.....ccaagtcggaatcaacga 318

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA.\*

1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	291.4	91.6	974	4	US-09-859-053-29
2	291	91.5	388	3	US-09-042-353-358
3	291	91.5	388	3	US-08-758-417A-206
4	283.4	89.1	420	3	US-09-042-353-420
5	283.4	89.1	420	3	US-08-758-417A-220
6	283.4	89.1	3819	3	US-09-042-353-393
7	283.4	89.1	4319	3	US-08-758-417A-243
8	277	87.1	439	3	US-08-042-353-360
9	277	87.1	384	1	US-08-758-417A-208
10	275.4	86.6	384	1	US-08-259-372A-13
11	275.4	86.6	384	1	US-08-468-671-13
12	268.4	84.9	321	3	US-09-240-274-109
13	268.4	84.9	321	3	US-09-240-274-199
14	263.6	82.9	321	3	US-09-240-274-98
15	263.6	82.9	321	3	US-09-240-274-102
16	263.6	82.9	321	3	US-09-240-274-218
17	263.6	82.9	321	3	US-09-240-274-221
18	263.6	82.9	321	3	US-09-240-274-222
19	262	82.4	321	3	US-09-240-274-215
20	262	82.4	321	3	US-09-240-274-217
21	260.4	81.9	324	2	US-09-240-274-113
22	259.4	81.6	324	2	US-08-378-939-31
23	259.4	81.6	324	2	US-08-378-939-33
24	259.4	81.6	714	4	US-09-472-087-62
25	258.8	81.4	321	4	US-09-240-274-107
26	258.4	81.3	720	4	US-09-192-854-1
27	257.8	81.1	390	2	US-08-646-367-2

28	257.2	80.9	321	3	US-09-240-274-105	Sequence 105, App
29	257.2	80.9	321	3	US-09-240-274-216	Sequence 216, App
30	257	80.8	324	3	US-09-240-274-206	Sequence 206, App
31	256.2	80.6	324	2	US-08-378-939-23	Sequence 23, App1
32	255.6	80.4	321	3	US-09-240-274-104	Sequence 104, App
33	255.6	80.4	321	3	US-09-240-274-201	Sequence 201, App
34	255.6	80.4	321	3	US-09-240-274-211	Sequence 211, App
35	255.4	80.3	324	3	US-09-240-274-101	Sequence 101, App
36	255.4	80.3	324	3	US-09-240-274-112	Sequence 112, App
37	255.4	80.3	324	3	US-09-240-274-210	Sequence 210, App
38	254.6	80.1	324	2	US-08-378-939-17	Sequence 17, App1
39	254	79.9	324	2	US-09-240-274-207	Sequence 207, App
40	253	79.6	324	2	US-08-378-939-15	Sequence 15, App1
41	252.4	79.4	321	3	US-09-240-274-106	Sequence 106, App
42	252.2	79.3	324	3	US-09-240-274-224	Sequence 224, App
43	250.8	78.9	321	3	US-09-240-274-205	Sequence 205, App
44	250.6	78.8	324	3	US-09-240-274-110	Sequence 110, App
45	250.2	78.7	417	4	US-09-472-087-48	Sequence 48, App1

## ALIGNMENTS

```
RESULT 1
US-09-859-053-29
; Sequence 29, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Takashi
; APPLICANT: Tezuka, Katsunari
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILM AND
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859, 053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; NAME/KEY: (39)...(746)
; LOCATION: (750)...(974)
; NAME/KEY: sig_peptide
; LOCATION: (39)...(104)
US-09-859-053-29

Query Match          91.6%; Score 291.4; DB 4; Length 974;
Best Local Similarity 95.0%; Pred. No. 9.5e-92;
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY      2 AGCTCAGCAGTCTTCATCTCCGTTGTCATCTGTAGAGACAGATCCATTAATT 61
DB      112 AGATGACCCAGTCTTCATCTCCGTTGTCATCTGTAGAGACAGATCCATTA 171
QY      62 GTCCGCGCAGTCCAGGATTTAGCAGTTGTTAGCCTGATCAGCAGAAACAGGAAAG 121
DB      172 GTCCGCGCAGTCCAGGATTTAGCAGTTGTTAGCCTGATCAGCAGAAACAGGAAAG 231
QY      122 CCCCTAACTCTGATCTATTTCTGCATCCAGTTTGCAAGTGGGGTCCGTCAGTTCA 181
DB      232 CCCCTAACTCTGATCTATTTCTGCATCCAGTTTGCAAGTGGGGTCCGTCAGTTCA 291
```

Qy	18	GGCGAGTGAATCTGGGACAGATTTTACGTCACCATCAGAGCGCTGGAGCTGAAGTT	241
Db	292	GGCGAGTGAATCTGGGACAGATTTTACGTCACCATCAGAGCGCTGGAGCTGAAGTT	351
Qy	242	CTGCAACTTACTTGTGTCAACAGGCTTACAGTTTCCGTCACATTTTGGCCAGGGACCA	301
Db	352	TTGCAACTTACTTGTGTCAACAGGCTTACAGTTTCCGTCACATTTTGGCCAGGGACCA	411
Qy	302	AGGTGAAATCAACGA	318
Db	412	AGGTGAAATCAACGA	428
RESULT 2			
US-09-042-353-358			
Sequence 358, Application US/09042353			
Patent No. 6255458			
GENERAL INFORMATION:			
APPLICANT: Lomborg, Nils			
APPLICANT: Kay, Robert M.			
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for			
NUMBER OF SEQUENCES: 421			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Townsend and Townsend and Crew LLP			
STREET: Two Embarcadero Center, Eighth Floor			
CITY: San Francisco			
STATE: California			
COUNTRY: USA			
ZIP: 94111-3834			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentin Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/042,353			
FILING DATE: 13-MAR-1998			
CLASSIFICATION: 800			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/810,279			
FILING DATE: 17-DEC-1991			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/853,408			
FILING DATE: 18-MAR-1992			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/904,068			
FILING DATE: 23-JUN-1992			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/990,860			
FILING DATE: 16-DEC-1992			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 08/053,131			
FILING DATE: 26-APR-1993			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 08/096,762			
FILING DATE: 22-JUL-1993			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 08/155,301			
FILING DATE: 18-NOV-1993			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 08/161,739			
FILING DATE: 03-DEC-1993			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 08/165,699			
FILING DATE: 10-DEC-1993			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 08/209,741			
FILING DATE: 09-MAR-1994			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 08/352,322			
FILING DATE: 07-DEC-1994			

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1      PRIOR APPLICATION DATA:
2      APPLICATION NUMBER: US 08/544,404
3      FILING DATE: 10-OCT-1995
4      PRIOR APPLICATION DATA:
5      APPLICATION NUMBER: US 08/728,463
6      FILING DATE: 10-OCT-1996
7      PRIOR APPLICATION DATA:
8      APPLICATION NUMBER: WO PCT/US96/16433
9      FILING DATE: 10-OCT-1996
10     PRIOR APPLICATION DATA:
11     APPLICATION NUMBER: US 08/758,417
12     FILING DATE: 02-DEC-1996
13     PRIOR APPLICATION DATA:
14     APPLICATION NUMBER: WO PCT/US97/21803
15     FILING DATE: 01-DEC-1997
16     ATTORNEY/AGENT INFORMATION:
17     NAME: Apple, Randolph T.
18     REGISTRATION NUMBER: 36,429
19     REFERENCE/DOCKET NUMBER: 014643-009040US
20     TELECOMMUNICATION INFORMATION:
21     TELEPHONE: (415) 576-0200
22     TELEFAX: (415) 576-0300
23     INFORMATION FOR SEQ ID NO: 358:
24     SEQUENCE CHARACTERISTICS:
25     LENGTH: 388 base pairs
26     TYPE: nucleic acid
27     STRANDEDNESS: single
28     TOPOLOGY: linear
29     MOLECULE TYPE: DNA
30     US-09-042-353-358

```

Query Match	91.5%	Score 291;	DB 3;	Length 388;
Best Local Similarity	95.2%	Pred. No. 8.3e-92;		
Matches 300; Conservative	0;	Mismatches 15;	Indels 0;	Gaps 0;

Oy	2	AGCTCAGCAGATCTCCATTTCCGTCTGCATCTGTAGGAGACAGAGTCAACCTACTT	61
Db	74	AGATGACCCAGATCTCCATCTTCCGTGTGCATCTGTAGGAGACAGAGTCAACATCTT	133
Oy	62	GTCGGGCGAGTCAGGGTATTTAGCACTGGTTAGCCTGGTATCAGCAGAAACAGGGGAAAG	121
Db	134	GTCGGGCGAGTCAGGATATTTAGCACTGGTTAGCCTGGTATCAGCATTAAACAGGGGAAAG	193
Oy	122	CCCTTAACTCTGATCTATTTCTGCATCCAGTTTGCAAAAGTGGGTCCCGTCAAGTTCA	181
Db	194	CCCTTAACTCTGATCTATGTGTGATCAAGTTTGCAAAAGTGGGTCCCATCAAGTTCA	253
Oy	182	GCGGCAGTGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCTTGAGATT	241
Db	254	GCGGCAGTGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCTTGAGATT	313
Oy	242	CTGCAACTTACTATTTGTCAACAGGCTAACAGTTTCCGTAACCTTTTGGCCAGGGGACCA	301
Db	314	TTTCAACTTACTATTTGTCAACAGGCTTAATAGTTTCCGTAACCTTTTGGCCAGGGGACCA	373
Oy	302	AGGTGAAATCAAC	316
Db	374	AGCTTGAGATCAAC	388

```

: RESULT 3
: US-08-758-417A-206
: Sequence 206, Application US/08758417A
: Patent No. 6300129
: GENERAL INFORMATION:
: APPLICANT: Lomborg, Nils
: Kay, Robert M.
: TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
: Producing Heterologous Antibodies
: NUMBER OF SEQUENCES: 417
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
:

```

CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,417A  
FILING DATE: 02-DEC-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Serafini, Andrew T.  
REGISTRATION NUMBER: 41,303  
REFERENCE/DOCKET NUMBER: 014643-009030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 206:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 388 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 206:  
US-08-758-417A-206

Query Match 91.5%; Score 291; DB 3; Length 388;  
Best Local Similarity 95.2%; Pred. No. 8.3e-92;  
Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

2 AGCTACCCACTTCCATCTCCGCTGCTGCATCTGTAGGAGACAGATCCCAATTT 61  
74 AGATGACCCAGCTTCATCTCCGCTGCTGCATCTGTAGGAGACAGATCCCAATTT 133  
62 GTCCGGCAGTCAAGGATTTAGCAGTTAGCTGATATCAGAGAAACAGGGAAG 121  
134 GTCCGGCAGTCAAGGATTTAGCAGTTAGCTGATATCAGAGAAACAGGGAAG 193  
122 CCCCTAACTCTGATCTATTTGATCAGATTCAGTTGCAAGTGGGTCCCGTCAAGTTCA 181  
194 CCCCTAACTCTGATCTATTTGATCAGATTCAGTTGCAAGTGGGTCCCGTCAAGTTCA 253  
182 GGGGAGAGGATCTGGGACAGATTTGATCAGATTCAGATTCAGAGCTGAGGCTGAAGATT 241  
254 GGGGAGAGGATCTGGGACAGATTTGATCAGATTCAGATTCAGAGCTGAGGCTGAAGATT 313  
242 CTGCAACTTACTATTGTCAACAGGCTAAAGTTTCCGTACACTTTTGCCAGGGGACCA 301

Db 314 TTGCAACTTACTATTGTCAACAGGCTAAATAGTTCCCGTACACTTTGGCCAGGGGACCA 373  
Cy 302 AGGTGAATATCAAC 316  
Db 374 AGCTGAGATCAAC 388

RESULT 4  
US-09-042-353-420  
Sequence 420, Application US/09042353  
Patent No. 6255458  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nile  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 421  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,353  
FILING DATE: 13-MAR-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:

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1  APPLICATION NUMBER:  WO PCT/US96/16433
2  FILING DATE:  10-OCT-1996
3  PRIOR APPLICATION DATA:
4  APPLICATION NUMBER:  US 08/758,417
5  FILING DATE:  02-DEC-1996
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER:  WO PCT/US97/21803
8  FILING DATE:  01-DEC-1997
9  ATTORNEY/AGENT INFORMATION:
10 NAME:  Apple, Randolph T.
11 REGISTRATION NUMBER:  36,429
12 REFERENCE/DOCKET NUMBER:  014643-009040US
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE:  (415) 576-0200
15 TELEFAX:  (415) 576-0300
16 INFORMATION FOR SEQ ID NO: 420:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH:  420 base pairs
19 TYPE:  nucleic acid
20 STRANDEDNESS:  single
21 TOPOLOGY:  linear
22 MOLECULE TYPE:  DNA
23 US-09-042-353-420

```

Query Match	89.1%;	Score 283.4;	DB 3;	Length 420;
Best Local Similarity	93.4%;	Pred. No. 4e-89;		
Matches 296;	Conservative	0;	Mismatches 21;	Indels 0;
				Gaps 0;

Qy	2	AGCTCAGCAGTGTCCATCTTCGATGCTGTGCATCTGTAGAGACAGAGTCAACATACTT	61
Db	80	AGATTAGCCAGTCTCCATCTTCGATGCTGTGCATCTGTAGAGACAGAGTCAACATACTT	139
Qy	62	GTCGGCGAGTCAGGGTATTAGACGTGTGTAGCTGTGATCAGCAGAAACAGGGAAG	121
Db	140	GTCGGCGAGTCAGAGTATTAGACGTGTGTAGCTGTGATCAGCAGTAAACAGGTAAG	199
Qy	122	CCCTTAACTCCTGATCTATTTCGATCCAGTTTGCAAAGTGGGTCCCGTCAAGTTCA	181
Db	200	CACCTAAGCTCTGATCTATTGCTGATCCAGTTTGCAAAGTGGTCTCCATCAAGTTCA	255
Qy	182	GCGCAGTGGATTTGGGACAGATTTCAGTCTACCATCAGCAGCTCGACGCTTAAGATT	241
Db	260	GCGAAGTGGATCTGGGACAGATTTCACCTCACATCAGCAGCTCGACGCTTAAGATT	319
Qy	242	CTGCAACTTACTATTGTCAACAGGCTTAAGTTTCCCGTCACTTTTGGCCAGGGGACCA	301
Db	320	TTTCAACTTACTATTGTCAACAGGCTTAAGTTTCCCGTCACTTTTGGTCAAGGAAACA	379
Qy	302	AGGTGAAATCAACGA	318
Db	380	AGCTGAGATCAACGA	396

RESULT 5  
 US-08-758-417A-220  
 : Sequence 220, Application US/08758417A  
 : Patent No. 6300129  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Lomborg, Nils  
 : Kay, Robert W.  
 :  
 : TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for  
 : Producing Heterologous Antibodies  
 :  
 : NUMBER OF SEQUENCES: 417  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Townsend and Townsend and Crew LLP  
 : STREET: Two Embarcadero Center, Eighth Floor  
 : CITY: San Francisco  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 94111-3834  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 :

```

?
?      OPERATING SYSTEM: PC-DOS/MS-DOS
?      SOFTWARE: Patentin Release #1.0, Version #1.30
?
?      CURRENT APPLICATION DATA:
?
?      APPLICATION NUMBER: US/08/758,417A
?      FILING DATE: 02-Dec-1996
?      CLASSIFICATION: <Unknown>
?
?      PRIOR APPLICATION DATA:  US 06/790,453

```

Query Match	89.1%;	Score 283.4;	DB 3;	Length 420;
Best Local Similarity	93.4%;	Pred. No. 4e-89;		
Matches 296;	Conservative 0;	Mismatches 21;	Indels 0;	Gaps 0;

[illegible]



RESULT 6  
US-09-042-353-393  
Sequence 393, Application US/09042353  
Patent No. 6255458  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 421  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,353  
FILING DATE: 13-MAR-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US96/16433  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/758,417  
FILING DATE: 02-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/21803

FILING DATE: 01-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 014643-009040US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 393:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3819 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-09-042-353-393  
Query Match 89.1%; Score 283.4; DB 3; Length 3819;  
Best Local Similarity 93.4%; Pred. No. 1.2e-88;  
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 2 AGCTCAGGCACTCCCATCTTCGCTGATCTGTAGAGAGAGTCACTTAATT 61  
DB 2513 AGATGACCCAGCTTCCTTCCTGCTGATCTGTAGAGAGAGTCACTTAATT 2572  
QY 62 GTCCGGCGAGTCAGGATATTAGCAGTTGTTAGCCTGTATCAGCAAAACAGGAAAG 121  
DB 2573 GTCCGGCGAGTCAGGATATTAGCAGTTGTTAGCCTGTATCAGCAAAACAGGAAAG 2632  
QY 122 CCCCTAACTCTGATCTATTTCTGATTCAGTTTGCAAAAGTGGGCTCCGTCAGAGTTCA 181  
DB 2633 CACCTAAGCTCTGATCTATCTGATTCAGTTTGCAAAAGTGGGCTCCGTCAGAGTTCA 2692  
QY 182 GCGGAGTGTATCTGGGACAGATTTTCACTCAGATCAGAGCTGTAGAGCTTGAAGTT 241  
DB 2693 GCGGAGTGTATCTGGGACAGATTTTCACTCAGATCAGAGCTGTAGAGCTTGAAGTT 2752  
QY 242 CTGCACTTACTATTGTCAACAGGCTTAACAGTTTCCGTCACCTTTGGCCAGGGAGCA 301  
DB 2753 TTGCACTTACTATTGTCAACAGGCTTAACAGTTTCCGTCACCTTTGGTCAGGAGCA 2812  
QY 302 AGGTGAATCAACGA 318  
DB 2813 AGGTGAATCAACGA 2829  
RESULT 7  
US-08-758-417A-243  
Sequence 243, Application US/08758417A  
Patent No. 6300129  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 417  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,417A  
FILING DATE: 02-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>

APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Serafini, Andrew T.  
REGISTRATION NUMBER: 41,303  
REFERENCE/DOCKET NUMBER: 014643-009030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 243:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3819 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 243:  
US-08-758-417A-243

Query Match 89.1%; Score 283.4; DB 3; Length 3819;  
Best Local Similarity 93.4%; Pred. No. 1.2e-88;  
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 AGCTCAGGAGCTCCGCTGCTGATGCTGTAGGAGACAGAGTCAACCACTT 61  
DB 2513 AGATGACCCAGCTCTCCGCTGCTGATGCTGTAGGAGACAGAGTCAACCACTT 2512  
QY 62 GTCCGGGAGTCAAGATTAAGAGTGGTGAAGCTGATCAGAGAAACAGGGAAG 121  
DB 2573 GTCCGGGAGTCAAGATTAAGAGTGGTGAAGCTGATCAGAGAAACAGGTAAG 2632  
QY 122 CCCTTAATCTCTGATCTATTCGATCAGTTGGCAAGTGGGGTCCCTGAAGTTCA 181  
DB 2633 CACCTAAGCTCTCTATCTATCTGATCAGTTGGCAAGTGGGGTCCCTGAAGTTCA 2692  
QY 182 GCGGAGTGCATCTGGGACAGATTTCACTCAGCATCAGAGAGCTGAGGCTGAAGATT 241  
DB 2693 GCGGAGTGCATCTGGGACAGATTTCACTCAGCATCAGAGAGCTGAGGCTGAAGATT 2752  
QY 242 CTGCACTTACTATTGTCAACAGGCTAACAGTTTCCCTAGACTTTTGGCAGGGGACCA 301  
DB 2753 TTGCACTTACTATTGTCAACAGGCTAACAGTTTCCCTAGACTTTTGGTCAAGGGAACA 2812  
QY 302 AGGTGAAATCAACGA 318  
DB 2813 AGCTGAGATCAACGA 2829

RESULT 8  
US-09-042-353-360  
Sequence 360, Application US/09042353  
Patent No. 6255458  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
APPLICANT: Kay, Robert M.

TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 421  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,353  
FILING DATE: 13-MAR-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US96/16433  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/758,417  
FILING DATE: 02-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/21803  
FILING DATE: 01-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 014643-009040US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 360:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 439 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-09-042-353-360

Query Match 87.1%; Score 277; DB 3; Length 439;  
Best Local Similarity 92.1%; Pred. No. 7,1e-87;  
Matches 292; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGCTCTCCATCTTCCGCTGTCGATCTGTAGAGACAGAGTCAACCAATTA 61  
DB 74 AGATGACCCAGTCTTCATCTCCTCAGTGTGATCTGTAGAGACAGAGTCAACCAATTA 133  
QY 62 GTGCGGCGAGTCAAGGATTTAGCAGTTGGTTAGCCTGTATCAGCAGAAACAGGAAAG 121  
DB 134 GTGCGGCGAGTCAAGGATTTAGCAGTTGGTTAGCCTGTATCAGCAGAAACAGGAAAG 193  
QY 122 CCCCTAACTCTGATCTATTTCTGATCTCAGTTTCCAAAGTGGGGTCCCTCAAGTTCA 181  
DB 194 CCCCTAACTCTGATCTATTTCTGATCTCAGTTTCCAAAGTGGGGTCCCTCAAGTTCA 253  
QY 182 GCGGCAAGTGAATCTGGGACAGATTTCACTCAGTCACCATCAGAGCCTGAGGCTGAAGATT 241  
DB 254 GCGGCAAGTGAATCTGGGACAGATTTCACTCAGTCACCATCAGAGCCTGAGGCTGAAGATT 313  
QY 242 CTGCAACTTACTATTGTGCACAGGCTTAACAGTTTCCCTAGACATTTTGGCCAGGGAGCA 301  
DB 314 TTGCAACTTACTATTGTGCACAGGCTTAACAGTTTCCCTAGACATTTTGGCCAGGGAGCA 373  
QY 302 AGTGGAAATCAACGA 318  
DB 374 AGCTGAGATCAACGA 390

## RESULT 9

US-08-758-417A-208  
; Sequence 208, Application US/08758417A  
; Patent No. 6300129

## GENERAL INFORMATION:

APPLICANT: Lonberg, Nils  
; Kay, Robert M.

TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for  
; Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 417  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,417A  
FILING DATE: 02-Dec-1996  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: US 08/209,741

FILING DATE: 09-MAR-1994  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Serafini, Andrew T.  
REGISTRATION NUMBER: 41,303  
REFERENCE/DOCKET NUMBER: 014643-009030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 208:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 439 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 208:  
US-08-758-417A-208

Query Match 87.1%; Score 277; DB 3; Length 439;  
Best Local Similarity 92.1%; Pred. No. 7,1e-87;  
Matches 292; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGCTCTCCATCTTCCGCTGTCGATCTGTAGAGACAGAGTCAACCAATTA 61  
DB 74 AGATGACCCAGTCTTCATCTCCTCAGTGTGATCTGTAGAGACAGAGTCAACCAATTA 133  
QY 62 GTGCGGCGAGTCAAGGATTTAGCAGTTGGTTAGCCTGTATCAGCAGAAACAGGAAAG 121  
DB 134 GTGCGGCGAGTCAAGGATTTAGCAGTTGGTTAGCCTGTATCAGCAGAAACAGGAAAG 193  
QY 122 CCCCTAACTCTGATCTATTTCTGATCTCAGTTTCCAAAGTGGGGTCCCTCAAGTTCA 181  
DB 194 CCCCTAACTCTGATCTATTTCTGATCTCAGTTTCCAAAGTGGGGTCCCTCAAGTTCA 253  
QY 182 GCGGCAAGTGAATCTGGGACAGATTTCACTCAGTCACCATCAGAGCCTGAGGCTGAAGATT 241  
DB 254 GCGGCAAGTGAATCTGGGACAGATTTCACTCAGTCACCATCAGAGCCTGAGGCTGAAGATT 313  
QY 242 CTGCAACTTACTATTGTGCACAGGCTTAACAGTTTCCCTAGACATTTTGGCCAGGGAGCA 301  
DB 314 TTGCAACTTACTATTGTGCACAGGCTTAACAGTTTCCCTAGACATTTTGGCCAGGGAGCA 373  
QY 302 AGTGGAAATCAACGA 318  
DB 374 AGCTGAGATCAACGA 390

## RESULT 10

US-08-259-372A-13  
; Sequence 13, Application US/08259372A  
; Patent No. 5563554

## GENERAL INFORMATION:

APPLICANT: Ostberg, Lars G.

TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL

NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA

COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/259,372A  
FILING DATE: 14-JUN-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/871,426  
FILING DATE: 21-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/676,036  
FILING DATE: 27-MAR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/538,796  
FILING DATE: 15-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/192,754  
FILING DATE: 11-MAY-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/925,196  
FILING DATE: 31-OCT-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/904,517  
FILING DATE: 05-SEP-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-50-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 384 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: Hybridoma  
CELL LINE: ZM1-2  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..384  
US-08-259-372A-13

Query Match 86.6%; Score 275.4; DB 1; Length 384;  
Best Local Similarity 91.8%; Pred. No. 2.4e-86;  
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGCTTCATCTTCCGCTGCTGCATCTGTAGAGAGAGAGTCAACCAATTT 61  
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DB 128 GTCCGGCAGTCAAGGATTTAGCAGTTGTTAGCCTGTTATCAGCAAGAAACAGGGAAG 187  
QY 122 CCCCTAACTCTGATCTATTCTGCATCAGTTTGCAAGTGGGTCCTCCGTCAGGTTCA 181  
DB 188 CCCCTAACTCTGATCTATTCTGCATCAGTTTGCAAGTGGGTCCTCCGTCAGGTTCA 247  
QY 182 GCGGAGGTGATCTGGGACAGATTTCACTTCACATCAGCAGGCTGAGAGCTGAAGATT 241  
DB 248 TCGGAGGTGATCTGGGACAGATTTCACTTCACATCAGCAGGCTGAGAGCTGAAGATT 307

QY 242 CTCGAATCTATTGTTCAACAGGCTTACAGCTTCCGCTGACCTTTGGCCAGGGACCA 301  
DB 308 TTGCACCTACTATTGTTCAACAGGCTGACAGTCTCCCTTACTTTGGCGGAGGACCA 367  
QY 302 AGTGAATCAACAGCA 318  
DB 368 AGTGAATCAACAGCA 384

RESULT 11  
US-08-468-671-13  
Sequence 13, Application US/08468671  
Patent No. 5648077  
GENERAL INFORMATION:  
APPLICANT: Ostberg, Lars G.  
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,671  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/259,372  
FILING DATE: 14-JUN-1994  
APPLICATION NUMBER: US 07/871,426  
FILING DATE: 21-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/676,036  
FILING DATE: 27-MAR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/538,796  
FILING DATE: 15-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/192,754  
FILING DATE: 11-MAY-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/925,196  
FILING DATE: 31-OCT-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/904,517  
FILING DATE: 05-SEP-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-50-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 384 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens

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; CELL TYPE: Hybridoma
; CELL LINE: Zm1-2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..384
US-08-468-671-13

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Query Match	86.6%	Score 275.4	DB 1	Length 384
Best Local Similarity	91.8%	Pred. No. 2.4e-86		
Matches 291, Conservative	0	Mismatches 26	Indels 0	Gaps 0

Oy 2 AGCTCAGCAGAGTCTTCATCTTCGATCTGCACTGTAGGACAGAGTACCATTACTT 61  
 Db 68 AGATGATCCAGATCTCCATCTTCGATCTGCACTGTAGGACAGAGTACCATTACTT 127  
 Oy 62 GTCCGGCCGAGTCAGGGTATTAGACGTTGGTTCCTGTATTCAGCAGAAACGAGGAAAG 121  
 Db 128 GTCCGGCCGAGTCAGGGTATTAGACGTTGGTTCCTGTATTCAGCAGAAACGAGGAAAG 187  
 Oy 122 CCCCTAACTCCTGATCTATTCTGCATCCAGTTTGCAGAAAGTGGGGTCCCGTCAAGTTCA 181b  
 Db 188 CCCCTAACTCCTGATCCATGCTGCATCCAGTTTGCAGAAAGTGGGGTCCCATCAAGTTCA 247  
 Oy 182 GCGGCAGTGAGATCTGGGACAGATTTAGTCTCAACATCAGACAGCTGACGCTGGAAGATT 241b  
 Db 248 TCGGCAGTGAGATCTGGGACAGATTTCACTCTCAACATCAGACAGCTGGAAGATT 307  
 Oy 242 CTGCAACTTACTAATTGTCAACAGGCTAAACAGTTTCCCGTACACTTTTGGCCAGGGACCA 301b  
 Db 308 TTGCAACCTTACTAATTGTCAACAGGCTGACAGTCTCCCTTTTACTTTCCGGGAGGAGACCA 367  
 Oy 302 AGGTGGAATCAAAACA 318  
 Db 368 AGGTGACTTCAAAACA 384

RESULT 12  
US-09-240-274-109  
; Sequence 109, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:

[illegible]

Qy	181	AGCGGCAGTGATCTGGGACAGATTTCAgTCTCAcCATCAGCAGCCTGCAGCCTTGAAGAT	240
Db	184	AGTGGCAGTGGATCTGGGACAGATTTCCACTCTCAGCAGCATCAGCAGTGTGCAACTGAAGAT	243
Qy	241	TCGCAACTTACTATATGTGCACAGGCTAAcAGTTTCCCGTACATTTTGGCGAGGGGACC	300
Db	244	TTTGGCAACTTATTATCTGTCAcAGCTTAATgTTAACCgTACACTTTTGGCGAGGGGACC	303
Qy	301	AAGGTGAATCAAACGA	318
Db	304	AAcCTGAGATCAAACGA	321

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RESULT 13
US-09-240-274-199
; Sequence 199, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-199

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Query Match	83.9%	Score 266.8;	DB 3;	Length 321;
Best Local Similarity	89.9%	Pred. No. 2.3e-83;		
Matches 286; Conservative	0;	Mismatches 32;	Indels 0;	Gaps 0;

Oy	1	GAGTACACGAGCTCATCTTCGCCGTCGTGATCTGTAGAGAGACAGATCACCATACT	60
Dd	4	GAGCTACCCAGTCTCATCTCTCCCTGTCATCTGTAGAGAGACAGATCACCATACT	63
Oy	61	TGTCGGGCGAGTCAGGGATATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAAACGAGGAAA	120
Dd	64	TGCCGGGCAGTATAGAGCATTTAGCAGCTATTAAATTGGTATCAGCAGAAAACGAGGAAA	122
Oy	121	GCCCTAAACCTCCTGATCTATTCTGCATCCAGTTTGCAAAAGTGGGGTCCCGTCAAGTTC	180
Dd	124	GCCCTAAAGTCTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTC	183
Oy	181	AGCGGAGTGGATCTTGGGACAGATTTCACTTCACCATCAGCAGCTTGACCTTGAAGAT	240
Dd	184	AGTGGAGTGGATCTGGGACAGATTTCACTTCACCATCAGGAGCTTGAAGAT	243
Oy	241	TTGCGAATTCTATTGTGCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC	300
Dd	244	TTTGCAACTTACTACTGTCAACAGATTACAGTAACTCCCTCACTTTTGGCCAGGGGACC	303
Oy	301	AAAGTGGAAATCAAAAGA 318	
Dd	304	AAAGTGGAGATCAAAAGA 321	

RESULT 14  
US-09-240-274-98

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; Sequence 98, Application US/09240274
; Patent No. 625345
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain F01
US-09-240-274-98
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Query March 82.9%; Score 263.6; DB 3; Length 321;
Best Local Similarity 89.3%; Pred. No. 3.1e-82;
Matches 284; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAGCTCAGCAGTCTCCATCTTCGCTGTCGATCTGTAGAGACAGAGTCACCATTAAT 60
DB 4 GAGCTCAGCAGTCTCCATCTTCGCTGTCGATCTGTAGAGACAGAGTCACCATTAAT 63
QY 61 TGTGGGCGAGTCAAGGTATTAGACGTTGTTAGCTGTATCAGCAGAAACCGAGGAAA 120
DB 64 TGCCTGAGAGTCAAGGTATTAGACGTTGTTAGCTGTATCAGCAGAAACCGAGGAAA 123
QY 121 GCCCTTAACCTCGATCTATTCGATCCAGTTGCAAGTGGGGTCCCGTCAAGGTTTC 180
DB 124 GCCCTTAACCTCGATCTATTCGATCCAGTTGCAAGTGGGGTCCCGTCAAGGTTTC 183
QY 181 AGCGCAGTGGATCTGGGACAGATTTCAGTCTCAGCATCAGAGCTGAGCTGAAGAT 240
DB 184 AGCGCAGTGGATCTGGGACAGATTTCAGTCTCAGCATCAGAGCTGAGCTGAAGAT 243
QY 241 TCTGCAACTTAATCTATTTGCAACAGGCTAACAGTTTCCGTAACACTTTTGGCCAGGGACC 300
DB 244 TCTGCAACTTAATCTATTTGCAACAGGCTAACAGTTTCCGTAACACTTTTGGCCAGGGACC 303
QY 301 AAGGTGAAATCAACGA 318
DB 304 AAGGTGAAATCAACGA 321
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RESULT 15
US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 625345
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102

Query March 82.9%; Score 263.6; DB 3; Length 321;
Best Local Similarity 89.3%; Pred. No. 3.1e-82;
Matches 284; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAGCTCAGCAGTCTCCATCTTCGCTGTCGATCTGTAGAGACAGAGTCACCATTAAT 60
DB 4 GAGCTCAGCAGTCTCCATCTTCGCTGTCGATCTGTAGAGACAGAGTCACCATTAAT 63
QY 61 TGTGGGCGAGTCAAGGTATTAGACGTTGTTAGCTGTATCAGCAGAAACCGAGGAAA 120
DB 64 TGCCTGAGAGTCAAGGTATTAGACGTTGTTAGCTGTATCAGCAGAAACCGAGGAAA 123
QY 121 GCCCTTAACCTCGATCTATTCGATCCAGTTGCAAGTGGGGTCCCGTCAAGGTTTC 180
DB 124 GCCCTTAACCTCGATCTATTCGATCCAGTTGCAAGTGGGGTCCCGTCAAGGTTTC 183
QY 181 AGCGCAGTGGATCTGGGACAGATTTCAGTCTCAGCATCAGAGCTGAGCTGAAGAT 240
DB 184 AGCGCAGTGGATCTGGGACAGATTTCAGTCTCAGCATCAGAGCTGAGCTGAAGAT 243
QY 241 TCTGCAACTTAATCTATTTGCAACAGGCTAACAGTTTCCGTAACACTTTTGGCCAGGGACC 300
DB 244 TCTGCAACTTAATCTATTTGCAACAGGCTAACAGTTTCCGTAACACTTTTGGCCAGGGACC 303
QY 301 AAGGTGAAATCAACGA 318
DB 304 AAGGTGAAATCAACGA 321
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Search completed: July 27, 2005, 12:41:22  
Job time : 88.6545 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:09:06 ; Search time 1819.51 Seconds  
(without alignments)  
8468.649 Million cell updates/sec

Title: US-10-027-725A-6  
Perfect score: 318  
Sequence: 1 gagctcagcagctctcctc.....ccaagtcggaatcaacga 318

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapect 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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2: gb\_hcg:\*  
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7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318	100.0	318	9 HSA458381	AJ458381 Homo sapi
2	316.4	99.5	705	12 HSI6KLC5	X85747 Synthetic c
3	291.4	91.6	974	6 AX305000	AX305000 Sequence
4	291.4	91.6	974	6 AX306529	AX306529 Sequence
5	291.4	91.6	974	6 BD131246	BD131246 Human mon
6	291	91.5	388	6 AR161375	AR161375 Sequence
7	291	91.5	388	6 AR369968	AR369968 Sequence
8	291	91.5	388	6 BD096602	BD096602 Transgeni
9	289.8	91.1	327	9 HSA388657	AJ388657 Homo sapi
10	289.4	91.0	322	9 AY043120	AY043120 Homo sapi
11	289.2	90.9	324	9 AF306360	AF306360 Homo sapi
12	288.2	90.6	324	9 AF146407	AF146407 Homo sapi
13	288.2	90.6	433	9 S59162	S59162 Ig V kappa
14	288.2	90.6	812	9 AB064045	AB064045 Homo sapi
15	288.2	90.6	936	9 BC073764	BC073764 Homo sapi
16	287.4	90.4	310	9 HSA408418	AJ408418 Homo sapi
17	287.4	90.4	318	9 AF103433	AF103433 Homo sapi
18	286.6	89.1	824	9 AY510107	AY510107 Homo sapi
19	286	89.9	324	9 AB095279	AB095279 Homo sapi

20	285.2	89.7	321	6 BD097622	BD097622 Antibody
21	285	89.6	330	9 AF240362	AF240362 Homo sapi
22	283.4	89.1	324	9 AB095282	AB095282 Homo sapi
23	283.4	89.1	420	6 AR161429	AR161429 Sequence
24	283.4	89.1	420	6 AR369974	AR369974 Sequence
25	283.4	89.1	420	6 BD096608	BD096608 Transgeni
26	283.4	89.1	3819	6 AR161402	AR161402 Sequence
27	283.4	89.1	3819	6 AR369997	AR369997 Sequence
28	283.4	89.1	3819	6 BD096631	BD096631 Transgeni
29	280.8	88.3	728	6 BD182353	BD182353 Ant1 CD40
30	280.8	88.3	728	6 AX327729	AX327729 Sequence
31	280.4	88.2	321	6 AX365137	AX365137 Sequence
32	278.6	87.6	324	9 AB063969	AB063969 Homo sapi
33	278.6	87.6	326	9 AF103397	AF103397 Homo sapi
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36	277.6	87.3	716	6 AX327727	AX327727 Sequence
37	277	87.1	439	6 AR161377	AR161377 Sequence
38	277	87.1	439	6 AR369970	AR369970 Sequence
39	275.4	86.6	324	6 BD096604	BD096604 Transgeni
40	275.4	86.6	324	6 AB095289	AB095289 Homo sapi
41	275.4	86.6	384	6 I27685	I27685 Sequence 13
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43	275.2	86.6	312	9 HUMIGKAAA	L03678 Homo sapien
44	275.2	86.5	312	9 HSGX98967	X98967 H.sapiens r
45	274.8	86.4	324	9 AB095284	AB095284 Homo sapi

#### ALIGNMENTS

RESULT 1	
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LOCUS	HSA458381 318 bp mRNA linear PRI 30-APR-2002
DEFINITION	Homo sapiens partial mRNA for immunoglobulin kappa light chain .
ACCESSION	AJ458381
VERSION	AJ458381.1 GI:20387061
KEYWORDS	IGKV gene; immunoglobulin kappa; light chain; variable region.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Flicker, S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y., Valent, P., Kraft, D. and Valenta, R.
TITLE	Conversion of grass allergen-specific human IgE into a protective IgG1 antibody
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 318)
AUTHORS	Flicker, S.
TITLE	Direct Submission
JOURNAL	Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA
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source	Location/Qualifiers 1..318 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="100" /rearranged 1..318 /gene="IGKV" /gene="IGKV" /codon_start=1 /product="immunoglobulin kappa light chain" /protein_id="CAD30443.1" /db_xref="GI:20387062" /translation="ELTQSPSSVASVGDVTVTCRASQGISIMLAWYQKPKAPKL LIVASVDSGVPSRFGSGGTGFTSLTSLTSLAPEDSATYVCCQANSPPTFGQGTKV EIKR"

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/product="immunoglobulin kappa light chain variable region"

ORIGIN

Query Match 100.0%; Score 318; DB 9; Length 318;  
Best Local Similarity 100.0%; Pred. No. 3e-89;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTCAGCAGATCTCCATCTCCGTCCTGTCATCTGTAGAGACAGAGTACCATTAAT 60  
DB 1 GAGCTCAGCAGATCTCCATCTCCGTCCTGTCATCTGTAGAGACAGAGTACCATTAAT 60  
QY 61 TGTGGGCGAGTCAGGGTATTAGACATTGTTAGCCTGCTATCAGCAGAAACAGGGAAA 120  
DB 61 TGTGGGCGAGTCAGGGTATTAGACATTGTTAGCCTGCTATCAGCAGAAACAGGGAAA 120  
QY 121 GCCCCTAAATCTCGATCTATTCGATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTTC 180  
DB 121 GCCCCTAAATCTCGATCTATTCGATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTTC 180  
QY 181 AGCGGAGTGGATCTGGGACAGATTTGATCTCAACATCAGACGCTGACGCTGAAGAT 240  
DB 181 AGCGGAGTGGATCTGGGACAGATTTGATCTCAACATCAGACGCTGACGCTGAAGAT 240  
QY 241 TCTGCAACTTACTATTTGTCACAGGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300  
DB 241 TCTGCAACTTACTATTTGTCACAGGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300  
QY 301 AAGGTGAAATCAACACA 318  
DB 301 AAGGTGAAATCAACACA 318

RESULT 2  
HISGLCS 705 bp RNA linear SYN 29-MAR-2001  
LOCUS DEFINITION Synthetic construct including Homo sapiens immunoglobulin kappa chain (clone: 5).

ACCESSION X95747  
VERSION X95747.1 GI:1514580  
KEYWORDS constant region; immunoglobulin; kappa light chain.  
SOURCE Synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Steinberger, P., Kraft, D. and Valenta, R.  
TITLE Construction of a combinatorial IgE library from an allergic patient. Isolation and characterization of human IgE Fabs with specificity for the major Timothy grass pollen allergen, Phl p 5  
JOURNAL J. Biol. Chem. 271 (18), 10967-10972 (1996)  
MEDLINE 96210038  
PUBMED 8631916  
REFERENCE 2 (bases 1 to 705)  
AUTHORS Valenta, R.L.S.  
TITLE Direct Submission  
JOURNAL Submitted (19-FEB-1996) R.L.S. Valenta, Institute of General & Experimental Pathology, General Hospital, Waehringer Guertel 18-20, 1090 Vienna, AUSTRIA

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ORIGIN

Query Match 99.5%; Score 316.4; DB 12; Length 705;  
Best Local Similarity 99.7%; Pred. No. 8.7e-89;  
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCTCAGCAGATCTCCATCTCCGTCCTGTCATCTGTAGAGACAGAGTACCATTAAT 60  
DB 67 GAGCTCAGCAGATCTCCATCTCCGTCCTGTCATCTGTAGAGACAGAGTACCATTAAT 126  
QY 61 TGTGGGCGAGTCAGGGTATTAGACATTGTTAGCCTGCTATCAGCAGAAACAGGGAAA 120  
DB 127 TGTGGGCGAGTCAGGGTATTAGACATTGTTAGCCTGCTATCAGCAGAAACAGGGAAA 186  
QY 121 GCCCCTAAATCTCGATCTATTCGATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTTC 180  
DB 187 GCCCCTAAATCTCGATCTATTCGATCCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTTC 246  
QY 181 AGCGGAGTGGATCTGGGACAGATTTGATCTCAACATCAGACGCTGACGCTGAAGAT 240  
DB 247 AGCGGAGTGGATCTGGGACAGATTTGATCTCAACATCAGACGCTGACGCTGAAGAT 306  
QY 241 TCTGCAACTTACTATTTGTCACAGGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300  
DB 307 TCTGCAACTTACTATTTGTCACAGGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 366  
QY 301 AAGGTGAAATCAACACA 318  
DB 367 AAGGTGAAATCAACACA 384



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ACCESSION	AX305000				
VERSION	AX305000.1	GI:17644678			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	1 Takashi, T., Katsunari, T. P. and Nobuaki, H.				
TITLE	Human monoclonal antibody against a costimulatory signal transduction molecule a11m and pharmaceutical use thereof				
JOURNAL	Patent: EP 1158004-A 29 28-NOV-2001, Japan Tobacco Inc. (JP)				
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Best Local Similarity	95.0%; Pred. No. 6.9e-81;				
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QY	2 AGCTCAGCAGCTCTCCATCTTCCTGCTGTCATCTGTAGGAGACAGAGTCACTAATT 61				
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QY	62 GTGGGGCAGGTGAGGGATTTAGCAGTTGATTAGCCTGGATCAGAGAAACAGGGAAAG 121				
DB	172 GTGGGGCAGGTGAGGGATTTAGCAGTTGATTAGCCTGGATCAGAGAAACAGGGAAAG 231				
QY	122 CCCCTAAACTCTGATCTATTTCTGATCAGATTGGCAAGTGGGGTCCCGTCAAGTTCA 181				
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QY	182 GCGCAGTGTGATCTGGGACAGATTTCACTTCACCATCAGACAGCTCGAGCTTGAAATT 241				
DB	292 GCGCAGTGTGATCTGGGACAGATTTCACTTCACCATCAGACAGCTCGAGCTTGAAATT 351				
QY	242 CTGCAACTTATTTGTCAGACAGGTTACAGTTTCCGTACACTTTTGGCAGGGGACCA 301				
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QY	302 AGGTGGAATCAACGA 318				
DB	412 AGGTGGAATCAACGA 428				
RESULT 4					
LOCUS	AX306529	974 bp	DNA	linear	PAT 11-DEC-2001
DEFINITION	Sequence 29 from Patent WO0187981.				
ACCESSION	AX306529				
VERSION	AX306529.1	GI:17645749			
KEYWORDS					

SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1
AUTHORS	Tsuji, T., Tezuka, K. and Hori, N.
TITLE	Human monoclonal antibody against a costimulatory signal transduction molecule aIlm and pharmaceutical use thereof
JOURNAL	Patent: WO 0187981-A 29 22-NOV-2001;
LOCATION	Japan Tobacco Inc. (Jp)
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sIg peptide	39..104
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Query Match	91.6%; Score 291.4; DB 6; Length 974;
Best Local Similarity	95.0%; Pred. No. 6.9e-81;
Matches 301; Conservative	0; Mismatches 16; Indels 0; Gaps 0;
Oy	2 AGCTCAGCGAGTCCTCCATCTTCGGTGTCGATCTGTAGGACAGAGTCAACATACTT 61
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Oy	62 GTCCGGCGAGTCAGGGATTATAGCAGTTGGTAGCCTGGTATCAGCAGAACAACAGGAAGA 121
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Oy	122 CCCTAAACTCTGATCTATTCTGCATCCAGATTGGCAAAGTGGGCTCCGTCAGAGTTCA 181
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Oy	182 GCGGCGAGTGCATCTGGGACAGATTTCAGTCTCACCACATCAGACGCTCAGGCTAAGTT 241
Db	292 GCGGCGAGTGCATCTGGGACAGATTTCAGTCTCACCACATCAGACGCTCAGGCTAAGTT 351
Oy	242 CTGCAACTTACTATTGTCACACAGGCTTAACAGTTCCCGTACACTTTTGGCCAGGGAGCA 301
Db	352 TTGCAACTTACTATTGTCACACAGGCTTAACAGTTCCCGTGGACGTTGGGCCAAGGAGCA 411
Oy	302 AGGTGAATCAACGA 318
Db	412 AGGTGAATCAACGA 428
RESULT 5	
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LOCUS	BD131246 974 bp DNA linear PAT 18-SEP-2002
DEFINITION	Human monoclonal antibody against consimulation transducer
ACCESSION	BD131246
VERSION	BD131246.1 GI:33226191
KEYWORDS	JP 2002034581-A/28.
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 974)
AUTHORS	Tsuji, T., Tezuka, K. and Hori, N.

TITLE Human monoclonal antibody against constitutively transduced  
JOURNAL molecule AILIM and medicinal utilization thereof  
Patent: JP 2002034581-A 28 05-FEB-2002;  
COMMENT JAPAN TOBACCO INC  
OS Homo sapiens (human)  
PN JP 2002034581-A/28  
PD 05-FEB-2002  
PF 30-MAR-2001 JP 2001099508  
PI TAKASHI TSUJI, KATSUNARI TEZUKA, NOBUAKI HORI  
PC C12N15/09, A61K31/7088, A61K39/395, A61K45/  
PC A61P43/00, A61P43/00, C07K16/28, C07K16/46, C07K19/00, C12N5/10, PC  
C12N15/02,  
PC C12P21/08, G01N33/15, G01N33/50, G01N33/53, G01N33/566, G01N33/577// PC  
(C12P21/08, C12P1:91), C12N15/00, A61K37/02, C12N5/00, C12N15/00 CC  
Human monoclonal antibody against constitutively transducer CC  
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CC and medicinal utilization thereof  
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FT CDS (39)..(749)  
FT 3'UTR (750)..(974)  
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Best Local Similarity 95.0%; Pred. No. 6.9e-81;  
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGTCTCCATCTTCGGTCTGCATCGTATGAGAGAGAGTCCATTAATT 61  
DB 112 AGATGACCCAGTCTCCATCTTCGGTCTGCATCGTATGAGAGAGAGTCCATTAATT 171  
QY 62 GTCGGGAGAGTCAAGGATTAAGAGTGGTGGTATGAGAGAGAGAGAGAGAGAGAG 121  
DB 172 GTCGGGAGAGTCAAGGATTAAGAGTGGTGGTATGAGAGAGAGAGAGAGAGAGAG 231  
QY 122 CCCCTAAATCTCTGATCTATCTGCATCCAGTTGGCAAGTGGGGTCCGTAAGTTCA 181  
DB 232 CCCCTAAATCTCTGATCTATCTGCATCCAGTTGGCAAGTGGGGTCCGTAAGTTCA 291  
QY 182 GCGGAGAGATCTGGGAGAGATTTCACTCCATCAGAGAGAGAGAGAGAGAGAGAG 241  
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QY 242 CTCGAACTTACTATTTGCAAGAGTAAAGTTCCCTGACACTTTTGGCCAGGAGCA 301  
DB 352 TTGCACTTACTATTTGCAAGAGTAAAGTTCCCTGACACTTTTGGCCAGGAGCA 411  
QY 302 AGTGGAAATCAACGA 318  
DB 412 AGTGGAAATCAACGA 428  
RESULT 6  
LOCUS AR161375 388 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 358 from patent US 6255458.  
ACCESSION AR161375  
VERSION AR161375.1 GI:16227235  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 388)  
AUTHORS Lonberg N. and Kay R.M.  
TITLE High affinity human antibodies and human antibodies against digoxin

JOURNAL Patent: US 6255458-A 358 03-JUL-2001;  
FEATURES Location/Qualifiers  
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Best Local Similarity 95.2%; Pred. No. 1e-80;  
Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
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DB 314 TTGCACTTACTATTTGCAAGAGTAAAGTTCCCTGACACTTTTGGCCAGGAGCA 373  
QY 302 AGTGGAAATCAAC 316  
DB 374 AGTGGAAATCAAC 388  
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LOCUS AR369968 388 bp DNA linear PAT 12-SEP-2003  
DEFINITION Sequence 206 from patent US 6300129.  
ACCESSION AR369968  
VERSION AR369968.1 GI:34606408  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 388)  
AUTHORS Lonberg N. and Kay R.M.  
TITLE Transgenic non-human animals for producing heterologous antibodies  
JOURNAL Patent: US 6300129-A 206 09-OCT-2001;  
FEATURES Location/Qualifiers  
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Best Local Similarity 95.2%; Pred. No. 1e-80;  
Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
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QY 122 CCCCTAAATCTCTGATCTATCTGCATCCAGTTGGCAAGTGGGGTCCGTAAGTTCA 181  
DB 194 CCCCTAAATCTCTGATCTATGAGTGCATCCAGTTGGCAAGTGGGGTCCGTAAGTTCA 253  
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Db      254 GCGGAGGATCTCGGAGCAGATTTCCTCCACCATGACAGCCTGAGCCTTAAGATT 313
Qy      242 CTGCAACTTACTATTTGTCAACAGGCTAAAGTTTCCGTACACTTTTGGCCAGGGGACCA 301
Db      314 TTGCAACTTACTATTTGTCAACAGGCTTAAGTTTCCGTACACTTTTGGCCAGGGGACCA 373
Qy      302 AGGTGAATCAAC 316
Db      374 AGCTGAGATCAAC 388

RESULT 8
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LOCUS   BD096602
DEFINITION Transgenic non-human animals capable of producing heterologous
antibodies.
ACCESSION BD096602
VERSION   BD096602.1 GI:22642190
KEYWORDS  JP 2001527386-A/129.
SOURCE    unidentified
ORGANISM  unidentified.
REFERENCE 1 (bases 1 to 388)
AUTHORS  Lomborg,N. and Kay,R.M.
TITLE     Transgenic non-human animals capable of producing heterologous
antibodies
JOURNAL   Patent: JP 2001527386-A 129 25-DEC-2001.
COMMENT   GENPHARM INTERNATIONAL
OS        Unidentified
PN        JP 2001527386-A/129
PD        25-DEC-2001
PR        01-DEC-1997 JP 1998525687
PT        NILS LOMBERG,ROBERT M KAY
PC        C12N5/00,C12N5/28,C12N5/24,C12N5/10,C07K16/00,A61K39/00 CC
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CC        Transgenic non-human animals capable of
producing heterologous
antibodies
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Best Local Similarity 95.2%; Pred. No. 1e-80;
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Qy      2 AGCTCAGCAGCTCCATCTCCGTGTGATCGTATGAGAGACAGATCCATAATT 61
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Qy      122 CCCCTAACTCTGATCTATTTGATCGATCAGTTGGCAAGTGGGGTCCGTCAGAGTTCA 181
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Qy      182 GCGGAGTGAATCTGGGAGCAGATTTCACTCAGTCACCATAGAGAGCTGAGGCTGAAGATT 241
Db      254 GCGGAGTGAATCTGGGAGCAGATTTCACTCAGTCACCATAGAGAGCTGAGGCTGAAGATT 313
Qy      242 CTGCAACTTACTATTTGTCAACAGGCTAAAGTTTCCGTACACTTTTGGCCAGGGGACCA 301

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Db      314 TTGCAACTTACTATTTGTCAACAGGCTTAAGTTTCCGTACACTTTTGGCCAGGGGACCA 373
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Db      374 AGCTGAGATCAAC 388

RESULT 9
HSA388657
LOCUS   HSA388657
DEFINITION Homo sapiens partial mRNA for immunoglobulin kappa chain variable
region (IGVK gene), sample GN30.
ACCESSION AJ388657
VERSION   AJ388657.1 GI:5578815
KEYWORDS  IGVK gene; immunoglobulin kappa chain; immunoglobulin light chain;
variable region.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS  Capello,D., Fais,F., Vivenza,D., Migliaretti,G., Chiorazzi,N.,
Gardano,G. and Ferrarini,M.
TITLE     Identification of three subgroups of B-cell chronic lymphocytic
leukemia based upon mutations of BCL-6 and IGV genes
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 327)
AUTHORS  Fais,F.
TITLE     Direct Submission
JOURNAL   Submitted (20-JUL-1999) Fais F., Clinical Immunology, Istituto
Nazionale per la Ricerca sul Cancro, L.go R. Benzi 1, 16132, ITALY

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CDS
gene

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ORIGIN
Query Match      91.1%; Score 289.8; DB 9; Length 327;
Best Local Similarity 94.6%; Pred. No. 2.6e-80;
Matches 300; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy      2 AGCTCAGCAGCTTCATCTTCCGTGTGATCGTATGAGAGACAGATCCATAACTT 61
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Qy      122 CCCCTAACTCTGATCTATTTGATCGATCAGTTGGCAAGTGGGGTCCGTCAGAGTTCA 181
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Qy      182 GCGGAGTGAATCTGGGAGCAGATTTCACTCAGTCACCATAGAGAGCTGAGGCTGAAGATT 241
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QY 302 AGGTGAATCAACGA 318  
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Db 308 AGGTGAATCAACGA 324  
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RESULT 10  
AY043120 322 bp mRNA linear PRI 31-DEC-2001  
LOCUS Homo sapiens MCLL047 immunoglobulin light chain variable region  
DEFINITION mRNA, partial cds.  
ACCESSION AY043120  
VERSION AY043120.1 GI:18025629  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Ghiotto, F., Fais, F., Valetto, A., Albesiano, E., Allen, S.,  
Schulman, P., Vinciguerra, V., Rai, K., Ferrarini, M. and Chiorazzi, N.  
TITLE Ig VL gene repertoire in B cell type chronic lymphocytic leukemia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 322)  
AUTHORS Ghiotto, F., Fais, F., Valetto, A., Albesiano, E., Allen, S.,  
Schulman, P., Vinciguerra, V., Rai, K., Ferrarini, M. and Chiorazzi, N.  
TITLE Direct Submission  
JOURNAL Submitted (29-JUN-2001) North Shore-LIJ Research Institute, 350  
Community Drive, Manhasset, NY 11030, USA  
FEATURES  
Source location/Qualifiers  
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ORIGIN  
Query Match 91.0%; Score 289.4; DB 9; Length 322;  
Best Local Similarity 94.9%; Pred. No. 3.4e-80;  
Matches 299; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGCTCCATCTCCGCTGTCATCTGTGAGACAGATCCATTAATT 61  
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Db 8 AGATGACCCAGCTTCATCTCCGCTGTCATCTGTGAGACAGATCCATTAATT 67  
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QY 302 AGGTGAATCAAC 316  
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Db 308 AGGTGAATCAAC 322  
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RESULT 11  
AF306360 324 bp mRNA linear PRI 28-JUN-2001  
LOCUS Homo sapiens clone TP2.4 immunoglobulin light chain variable region  
DEFINITION mRNA, partial cds.  
ACCESSION AF306360  
VERSION AF306360.1 GI:14573216  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Pichurin, P., Guo, J., Yan, X., Rapoport, B. and McLachlan, S.M.  
TITLE Human monoclonal autoantibodies to B-cell epitopes outside the  
thyroid peroxidase autoantibody immunodominant region  
JOURNAL Thyroid 11 (4), 301-313 (2001)  
MEDLINE 21247463  
PUBMED 11349828  
REFERENCE 2 (bases 1 to 324)  
AUTHORS McLachlan, S.M., Rapoport, B., Pichurin, P., Guo, J. and Yan, X.  
TITLE Direct Submission  
JOURNAL Submitted (18-SEP-2000) Medicine, Cedars-Sinai Medical Center, 8700  
Beverly Blvd, B-131, Los Angeles, CA 90048, USA  
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Best Local Similarity 94.3%; Pred. No. 4e-80;  
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	DEFINITION Homo sapiens antibody light chain variable region (EU-14) mRNA,	
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	ACCESSION AF146407	
	VERSION AF146407.1	GI:5081718
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	ORGANISM Homo sapiens	
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	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
	REFERENCE 1 (bases 1 to 324)	
	AUTHORS van den Brink, E.N., Tuenhout, E.A., Davies, J., Boevenschen, N.,	
	Fijnvandraat, K., Ouwendijk, W.H., Peters, M. and Voorberg, V.	
	Human antibodies with specificity for the C2 domain of factor VIII	
	are derived from VH1 germ-line genes	
	Blood 95 (2), 558-563 (2000)	
	JOURNAL MEDLINE	
	PUBMED 20094679	
	REFERENCE 2 (bases 1 to 324)	
	AUTHORS van den Brink, E.N. and Voorberg, J.	
	Direct Submission	
	TITLE Submitted (28-APR-1999) Blood Coagulation, CLB, Sanguin Blood	
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Dd	127 GCCCTAAGCTCTGATCTATGCTGCATCCAGTTGGCAAAGGGGGTCCCATCAAGGTTG	186
Dy	181 AGCGGAGTGAATCTGGGACAGATTTCAGTCTCACCATCAGCAGCTGACCTGGAAGAT	240
Dd	187 AGCGGAGTGAATCTGGGACAGATTTCAGTCTCACCATCAGCAGCTGGAAGAT	246
Dy	241 TTGTGAACCTTCTATTTGTCACAAGGCTAACAGTTTCCCGTACACTTTGGCCAGGGACC	300
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VERSION AB064045.1 GI:21669296  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hiroo, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsun, H., Okada, J., Miura, K. and Kurosawa, Y.  
TITLE Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 812)  
AUTHORS Kurosawa, Y.  
TITLE Direct Submission  
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsunake-cho, Toyosake 470-1192, Japan  
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)  
COMMENT Please visit our web site  
URL: <http://www.fujita-hu.ac.jp/immunity/>.

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Matches 299; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2 AGCTACGCACTTCCTTCCTGCTGATCTGTAGAGACAGACTCCATTAATT 61  
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Db 74 AGATGACCCAGATTCCTCCGCTGCTGTAGAGAGAGAGACTCAACATCACTT 133  
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QY 62 GTCCGGGCAAGTCAGGATTTAGCACTTGCTTACCTGATTCAGCAAAACAGGAAAG 121  
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Db 254 GCGGCACTGATCTGGGACAGATTTTCAGTCTCAACATCAGACGCTGACCTGAAATTT 313  
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QY 242 CTGCACTTACTATTGTCACAGGCTAACAGTTTCCGTCACCTTTTGGCGGAGGACCA 301  
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Db 374 AGGTGAGATCAACGA 390  
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RESULT 15  
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LOCUS Homo sapiens cDNA clone MGC:88771 IMAGE:4576136, complete cds.  
ACCESSION BC073764  
VERSION BC073764.1 GI:49256424  
KEYWORDS  
SOURCE MGC.  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 936)  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Utsch, T.B., Tomshyuk, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Heltan, E., Ketterman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Diatchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schermer, A., Schein, J.E., Jones, S.V., and Marra, M.A.  
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
PUBMED 12477932  
JOURNAL 2 (bases 1 to 936)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (23-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
CONTACT NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Louis Staudt  
cDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (ULNI)  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [md@paxil.stanford.edu](mailto:md@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
Series: IRAL Plate: 58 Row: c Column: 10  
This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction, Similarity but not identity to protein.

## Location/Qualifiers

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## CDS

## ORIGIN

Query Match 90.6%; Score 288.2; DB 9; Length 936;  
Best Local Similarity 94.3%; Pred. No. 7.2e-80;  
Matches 299; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Db 85 AGATGACCCAGTCTCCATCTCCGCTGTCATCTGTAGAGACAGAGTCAACATTAATT 144
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Db 145 GTCCGGCGAGTCAGGGTATTAGCAGTTGTTAGCTGTATCAGCAGAAACAGGGAAG 204
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QY 302 AGGTGAATCAACGA 318
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:15:56 ; Search time 1958.75 Seconds

(without alignments)  
6179.670 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Database : Listing first 45 summaries

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1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsal:\*  
9: gb\_gsal2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	283.4	89.1	558	5	CD690030 EST6553 h
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10	281.8	88.6	472	6	CD702614 EST19139
11	280.2	88.1	497	6	CD696718 EST13241
12	278.6	87.6	912	2	BF129120 601811580
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14	275.4	86.6	561	6	CD706288 EST2815
15	274.6	86.4	851	4	BG686018 602638582
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DEFINITION 602245105P1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4336225 5', mRNA sequence.  
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VERSION BF976230.1 GI:12343445  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 943)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
COMMENT Email: cgaaba-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.lnl.gov  
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High quality sequence stop: 721.

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#### ORIGIN

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DB 271 GCGGCACTGATCTGGGACAGATTTCAGTCTACCATCAGAGCCTGAGCCTGAAGATT 330  
QY 242 CTGCACTTACTATTGTCAACAGGCTAACAGTTTCCGTCACCTTTGGCCAGGGAGCA 301  
DB 331 TTGCACTTACTATTGTCAACAGGCTAACAGTTTCCGTCACCTTTGGCCAGGGAGCA 390  
QY 302 AGGTGAAATCAACGA 318  
DB 391 AGGTGAAATCAACGA 407

RESULT 2  
BX336281 774 bp mRNA linear EST 08-APR-2004  
LOCUS BX336281 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
DEFINITION clone CSOD1026Y122 5-PRIME, mRNA sequence.  
ACCESSION BX336281  
VERSION BX336281.2 GI:46279255  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 774)  
AUTHORS Li, M.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length CDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On May 2, 2003 this sequence version replaced gi:30341499.  
CONTACT Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by life technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
1696.r

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?cs=CSOD1026DF11QPI&c=1696.r.

FEATURES  
source 1..774  
location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSOD1026Y122"  
/issue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
Query Match 91.1%; Score 289.8; DB 5; Length 774;

Best Local Similarity 94.6%; Pred. No. 4e-81;  
Matches 300; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCATCTCCGTCCTGTCATCTGTAGAGACAGATCCATTAATT 61  
DB 22 AGATGACCCAGTCTCCATCTTCGTCGTCTGATCTGTAGAGACAGATCCATTAATT 81  
QY 62 GTCGGGCGAGTCAGGGATTATAGCAGTTGGTTCAGCTGTATCAGCAAAACAGGAAAG 121  
DB 82 GTCGGGCGAGTCAGGGATTATAGCAGTTGGTTCAGCTGTATCAGCAAAACAGGAAAG 141  
QY 122 CCCCTAATCCGATCTATCTGATCCATTCAGTTGGCAAGGGGTCCTCCGTCAGTTCA 181  
DB 142 CCCCTAATCCGATCTATCTGATCCATTCAGTTGGCAAGGGGTCCTCCGTCAGTTCA 201  
QY 182 GCGGCACTGATCTGGGACAGATTTCAGTCTACCATCAGAGCCTGAGCCTGAAGATT 241  
DB 202 GCGGCACTGATCTGGGACAGATTTCAGTCTACCATCAGAGCCTGAGCCTGAAGATT 261  
QY 242 CTGCACTTACTATTGTCAACAGGCTAACAGTTTCCGTCACCTTTGGCCAGGGAGCA 301  
DB 322 TTGCACTTACTATTGTCAACAGGCTAACAGTTTCCGTCACCTTTGGCCAGGGAGCA 321  
QY 302 AGGTGAAATCAACGA 318  
DB 322 AGGTGAAATCAACGA 338

RESULT 3  
BE939490 554 bp mRNA linear EST 02-OCT-2000  
LOCUS BE939490 QVO-UM0093-250800-360-a09 UM0093 Homo sapiens CDNA, mRNA sequence.  
DEFINITION BE939490  
ACCESSION BE939490.1 GI:10467987  
VERSION BE939490.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 554)  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goulden, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brenhan, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=kt2=QVO-UM0093-250  
800-360-a09&kt3=2000-08-25&kt4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 21  
High quality sequence stop: 547.  
Location/Qualifiers  
1..554  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="UM0093"

/note="Organ: uterus; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 90.6%; Score 288.2; DB 2; Length 554;

Best Local Similarity 94.3%; Pred. No. 1.2e-80;

Matches 299; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCCGTCGTGATCTGTAGAGACAGATCCATTAATT 61  
DB 36 AGATGACCCAGTCTCCATCTTCCGTCGTGATCTGTAGAGACAGATCCATTAATT 95  
QY 62 GTCCGGGCGAGTCAGGATTTAGCAGTTGGTTAGCTGGTATCAGAGAACCCAGGAAAG 121  
DB 96 GTCCGGGCGAGTCAGGATTTAGCAGTTGGTTAGCTGGTATCAGAGAACCCAGGAAAG 155  
QY 122 CCCCTAACTCTGATCTATCTGATCTGATCCAGTTCGAAAGGGGTCCCTCAAGTTCA 181  
DB 156 CCCCTAACTCTGATCTATCTGATCTGATCCAGTTCGAAAGGGGTCCCTCAAGTTCA 215  
QY 182 GCGGCAAGTGTCTGGGACAGATTTTCCAGTTCACCATCAGAGCCTGAGGCTGAAGATT 241  
DB 216 GCGGCAAGTGTCTGGGACAGATTTTCCAGTTCACCATCAGAGCCTGAGGCTGAAGATT 275  
QY 242 CTGCACTTACTATTTGTCACAGGCTAACAGTTTCCCTGATCACTTTGGCCAGGGGACCA 301  
DB 276 TTGCACTTACTATTTGTCACAGGCTAACAGTTTCCCTGATCACTTTGGCCAGGGGACCA 335  
QY 302 AGGTGAATCAACGA 318  
DB 336 AGCTGAGATCAACGA 352

## RESULT 4

LOCUS BF663472 1100 bp mRNA linear EST 21-DEC-2000  
DEFINITION 602144635F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4297736 5',  
mRNA sequence.

ACCESSION BF663472

VERSION BF663472.1 GI:11937367

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1100)  
NIH-MGC http://mgi.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cga@b-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/MLML at:

http://image.llnl.gov

Plate: L10M152 row: F column: 09

High quality sequence stop: 704.

Location/Qualifiers

1. .1100

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone\_image="4297736"

/tissue\_type="Primary B-cells from tonsils (cell line)"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_48"

/note="Organ: B-cells; Vector: pOTB7; Site\_1: XhoI;

Site\_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GCGACAG(G) size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 90.1%; Score 286.6; DB 2; Length 1100;

Best Local Similarity 94.0%; Pred. No. 4.6e-80;

Matches 298; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCCGTCGTGATCTGTAGAGACAGATCCATTAATT 61  
DB 81 AGATGACCCAGTCTCCATCTTCCGTCGTGATCTGTAGAGACAGATCCATTAATT 140  
QY 62 GTCCGGGCGAGTCAGGATTTAGCAGTTGGTTAGCTGGTATCAGAGAACCCAGGAAAG 121  
DB 141 GTCCGGGCGAGTCAGGATTTAGCAGTTGGTTAGCTGGTATCAGAGAACCCAGGAAAG 200  
QY 122 CCCCTAACTCTGATCTATCTGATCTGATCCAGTTCGAAAGGGGTCCCTCAAGTTCA 181  
DB 201 CCCCTAACTCTGATCTATCTGATCTGATCCAGTTCGAAAGGGGTCCCTCAAGTTCA 260  
QY 182 GCGGCAAGTGTCTGGGACAGATTTTCCAGTTCACCATCAGAGCCTGAGGCTGAAGATT 241  
DB 261 GCGGCAAGTGTCTGGGACAGATTTTCCAGTTCACCATCAGAGCCTGAGGCTGAAGATT 320  
QY 242 CTGCACTTACTATTTGTCACAGGCTAACAGTTTCCCTGATCACTTTGGCCAGGGGACCA 301  
DB 321 TTGCACTTACTATTTGTCACAGGCTAACAGTTTCCCTGATCACTTTGGCCAGGGGACCA 380  
QY 302 AGGTGAATCAACGA 318  
DB 381 AGCTGAGATCAACGA 397

## RESULT 5

LOCUS CD690290 606 bp mRNA linear EST 25-JUN-2003  
DEFINITION EST6813 human nasopharynx Homo sapiens cDNA, mRNA sequence.

ACCESSION CD690290

VERSION CD690290.1 GI:32210896

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 606)

Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and

Zeng, Y.-X.

Transcriptional Gene Expression Profile of Human Nasopharynx

Unpublished (2003)

CONTACT: Yixin Zeng

Cancer Center

Sun Yat-sen University

651 Dongfeng Road East, Guangzhou 510060, China

Tel: 86-1380-9770-743

Fax: 86-20-8775-4506

Email: yxzeng@gzsums.edu.cn.

Location/Qualifiers

1. .606

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="normal nasopharynx"

/clone\_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

## ORIGIN

Query Match 89.6%; Score 285; DB 6; Length 606;  
Best Local Similarity 93.7%; Pred. No. 1.3e-79;  
Matches 297; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGCTCCATCTTCCGTCTGATCTGTAGAGAGACAGTCCATACTT 61  
DB 141 AGATGACCCAGTCTCCATCTTCTGTCTGATCTGTAGAGAGACAGTCCATACTT 200  
QY 62 GTGCGGCGAGTCAAGGATTTAGCAGTTGTTAGCCTGTATCAGCAAAACAGGAAAG 121  
DB 201 GTGGGGGAGTCAAGGATTTAGCAGTGTGTTAGCCTGTATCAGCAAAACAGGAAAG 260  
QY 122 CCGCTTAACCTCTGATCTTATCTGCATCCAGTTGGCAAAGTGGGTCCTCAAGTTCA 181  
DB 261 CCGCTTAACCTCTGATCTTATCTGCATCCAGTTGGCAAAGTGGGTCCTCAAGTTCA 320  
QY 182 GCGGCACTGATCTGGGAGATTTGATCTCAACATCAGAGCTGACGCTGAAGATT 241  
DB 321 GCGGCACTGATCTGGGAGATTTGATCTCAACATCAGAGCTGACGCTGAAGATT 380  
QY 242 CTGCACTTACTATTTGCAACAGGCTTAACAGTTTCCGTACACTTTTGGCCAGGGACA 301  
DB 381 TTGCACTTACTATTTGCAACAGGCTTAACAGTTTCCGTACACTTTTGGCCAGGGACA 440  
QY 302 AGGTGGAATCAACGA 318  
DB 441 AGGTGGAATCAACGA 457

RESULT 6  
CD690030 558 bp mRNA linear EST 25-JUN-2003  
LOCUS  
DEFINITION  
EST6553 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION  
CD690030  
VERSION  
CD690030.1 GI:32210387  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

REFERENCE  
1 (bases 1 to 558)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS  
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and  
Zeng, Y.-X.  
TITLE  
Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Yixun Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gzsums.edu.cn

## FEATURES

source  
1..558  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/issue\_type="normal nasopharynx"  
/clone\_lib="human nasopharynx"  
/note="ESTs generated from a normal nasopharynx cDNA  
library from southern Chinese"

## ORIGIN

Query Match 89.1%; Score 283.4; DB 6; Length 558;  
Best Local Similarity 93.4%; Pred. No. 4e-79;  
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGCTCCATCTTCCGTCTGATCTGTAGAGAGACAGTCCATACTT 61  
DB 123 AGATGACCCAGTCTCCATCTTCCGTCTGATCTGTAGAGAGACAGTCCATACTT 182

## QY

62 GTGCGGCGAGTCAAGGATTTAGCAGTTGTTAGCCTGTATCAGCAAAACAGGAAAG 121  
DB 183 GTGGGGGAGTCAAGGATTTAGCAGTGTGTTAGCCTGTATCAGCAAAACAGGAAAG 242  
QY 122 CCGCTTAACCTCTGATCTTATCTGCATCCAGTTGGCAAAGTGGGTCCTCAAGTTCA 181  
DB 243 CCGCTTAACCTCTGATCTTATCTGCATCCAGTTGGCAAAGTGGGTCCTCAAGTTCA 302  
QY 182 GCGGCACTGATCTGGGAGATTTGATCTCAACATCAGAGCTGACGCTGAAGATT 241  
DB 303 GCGGCACTGATCTGGGAGATTTGATCTCAACATCAGAGCTGACGCTGAAGATT 362  
QY 242 CTGCACTTACTATTTGCAACAGGCTTAACAGTTTCCGTACACTTTTGGCCAGGGACA 301  
DB 363 TTGCACTTACTATTTGCAACAGGCTTAACAGTTTCCGTACACTTTTGGCCAGGGACA 422  
QY 302 AGGTGGAATCAACGA 318  
DB 423 AGGTGGAATCAACGA 439

RESULT 7  
BX336280 745 bp mRNA linear EST 07-APR-2004  
LOCUS  
DEFINITION  
BX336280 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CSOD1026Y122 3-PRIME, mRNA sequence.  
ACCESSION  
BX336280  
VERSION  
BX336280.2 GI:46274765  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

REFERENCE  
1 (bases 1 to 745)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS  
Liu, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE  
Full-length cDNA libraries and normalization  
JOURNAL  
Unpublished (2001)  
COMMENT  
On May 2, 2003 this sequence version replaced gi:30339485.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
1696.r

For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdnas=CSOD1026Y122&P1=1696.r>.

Location/Qualifiers

source  
1..745  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSOD1026Y122"  
/issue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 89.1%; Score 283.4; DB 5; Length 745;  
Best Local Similarity 92.4%; Pred. No. 4.3e-79;  
Matches 293; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGCTCCATCTTCCGTCTGATCTGTAGAGAGACAGTCCATACTT 61  
DB 685 AGATGACCCAGTCTCCATCTTCCGTCTGATCTGTAGAGAGACAGTCCATACTT 626  
QY 62 GTGCGGCGAGTCAAGGATTTAGCAGTTGTTAGCCTGTATCAGCAAAACAGGAAAG 121

Db 625 GTCCGGGAGTCAGGATTAAGCAGCTGGTTAGCGCTGGTTTCAGCAGAAACAGGAAAG 566  
 Qy 122 CCCCTAAACTCTGATCTATCTGCATCTCAGTTTGGCAAGGGGATCCCGTCAAGTTCA 181  
 Db 565 CCCCTAAGCTCTGATCTATCTGCATCTCAGTTTGGCAAGGGGATCCCGTCAAGTTCA 506  
 Qy 182 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGAGCCTGAAGATT 241  
 Db 505 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGAGCCTGAAGATT 446  
 Qy 242 CTGCACTTACTATTGTCAACAGGCTTACAGTTTCCGCTACACTTTGGCCAGGGACCA 301  
 Db 445 TTGCACTTACTATTGTCAACAGGCTTACAGTTTCCGCTACAGTTTGGCCAGGGACCA 386  
 Qy 302 AGGTGAATCAACGA 318  
 Db 385 AGGTGAATCAACGA 369

RESULT 8  
 LOCUS BG533970 755 bp mRNA linear EST 03-APR-2001  
 DEFINITION 602553071.F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4663096 5',  
 mRNA sequence.

ACCESSION BG533970  
 VERSION BG533970.1 GI:13525510  
 EST.

KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 755)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: csaasb@mail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.lnl.gov  
 Plate: LNCM1464 row: m column: 17  
 High quality sequence stop: 726.

#### FEATURES

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 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4663096"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_id="NIH\_MGC\_77"  
 /note="Torgan: lung; Vector: pMDR-LIB (Clontech); Site 1:  
 SfiI (ggcgccctcgcc); Site 2: SfiI (ggcgcttaagcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGCCATTATGCCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCCGAGCGCGCCGACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.9  
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

#### ORIGIN

Query Match 89.1%; Score 283.4; DB 4; Length 755;  
 Best Local Similarity 93.4%; Pred. No. 4,4e-79;  
 Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
 2 AGCTCAGCAGTCTCATCTTCCGTGTCATCTGTAGAGACAGAGTCAACATTAATT 61

Db 101 AGATGACCCAGTCTCCATCTTCGCTGTCGATCTGTAGAGACGAGTCAACATCACTT 160  
 Qy 62 GTCCGGGAGTCAGGATTAAGCAGTTGTTAGCTTGATTCAGCAGAAACAGGAAAG 121  
 Db 161 GTCCGGGAGTCAGGATTAAGCAGTTGTTAGCTTGATTCAGCAGAAACAGGAAAG 220  
 Qy 122 CCCCTAAACTCTGATCTATCTGCATCTCAGTTTGGCAAGGGGATCCCGTCAAGTTCA 181  
 Db 221 CCCCTAAGCTCTGATCTATCTGCATCTCAGTTTGGCAAGGGGATCCCGTCAAGTTCA 280  
 Qy 182 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGAGCCTGAAGATT 241  
 Db 281 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGAGCCTGAAGATT 340  
 Qy 242 CTGCACTTACTATTGTCAACAGGCTTACAGTTTCCGCTACACTTTGGCCAGGGACCA 301  
 Db 341 TTGCACTTACTATTGTCAACAGGCTTACAGTTTCCGCTACACTTTGGCCAGGGACCA 400  
 Qy 302 AGGTGAATCAACGA 318  
 Db 401 AGGTGAATCAACGA 417

RESULT 9  
 LOCUS CD688415 605 bp mRNA linear EST 25-JUN-2003  
 DEFINITION EST4937 human nasopharynx Homo sapiens cDNA, mRNA sequence.

ACCESSION CD688415  
 VERSION CD688415.1 GI:32207195  
 EST.

KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 605)  
 Lhu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and  
 Zeng, Y.-X.  
 Transcriptional Gene Expression Profile of Human Nasopharynx  
 Unpublished (2003)  
 COMMENT Contact: Yixun Zeng  
 Cancer Center  
 Sun Yat-sen University  
 651 Dongfeng Road East, Guangzhou 510060, China  
 Tel: 86-1380-9770-743  
 Fax: 86-20-8775-4506  
 Email: yxzeng@zsune.edu.cn.

#### FEATURES

source

1..605  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="normal nasopharynx"  
 /clone\_id="human nasopharynx"  
 /note="ESTs generated from a normal nasopharynx cDNA  
 library from southern Chinese"

#### ORIGIN

Query Match 88.7%; Score 282; DB 6; Length 605;  
 Best Local Similarity 93.6%; Pred. No. 1.1e-78;  
 Matches 294; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 5 TCAGGAGTTCCTCATCTTCGCTGTCGATCTGTAGAGACAGAGTCAACATTAATTTC 64  
 Db 123 TGACCCAGTCTCATCTTCTGCTGTCGATCTGTAGAGACAGAGTCAACATTAATTTC 182  
 Qy 65 GCGGAGTCAAGGATTAAGCAGTTGTTAGCTTGATTCAGCAGAAACAGGAAAGCC 124  
 Db 183 GCGGAGTCAAGGATTAAGCAGTTGTTAGCTTGATTCAGCAGAAACAGGAAAGCC 242  
 Qy 125 CTAAATCTCTGATCTATCTGCATCTCAGTTTGGCAAGGGGATCCCGTCAAGTTCAAG 184  
 Db 243 CTAAATCTCTGATCTATCTGCATCTCAGTTTGGCAAGGGGATCCCGTCAAGTTCAAG 302

QY 185 GCAGTGATCTGGGACAGATTTCAGTCTCACCATCAGACGCTGCAAGCTGGAATTCTG 244  
Db 303 GCAGTGATCTGGGACAGATTTCAGTCTCACCATCAGACGCTGCAAGCTGGAATTCTG 362  
QY 245 CAACCTACTATTGTCAACAGGCTTAACAGTTCCCGTACACTTTGGCCAGGAGCAACG 304  
Db 363 CAACCTACTATTGTCAACAGGCTTAACAGTTCCCGTACACTTTGGCCAGGAGCAACG 422  
QY 305 TGGAAATCAACGA 318  
Db 423 TGGAGATCAACGA 436  
RESULT 10  
CD702614 472 bp mRNA linear EST 25-JUN-2003  
LOCUS EST19139 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD702614  
VERSION CD702614.1 GI:32233244  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and  
AUTHORS Zeng,Y.-X.  
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gzsums.edu.cn.  
FEATURES  
source Location/Qualifiers  
1..472  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="normal nasopharynx"  
/clone\_lib="human nasopharynx"  
/note="ESTs generated from a normal nasopharynx cDNA  
library from southern Chinese"

ORIGIN  
Query Match 88.6%; Score 281.8; DB 6; Length 472;  
Best Local Similarity 93.1%; Pred. No. 1.2e-78;  
Matches 295; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGTCTCCATCTTCGTCGTCATCTGTAGAGAGAGAGTCAACCAATTT 61  
Db 125 AGATGACCCAGTCTCCATCTTCGTCGTCATCTGTAGAGAGAGAGTCAACCAATTT 184  
QY 62 GTCGGGAGAGTCAAGGATTAAGCAGTTGGTTAGCTGGTATCAGAGAAACAGGGAAG 121  
Db 185 GTCGGGAGAGTCAAGGATTAAGCAGTTGGTTAGCTGGTATCAGAGAAACAGGGAAG 244  
QY 122 CCCCTAACTCTGATCTATCTGCATCCAGTTGGCAAGGGGTCGCCGCAAGTTCA 181  
Db 245 CCCCTAACTCTGATCTATCTGCATCCAGTTGGCAAGGGGTCGCCGCAAGTTCA 304  
QY 182 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGACGCTGCAAGCTGGAATT 241  
Db 305 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGACGCTGCAAGCTGGAATT 364  
QY 242 CTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCCGTACACTTTGGCCAGGAGCA 301  
Db 365 TTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCCGTACACTTTGGCCAGGAGCA 424  
QY 302 AGGTGAATCAACGA 318  
Db 423 TGGAGATCAACGA 436

Db 425 AGGTGAATCAACGA 441  
RESULT 11  
CD696718 497 bp mRNA linear EST 25-JUN-2003  
LOCUS EST13241 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD696718  
VERSION CD696718.1 GI:32223477  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and  
AUTHORS Zeng,Y.-X.  
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gzsums.edu.cn.  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/tissue\_type="normal nasopharynx"  
/clone\_lib="human nasopharynx"  
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library from southern Chinese"

ORIGIN  
Query Match 88.1%; Score 280.2; DB 6; Length 497;  
Best Local Similarity 92.7%; Pred. No. 4.1e-78;  
Matches 294; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGTCTCCATCTTCGTCGTCATCTGTAGAGAGAGTCAACCAATTT 61  
Db 120 AGATGACCCAGTCTCCATCTTCGTCGTCATCTGTAGAGAGAGTCAACCAATTT 179  
QY 62 GTCGGGAGAGTCAAGGATTAAGCAGTTGGTTAGCTGGTATCAGAGAAACAGGGAAG 121  
Db 180 GTCGGGAGAGTCAAGGATTAAGCAGTTGGTTAGCTGGTATCAGAGAAACAGGGAAG 239  
QY 122 CCCCTAACTCTGATCTATCTGCATCCAGTTGGCAAGGGGTCGCCGCAAGTTCA 181  
Db 240 CCCCTAACTCTGATCTATCTGCATCCAGTTGGCAAGGGGTCGCCGCAAGTTCA 299  
QY 182 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGACGCTGCAAGCTGGAATT 241  
Db 300 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGACGCTGCAAGCTGGAATT 359  
QY 242 CTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCCGTACACTTTGGCCAGGAGCA 301  
Db 360 TTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCCGTACACTTTGGCCAGGAGCA 419  
QY 302 AGGTGAATCAACGA 318  
Db 420 AAGTGATATCAACGA 436  
RESULT 12  
BF129120 912 bp mRNA linear EST 24-OCT-2000  
LOCUS BF129120  
DEFINITION 601811580F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4054530 5',  
mRNA sequence.  
ACCESSION BF129120  
VERSION BF129120.1 GI:10968160

KEYWORDS EST. Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 912)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>  
Plate: LNCM894 row: p column: 19  
High quality sequence stop: 695.  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:4054530"  
/tissue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_48"  
/note="Organ: B-cells; Vector: pORF7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 87.6%; Score 278.6; DB 2; Length 912;  
Best Local Similarity 92.4%; Pred. No. 1.6e-77;  
Matches 293; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGTCTCCATCTCCGTCGTCATCTGTAGAGACAGAGTCCATTAATT 61  
DB 72 AGATGACCCAGTCTCCATCTCCGTCGTCATCTGTAGAGACAGAGTCCATTAATT 131  
QY 62 GTCCGGCGAGTCAGGGATTAGCAGTTGGTTAGCTGTATCAGAGAAACAGGGAAG 121  
DB 132 GTCCGGCGAGTCAGGGATTAGTGTAGTTAGCTGTATCAGAGAAACAGGGAAG 191  
QY 122 CCCCTAAATCTCTATCTATCTGATCAGTTGGCAAGTGGGGTCCCTCAAGTTCA 181  
DB 192 CCCCTAAATCTCTATCTATCTGATCAGTTTCAAAAGTGGGGTCCCTCAAGTTCA 251  
QY 182 GCGGAGTGTATCTGGGACAGATTTCATCTCAGATCAGAGAGCTGAGAGTT 241  
DB 252 GCGGAGTGTATCTGGGACAGATTTCATCTCAGATCAGAGAGCTGAGAGTT 311  
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTGTAAGTTGGCCAGGAGCA 301  
DB 312 TTGCAACTTACTATTGTCTACAGACTAACAGTTTCCCTGTAAGTTGGCCAGGAGCA 371  
QY 302 AGGTGAAATCAACGA 318  
DB 372 AAGTGATATCAACGA 388

RESULT 13  
BG341803 894 bp mRNA linear EST 27-FEB-2001  
LOCUS BG341803  
DEFINITION 602463535F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4576136 5',

ACCESSION mRNA sequence.  
VERSION BG341803  
KEYWORDS BG341803.1 GI:13148241  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 894)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>  
Plate: LNCM1288 row: f column: 09  
High quality sequence stop: 636.  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:4576136"  
/tissue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_48"  
/note="Organ: B-cells; Vector: pORF7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 86.9%; Score 276.2; DB 4; Length 894;  
Best Local Similarity 94.0%; Pred. No. 9.1e-77;  
Matches 298; Conservative 0; Mismatches 18; Indels 1; Gaps 1;  
QY 2 AGCTCAGCAGTCTCCATCTCCGTCGTCATCTGTAGAGACAGAGTCCATTAATT 61  
DB 86 AGATGACCCAGTCTCCATCTCCGTCGTCATCTGTAGAGACAGAGTCCATTAATT 145  
QY 62 GTCCGGCGAGTCAGGGATTAGCAGTTGGTTAGCTGTATCAGAGAAACAGGGAAG 121  
DB 146 GTCCGGCGAGTCAGGGATTAGCAGTTGGTTAGCTGTATCAGAGAAACAGGGAAG 204  
QY 122 CCCCTAAATCTCTATCTATCTGATCAGTTGGCAAGTGGGGTCCCTCAAGTTCA 181  
DB 205 CCCCTAAATCTCTATCTATCTGATCAGTTTCAAAAGTGGGGTCCCTCAAGTTCA 264  
QY 182 GCGGAGTGTATCTGGGACAGATTTCATCTCAGATCAGAGAGCTGAGAGTT 241  
DB 265 GCGGAGTGTATCTGGGACAGATTTCATCTCAGATCAGAGAGCTGAGAGTT 324  
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTGTAAGTTGGCCAGGAGCA 301  
DB 325 TTGCAACTTACTATTGTCTACAGACTAACAGTTTCCCTGTAAGTTGGCCAGGAGCA 384  
QY 302 AGGTGAAATCAACGA 318  
DB 385 AAGTGATATCAACGA 401

RESULT 14



CD706288  
LOCUS CD706288 561 bp mRNA linear EST 25-JUN-2003  
DEFINITION EST22815 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD706288  
VERSION CD706288.1 GI:32236918  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 561)  
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.  
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gzsums.edu.cn.  
location/Qualifiers  
1..561  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="normal nasopharynx"  
/clone\_lib="human nasopharynx"  
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN  
Query Match 86.6%; Score 275.4; DB 6; Length 561;  
Best Local Similarity 91.8%; Pred. No. 1.4e-76;  
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGTCTTCATCTTCGTCGATCTGTAGAGACAGAGTCACCACTT 61  
Db 117 AGATGACCCAGTCTTCATCTTCGTCGATCTGTAGAGACAGAGTCACCACTT 176  
QY 62 GTGGGGGAGTCAGGATATTAGCAGTTGGTAGCCTGATCAGAGAAACAGGGAAG 121  
Db 177 GTGGGGGAGTCAGGATATTAGCAGTTGGTAGCCTGATCAGAGAAACAGGGAAG 236  
QY 122 CCCCTAACTCTGATCTATTTCTGATCCAGTTTGCAAGTGGGTCCTCAAGTTCA 181  
Db 237 CCCCTAACTCTGATCTATGCTGATCCAGTTTGCAAGTGGGTCCTCAAGTTTA 296  
QY 182 GCGGCACTGATCTGGGACAGATTTCACTTCACCATCAGAGCCTGCAAGCTTA 241  
Db 297 GCGGCACTGATCTGGGACAGATTTCACTTCACCATCAGAGCCTGCAAGCTTA 356  
QY 242 CTGCACTTACTATTGTCAAGGCTAACAGTTTCCCTACACTTTTGGCCAGGGAACA 301  
Db 357 TTGCACTTACTATTGTGAGAGACTTAACAGTTTCCCTGCACTTTGGCCAGGGAACA 416  
QY 302 AGGTGAATCAACGA 318  
Db 417 AGGTGAATCAACGA 433

RESULT 15  
LOCUS BG686018 851 bp mRNA linear EST 01-MAY-2001  
DEFINITION 602638582F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4766157 5', mRNA sequence.  
ACCESSION BG686018  
VERSION BG686018.1 GI:13917415  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 851)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strauberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: L1CM1626 row: c column: 22  
High quality sequence stop: 851.  
location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4766157"  
/tissue\_type="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_48"  
/note="Organ: B-cells; Vector: pOTB7, Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

ORIGIN  
Query Match 86.4%; Score 274.6; DB 4; Length 851;  
Best Local Similarity 93.7%; Pred. No. 2.9e-76;  
Matches 297; Conservative 0; Mismatches 19; Indels 1; Gaps 1;  
QY 2 AGCTCAGCAGTCTTCATCTTCGTCGATCTGTAGAGACAGAGTCACCACTT 61  
Db 81 AGATGACCCAGTCTTCATCTTCGTCGATCTGTAGAGACAGAGTCACCACTT 140  
QY 62 GTGGGGGAGTCAGGATATTAGCAGTTGGTAGCCTGATCAGAGAAACAGGGAAG 121  
Db 141 GTGGGGGAGTCAGGATATTAGCAGTTGGTAGCCTGATCAGAGAAACAGGGAAG 199  
QY 122 CCCCTAACTCTGATCTATTTCTGATCCAGTTTGCAAGTGGGTCCTCAAGTTCA 181  
Db 200 CCCCTAACTCTGATCTATGCTGATCCAGTTTGCAAGTGGGTCCTCAAGTTCA 259  
QY 182 GCGGCACTGATCTGGGACAGATTTCACTTCACCATCAGAGCCTGCAAGCTTA 241  
Db 260 GCGGCACTGATCTGGGACAGATTTCACTTCACCATCAGAGCCTGCAAGCTTA 319  
QY 242 CTGCACTTACTATTGTCAAGGCTAACAGTTTCCCTACACTTTTGGCCAGGGAACA 301  
Db 320 TTGCACTTACTATTGTCAAGGCTAACAGTTTCCCTACACTTTTGGCCAGGGAACA 379  
QY 302 AGGTGAATCAACGA 318  
Db 380 AGGTGAATCAACGA 396

Search completed: July 27, 2005, 12:32:16  
Job time : 1962.75 secs





PF 27-DEC-2001; 2001WO-SE002908.  
XX  
XX 29-DEC-2000; 2000SE-00004892.  
XX  
XX (PMAA ) PHARMACIA DIAGNOSTICS AB.  
XX  
XX Flicker S, Steinberger P, Kraft D, Valenta R,  
XX WPI; 2002-583604/62.  
XX P-PSDB; ABG30450.  
XX  
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
PT diagnosing or passive immunotherapy of type I allergy, for environmental  
XX allergen detection.  
XX  
XX Disclosure; Page 35-36; 45pp; English.  
XX  
XX This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE Fabs and methods for their use. The proteins  
CC of the invention may have anti-allergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE  
CC antibodies to Phl p 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific Fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The Fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific Fabs of the invention are useful for  
CC inner alla, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergic patients  
CC IgE antibodies to Phl p 2. The present sequence represents the DNA  
CC encoding the human IgG Fab, clone 100 light chain protein of the  
XX invention  
XX  
XX Sequence 318 BP; 80 A; 81 C; 81 G; 76 T; 0 U; 0 Other:  
SQ  
Query Match 100.0%; Score 318; DB 6; Length 318;  
Best Local Similarity 100.0%; Pred. No. 9.6e-93;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCTCAGCGAGTCTCCATCTTCGTCGATCTGTAGAGACAGAGTCAACCTACT 60  
DB 1 GAGCTCAGCGAGTCTCCATCTTCGTCGATCTGTAGAGACAGAGTCAACCTACT 60  
QY 61 TGTGCGGAGTCAAGGATATTAGAGTGTAGAGTGTATCAGACAGAAACAGAGGAAA 120  
DB 61 TGTGCGGAGTCAAGGATATTAGAGTGTAGAGTGTATCAGACAGAAACAGAGGAAA 120  
QY 121 GCCCTTAACTCTGATCTATTTCGATCCAGTTTGCAAGTGGGCTCCGTCAGAGTTTC 180  
DB 121 GCCCTTAACTCTGATCTATTTCGATCCAGTTTGCAAGTGGGCTCCGTCAGAGTTTC 180  
QY 181 AGCGGCGAGTGAATTCGGAGAGATTTGATCTCAACATCAGACAGCGCTGACCTGAAGAT 240  
DB 181 AGCGGCGAGTGAATTCGGAGAGATTTGATCTCAACATCAGACAGCGCTGACCTGAAGAT 240  
QY 241 TCTGCAACTTACTATTGTCACAGAGCTTAACAGTTTCCGTCACACTTTTGGCAGAGGAGCC 300  
DB 241 TCTGCAACTTACTATTGTCACAGAGCTTAACAGTTTCCGTCACACTTTTGGCAGAGGAGCC 300  
QY 301 AAGGTGGAATCAACGA 318  
DB 301 AAGGTGGAATCAACGA 318  
RESULT 2  
AAS99473  
ID AAS99473 standard; cDNA; 974 BP.  
XX AAS99473;  
AC  
XX  
DT 12-MAR-2002 (first entry)

XX  
XX Anti-human AILIM monoclonal antibody clone Jmab-136, light chain cDNA.  
DE  
XX  
XX Human; antirheumatic; antiarthritis; antidiabetic; antipsoriatic;  
KW antiallergic; antitumor; neuroprotective; antihypertoid; vasotrophic;  
KW immunosuppressive; dermatological; antinflammatory; hepatotropic;  
KW activation inducible lymphocyte immunomodulatory molecule; AILIM;  
KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;  
KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;  
KW allergic contact-type dermatitis; chronic inflammatory dermatosis;  
KW systemic lupus erythematosus; autoimmune disorder; inflammation; SS;  
KW graft versus host reaction; immune rejection; intestinal immunity;  
KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.  
XX  
XX Homo sapiens.  
XX  
XX WO200187981-A2.  
XX  
XX 22-NOV-2001.  
XX  
XX 15-MAY-2001; 2001WO-JP004035.  
XX  
XX 18-MAY-2000; 2000JP-00147116.  
XX 30-MAR-2001; 2001JP-00099508.  
XX  
XX (NISE ) JAPAN TOBACCO INC.  
XX  
XX Tsuji T, Tezuka K, Hori N;  
XX WPI; 2002-075313/10.  
XX P-PSDB; AAU74297.  
XX  
XX New human monoclonal antibody that binds to activation inducible  
PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid  
PT arthritis, multiple sclerosis and inflammation.  
XX  
XX Claim 45; Page 267-270; 300pp; English.  
XX  
XX The invention relates to a novel human antibody (I), preferably a human  
CC monoclonal antibody which binds to an activation inducible lymphocyte  
CC immunomodulatory molecule (AILIM). (I) is useful for modulating signal  
CC transduction into a cell mediated by AILIM, for modulating proliferation  
CC of AILIM-expressing cells, for modulating production of a cytokine from  
CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity  
CC against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of  
CC AILIM-expressing cells. (I) is useful for treating, preventing or  
CC prophylaxis of delayed type allergy. (I) is useful for treating and  
CC preventing various diseases associated with AILIM-mediated costimulatory  
CC transduction, and for inhibiting the onset and/or advancement of the  
CC diseases. (I) is useful for suppression, prevention and/or treatment of  
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,  
CC allergic contact-type dermatitis, chronic inflammatory dermatosis,  
CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,  
CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus  
CC host reaction, graft versus host disease, immune rejection, disorders  
CC caused by abnormal intestinal immunity, specifically inflammatory  
CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,  
CC nephritis, vasculitis, and pancreatitis. (I) induces no serious  
CC immunorejection due to antigenicity to human, i.e., human anti-mouse  
CC antigenicity (HAMA) in a host. AAS99444-AAS99477 represent anti-human  
CC AILIM monoclonal antibody coding sequences and PCR primers of the  
XX invention  
XX  
SQ Sequence 974 BP; 246 A; 282 C; 232 G; 214 T; 0 U; 0 Other;  
Query Match 91.6%; Score 291.4; DB 6; Length 974;  
Best Local Similarity 95.0%; Pred. No. 6.4e-84;  
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
QY 2 AGCTCAGCGAGTCTCCATCTTCGTCGATCTGTAGAGACAGAGTCAACCTACT 61  
DB 112 AGATGACCCAGTCTCCATCTTCGTCGATCTGTAGAGACAGAGTCAACCTACT 171

QY 62 GTCCGGCGAGTCAGGGTATTAGCACTTGTTAGCTGGTATCAGCAAGAAACAGGGAAG 121  
Db 172 GTCCGGCGAGTCAGGGTATTAGCACTTGTTAGCTGGTATCAGCAAGAAACAGGGAAG 231  
QY 122 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGGGGTCCTCCGTCAAGGTTCA 181  
Db 232 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGGGGTCCTCCGTCAAGGTTCA 291  
QY 182 GCGGCAAGTGAATCTGGGACAGATTTCACTTCACATCAGAGCCTGAGCTGAAGATT 241  
Db 292 GCGGCAAGTGAATCTGGGACAGATTTCACTTCACATCAGAGCCTGAGCTGAAGATT 351  
QY 242 CTGCACTTACTATTTGTCACAGGCTAACAGTTCCGTAACCTTTGGCCAGGGGACCA 301  
Db 352 TTGCACTTACTATTTGTCACAGGCTAACAGTTCCGTAACCTTTGGCCAGGGGACCA 411  
QY 302 AGGTGAAATCAACGA 318  
Db 412 AGGTGAAATCAACGA 428

## RESULT 3

AAV73441  
ID AAT73441 standard, DNA, 388 BP.

AAV73441;

03-DEC-1997 (first entry)

Human immunoglobulin light chain variable region partial transcript.

Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;  
transgenic; mouse; CD4; antibody; autoimmune; inflammatory;

transplant rejection; ss.

Homo sapiens.

MO9713852-A1.

17-APR-1997.

10-OCT-1996; 96WO-US016433.

10-OCT-1995; 95US-00544404.

(GENP-) GENPHARM INT INC.

Lonberg N, Kay RM;

WPI, 1997-235888/21.

Novel anti-CD4 antibody produced by transgenic mice - used in the  
treatment of auto-immune disease etc.

Claim 44; Page 255; 396pp; English.

A novel composition has been developed which comprises an immunoglobulin  
(Ig) having an affinity constant (Ka) of at least 2 multiply 100000000 M  
-1 for binding to a predetermined human antigen. The present sequence  
represents a human light chain variable region partial nucleotide  
sequence, 10C5 kappa, which encodes an amino acid sequence from a claimed  
immunoglobulin that specifically binds human CD4. The anti-CD4 antibodies  
may be used in therapeutic and diagnostic applications, especially for  
the treatment of human diseases. These antibodies reduce activity of CD4  
cells and reduce undesirable autoimmune reactions, inflammatory response  
and transplant rejection. Transgenic animals are capable of producing  
heterologous antibodies of multiple isotypes by undergoing isotype  
switching. These animals produce a first Ig type that is necessary for  
antigen-stimulated B-cell maturation and can switch to encode and produce  
one or more subsequent heterologous isotypes

Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 U; 0 Other;

Query Match 91.5%; Score 291; DB 2; Length 388;  
Best Local Similarity 95.2%; Pred. No. 6e-84;  
Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 AGCTCAACCACTCTCCATCTCCGCTGCTGATCTGTGAGAGACAGATCCATCACTT 61  
Db 74 AGATGACCACTCTCCATCTCCGCTGCTGATCTGTGAGAGAGACAGATCCATCACTT 133  
QY 62 GTCCGGCGAGTCAGGGTATTAGCACTTGTTAGCTGGTATCAGCAAGAAACAGGGAAG 121  
Db 134 GTCCGGCGAGTCAGGGTATTAGCACTTGTTAGCTGGTATCAGCAAGAAACAGGGAAG 193  
QY 122 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGGGGTCCTCCGTCAAGGTTCA 181  
Db 194 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGGGGTCCTCCGTCAAGGTTCA 253  
QY 182 GCGGCAAGTGAATCTGGGACAGATTTCACTTCACATCAGAGCCTGAGCTGAAGATT 241  
Db 254 GCGGCAAGTGAATCTGGGACAGATTTCACTTCACATCAGAGCCTGAGCTGAAGATT 313  
QY 242 CTGCACTTACTATTTGTCACAGGCTAACAGTTCCGTAACCTTTGGCCAGGGGACCA 301  
Db 314 TTGCACTTACTATTTGTCACAGGCTAACAGTTCCGTAACCTTTGGCCAGGGGACCA 373  
QY 302 AGGTGAAATCAAC 316  
Db 374 AGGTGAAATCAAC 388

## RESULT 4

AAV39239  
ID AAV39239 standard, DNA, 388 BP.

AAV39239;

18-DEC-1998 (first entry)

Functional kappa transcript isolated from transgenic cell line 10C5.

Transgenic animal; human heterologous antibody; transgene;

isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;

autoimmune reaction; inflammatory response; transplant rejection;

acid induced lung injury; acute adult respiratory distress syndrome;

ARDS; vasculitis; septic shock; allergic reaction; asthma;

cystic fibrosis; ss.

Synthetic.

Homo sapiens.

Mus sp.

MO9824884-A1.

11-JUN-1998.

01-DEC-1997; 97WO-US021803.

02-DEC-1996; 96US-00758417.

(GENP-) GENPHARM INT.

Lonberg N, Kay RM;

WPI, 1998-333306/29.

Hybridoma producing antibody specific for interleukin-8 - used to prevent  
efflux of neutrophils from vasculature, and treat reperfusion injury.

Example 41; Page 304; 452pp; English.

AAV39232-41 represent functional transcripts of a human IgGkappa anti-CD4

antibody. The sequences are isolated from 5 different transgenic mouse

hybridoma cell lines. The specification describes transgenic non-human

animals, especially a mouse, which are capable of producing a human

CC heterologous antibodies of multiple isotypes by undergoing isotype  
 CC switching. The transgenic animals have human heavy and light chain  
 CC transgenes. The transgenes are capable of functionally rearranging a  
 CC heterologous diversity (D) gene in a variable-diversity-junction (V-D-J)  
 CC recombination. The transgenes include a heavy chain transgene comprising  
 CC at least one V, D and J gene segment, and one constant region gene  
 CC segment. The immunoglobulin (Ig) light chain transgene comprises at least  
 CC one V and J gene segment and one constant region gene segment. The gene  
 CC segments are heterologous to the transgenic animal. The antibody can be  
 CC used to prevent efflux of neutrophils from vasculature. It can also be  
 CC used to treat reperfusion injury. CD4 binding antibodies are used to  
 CC reduce undesirable autoimmune reactions, inflammatory responses and  
 CC rejection of transplanted organs. The anti-IL-8 antibodies can reduce  
 CC tissue damage and prolong survival in animal models of acute adult  
 CC respiratory distress syndrome (ARDS) and acid induced lung injury. The  
 CC anti-IL-8 antibodies can also be used for the treatment of vasculitis,  
 CC septic shock, allergic reactions (e.g. asthma) and cystic fibrosis  
 XX  
 SQ Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 U; 0 Other;  
 Query Match 91.5%; Score 291; DB 2; Length 388;  
 Best Local Similarity 95.2%; Pred. No. 6e-84;  
 Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
 QY 2 AGCTCAGGCAAGTCCCATCTCCGTCCTGATCTGTAGAGACAGAGTCAACCACTT 61  
 Db 74 AGATGACCCAGTCCCATCTCCGTCCTGATCTGTAGAGACAGAGTCAACCACTT 133  
 QY 62 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTCGCTGATCAGCAGAAACAGGGAAG 121  
 Db 134 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTCGCTGATCAGCAGAAACAGGGAAG 193  
 QY 122 CCCCTAACTCTGATCTATTCTGCATCCAGTTTGCAAAAGTGGGGTCCGTCAGAGTTCA 181  
 Db 194 CCCCTAACTCTGATCTATTCTGCATCCAGTTTGCAAAAGTGGGGTCCGTCAGAGTTCA 253  
 QY 182 GCGGCAGTGGATCTGGGACAGATTTCAGTCCACATCAGAGCCTGAGAGCTTAAGATT 241  
 Db 254 GCGGCAGTGGATCTGGGACAGATTTCAGTCCACATCAGAGCCTGAGAGCTTAAGATT 313  
 QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGTAACATTTTGGCCAGGGGACCA 301  
 Db 314 TTGCAACTTACTATTGTCAACAGGCTTAATAGTTTCCGTAACATTTTGGCCAGGGGACCA 373  
 QY 302 AGGTGAATCAAC 316  
 Db 374 AGCTGAGATCAAC 388  
 RESULT 5  
 AA221993 standard; DNA; 388 BP.  
 AC AA221993;  
 XX  
 DT 24-NOV-1999 (first entry)  
 XX  
 DE Partial nucleotide sequence for a functional transcript 10C5-kappa.  
 XX  
 KW Transgenic animal; heterologous antibody; hybridoma; B cell;  
 KW transgenic mouse; human heavy chain transgene; digoxin; PCR primer;  
 KW human light chain transgene; immortalized cell; immunoglobulin;  
 KW Shiga-like toxin; autoimmune disease; cancer; infectious disease;  
 KW transplant rejection; blood disorder; coagulation disorder; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX MO9945962-A1.  
 XX  
 XX 16-SEP-1999.  
 PD  
 XX 12-MAR-1999; 99WO-US005535.  
 PF

XX  
 PR 13-MAR-1998; 98US-00042353.  
 XX  
 PA (GENP-) GENPHARM INT INC.  
 XX  
 PI Lonberg N, Fishwild DM, Ball WJ;  
 DR WPI; 1999-551219/46.  
 XX  
 PR Novel transgenic non-human animals used to produce heterologous  
 PR antibodies.  
 XX  
 PS Example 41; Page 305; 484pp; English.  
 XX  
 CC The specification describes transgenic animals that are capable of  
 CC producing a heterologous antibody. The antibodies are isolated from a  
 CC hybridoma, comprising B cells, that is obtained from a transgenic mouse  
 CC having a genome comprising a human heavy chain transgene and a human  
 CC light chain transgene. The B cells are fused to immortalized cells  
 CC suitable for generating a hybridoma, which produces a detectable amount  
 CC of an immunoglobulin that specifically binds digoxin or Shiga-like  
 CC toxin. B cells from transgenic animals can be used to generate hybridomas  
 CC expressing monoclonal high affinity human sequence antibodies. Antibodies  
 CC produced from the transgenic animals of the invention can be used to  
 CC treat human diseases, e.g. autoimmune diseases, cancer, infectious  
 CC disease, transplant rejection, blood disorders such as coagulation  
 CC disorders and other diseases. The present sequence represents a partial  
 CC nucleotide sequence for a functional transcript used in the course of the  
 CC invention  
 XX  
 SQ Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 U; 0 Other;  
 Query Match 91.5%; Score 291; DB 2; Length 388;  
 Best Local Similarity 95.2%; Pred. No. 6e-84;  
 Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
 QY 2 AGCTCAGGCAAGTCCCATCTCCGTCCTGATCTGTAGAGACAGAGTCAACCACTT 61  
 Db 74 AGATGACCCAGTCCCATCTCCGTCCTGATCTGTAGAGACAGAGTCAACCACTT 133  
 QY 62 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTCGCTGATCAGCAGAAACAGGGAAG 121  
 Db 134 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTCGCTGATCAGCAGAAACAGGGAAG 193  
 QY 122 CCCCTAACTCTGATCTATTCTGCATCCAGTTTGCAAAAGTGGGGTCCGTCAGAGTTCA 181  
 Db 194 CCCCTAACTCTGATCTATTCTGCATCCAGTTTGCAAAAGTGGGGTCCGTCAGAGTTCA 253  
 QY 182 GCGGCAGTGGATCTGGGACAGATTTCAGTCCACATCAGAGCCTGAGAGCTTAAGATT 241  
 Db 254 GCGGCAGTGGATCTGGGACAGATTTCAGTCCACATCAGAGCCTGAGAGCTTAAGATT 313  
 QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGTAACATTTTGGCCAGGGGACCA 301  
 Db 314 TTGCAACTTACTATTGTCAACAGGCTTAATAGTTTCCGTAACATTTTGGCCAGGGGACCA 373  
 QY 302 AGGTGAATCAAC 316  
 Db 374 AGCTGAGATCAAC 388  
 RESULT 6  
 ADM47072 standard; DNA; 711 BP.  
 ID ADM47072  
 XX  
 XX ADM47072;  
 AC  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Mouse anti-human G-CSF antibody light chain gene.  
 XX  
 XX methyloctroph yeast; mammalian sugar chain; OCH1; alpha-1,  
 KW 6-mannosyl transferase; alpha-1; 2-mannosidase;  
 KW



Query Match	90.2%	Score 286.8;	DB 12;	Length 321;
Best Local Similarity	94.6%;	Pred. No. 1.3e-82;		
Matches 297;	Conservative	0;	Mismatches 17;	Indels 0;
			Gaps	0
QY	2	AGCTACCCAGCTCCATCTTCGCGTCTGCACTCTGTAGAGACAGAGTCCACATTA	61	
Db	8	AGATGACCCAGTCTCCATCTTCGCGTCTGCACTCTGTAGAGACAGAGTCCACATTA	67	
QY	62	GTCCGGCCAGTTCAGGGATTTAGACAGTTGGTGTAGCTGTATACAGCAAAACAGGAAAG	121	
Db	68	GTCCGGCCAGTTCAGGGATTTAGACAGTTGGTGTAGCTGTATACAGCAAAACAGGAAAG	127	
QY	122	CCCTTAACTCTGATCTTATTTGTCATCCAGTTTGCAAAAGTGGGGTCCGCTCAAGTTCA	181	
Db	128	CCCTTAACTCTGATCTTATTTGTCATCCAGTTTGCAAAAGTGGGGTCCGCTCAAGTTCA	187	
QY	182	GCGGAGTGTGATCTTGGGAGACAGATTTCAGTCTCACCATCAGACCCCTGACCTGGAAGATT	241	
Db	188	GCGGAGTGTGATCTTGGGAGACAGATTTCAGTCTCACCATCAGACCCCTGGAAGATT	247	
QY	242	CTGCAACTTACTATTGTCAACAGAGGCTTAAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA	301	
Db	248	TTGCAAGTACTATTGTGTCAACAGGCTTAAACAGTTTCCCGTGGACGTTTCGACCAAGGACCA	307	
QY	302	AGGTGAAATCAAA 315		
Db	308	AGGTGAAATCAAA 321		
RESULT 8				
ABZ22309				
ID	ABZ22309	standard;	DNA;	632 BP.
XX	ABZ22309;			
AC	ABZ22309;			
XX				
XX	20-MAR-2003 (first entry)			
DE	S. pneumoniae PPS-3 antibody 3H1 light chain DNA sequence SEQ ID NO:4.			
XX				
KW	Antipneumococcal; antibody; monoclonal antibody; infection; PPS-3;			
KW	Streptococcus pneumoniae; capsular polysaccharide; gene; de.			
XX				
OS	Streptococcus pneumoniae.			
XX	Synthetic.			
FN	WO200292017-A2.			
XX				
PD	21-NOV-2002.			
XX				
PF	16-MAY-2002; 2002MO-US018363.			
XX				
PR	16-MAY-2001; 2001US-0291492P.			
XX				

PA	(PIRO/)	PIROFSKY L.
PA	(ZHON/)	ZHONG Z.
PA	(CHAN/)	CHANG Q.
XX		
PI	Pirofsky L,	Zhong Z, Chang Q;
DR	WPI; 2003-120598/11.	
XX		
PT	New antibody or its antigen-binding fragment that specifically binds the	
PT	capsular polysaccharide of <i>Streptococcus pneumoniae</i> serotype 3, useful	
PT	for treating, inhibiting or preventing <i>S. pneumoniae</i> infections.	
XX		
PS	Claim 13; Fig 6B; 56pp; English.	
XX		
CC	The present invention describes an antibody or its antigen-binding	
CC	fragment (I) that specifically binds the capsular polysaccharide of	
CC	<i>Streptococcus pneumoniae</i> serotype 3 ( <i>S. pneumoniae</i> PS-3), comprising a	
CC	heavy and/or light chain amino acid sequence. (I) has antibacterial	
CC	activity and can be used in vaccines. The anti- <i>S. pneumoniae</i> PS-3	
CC	antibody or its antigen-binding fragment is useful for treating,	
CC	inhibiting or preventing <i>S. pneumoniae</i> infections or conditions or	
CC	disorders caused by the infection. Methods from the present invention can	
CC	be used for preventing or reducing the severity of conditions or	
CC	disorders caused by <i>S. pneumoniae</i> serotype 3 infection, or for increasing	
CC	the resistance of a subject to infection by <i>S. pneumoniae</i> serotype 3. The	
CC	present sequence represents a <i>S. pneumoniae</i> PS-3 antibody light chain	
CC	DNA sequence from the present invention	
XX		
Q0	Sequence 613BP; 165 A; 175 C; 159 G; 133 T; 0 U; 0 Other;	

Query Match	90.1%	Score 286.4	DB 8	Length 632
Best Local Similarity	94.9%	Pred. No. 2,36-82		
Matches 296	Conservative 0	Mismatches 16	Indels 0	Gaps 0
Qy	7	ACGCACTCTCCATCTTCCGTGTCTGCACTCTGTAGAGACAGAGTCACCATTACTTGTGG	66	
Db	12	ACGCAGTCTCCATCTTCCGTGTCTGCACTCTGTAGAGACAGAGTCACCATTACTTGTGG	71	
Qy	67	GCGAGTCAGAGGATTTAGCAGTTGGTTAACCTCGGATATCAGCAGAAACCAAGGAAAGCCCTT	126	
Db	72	GCGAGTCAGAGGATTTAGCAGCTCGTGTACCTCGGATATCAGCAGAAACCAAGGAAAGCCCTT	131	
Qy	127	AAACTCCTGATCTAATCTCTGCACTCAGTTTGGAAAAGTGGGGTCCCGTCAAGTTTCAGCGGC	186	
Db	132	AAACTCCTGATCTAATCTCTGCACTCAGTTTGGAAAAGTGGGGTCCCGTCAAGTTTCAGCGGC	191	
Qy	187	AGTGAATCTGGGACAGATTTCACTCAACATCAGACAGCTGACCGCTGAAGATTCTGCA	246	
Db	192	AGTGAATCTGGGACAGATTTCACTCAACATCAGACAGCTGACCGCTGAAGATTCTGCA	251	
Qy	247	ACTTACTATTTGTCACAGGCTTAACAGTTTCCCGTACCTTTTGGCCAGGGAGCCAGAGTGG	306	
Db	252	ACTTACTATTTGTCACAGGCTTAACAGTTTCCCGTACCTTTTGGCCAGGGAGCCAGAGTGG	311	
Qy	307	GAAATCAACGA 318		
Db	312	GAAATCAACGA 323		
RESULT 9				
ID	AAH47735	standard; DNA; 321 BP.		
XX	AAH47735;			
AC	AAH47735;			
XX	30-NOV-2001 (first entry)			
XX	Nucleotide sequence of seq Id No. 78.			
DE	Gene library; immunoglobulin; antibody library; human; ds.			
XX	Homo sapiens.			
OS				

PN WO200162907-A1.  
XX  
XX 30-AUG-2001.  
XX  
XX 22-FEB-2001; 2001WO-JP001298.  
XX  
XX 22-FEB-2000; 2000JP-00050543.  
XX  
XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.  
XX  
XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M,  
PI Okuno Y, Shiraki K;  
XX WPI; 2001-565420/63.  
XX P-PSDB; AAG65571.  
XX  
XX Producing gene libraries and antibody libraries, involves selecting a  
PT light chain that binds to a heavy chain product to produce a functional  
PT formation, and producing a gene library of the light chain variable  
PT regions.  
XX  
XX Examples; p 151; 181pp; Japanese.  
XX  
XX The invention relates to producing gene libraries, comprising  
CC immunoglobulin light and heavy variable region. The method involves  
CC selecting light chain that binds with the heavy chain product to produce  
CC a functional conformation, producing a gene library comprising a  
CC collection of these light chain variable genes, and combining with gene  
CC library of heavy chain variable genes. The method is used for production  
CC of gene and antibody libraries  
XX  
SQ Sequence 321 BP; 80 A; 85 C; 80 G; 76 T; 0 U; 0 Other;  
Query Match 89.7%; Score 285.2; DB 4; Length 321;  
Best Local Similarity 94.3%; Pred. No. 4.3e-82;  
Matches 296; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGTCTCATCTTCCGTCGATCTGTAGAGACAGAGTCAACATTAATT 61  
DB 8 AGATGACCCAGTCTTCATCTTCCGTCGATCTGTAGAGACAGAGTCAACATTAATT 67  
QY 62 GTCCGGCGAGTCAAGGATTAAGAGTTGGTAGCTGTATCAGAGAAACAGGAAAG 121  
DB 68 GTCCGGCGAGTCAAGGATTAAGAGTTGGTAGCTGTATCAGAGAAACAGGAAAG 127  
QY 122 CCCCTAACTCTGATCTATTCTGATCCAGTTTGCAAAAGTGGGGTCCCGTCAAGTTCA 181  
DB 128 CCCCTAACTCTGATCTATTCTGATCCAGTTTGCAAAAGTGGGGTCCCGTCAAGTTCA 187  
QY 182 GCGGAGTGAATCTGGGACAGATTTCACTCACCATCAGAGCCTGAGGCTGAAGATT 241  
DB 188 GCGGAGTGAATCTGGGACAGATTTCACTCACCATCAGAGCCTGAGGCTGAAGATT 247  
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGTACACTTTTGGCCAGGGAGCA 301  
DB 248 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGTACACTTTTGGCCAGGGAGCA 307  
QY 302 AGGTGGAATCAAA 315  
DB 308 AGGTGAGATCAAA 321  
RESULT 10  
ADHS6388  
ID ADHS6388 standard; DNA; 401 BP.  
XX  
XX ADHS6388;  
XX  
XX 25-MAR-2004 (first entry)  
XX  
XX Variable region of the human 9F11 antibody k-chain DNA SEQ ID NO:2.  
XX  
XX human; immunoglobulin M; IgM; monoclonal antibody; HIV infection;

KW anti-HIV; HIV; human 9F11 antibody; gene; ds.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX WO2004003196-A1.  
XX  
XX 08-JAN-2004.  
XX  
XX 30-JUN-2003; 2003WO-JP008306.  
XX  
XX 01-JUL-2002; 2002JP-00227952.  
XX  
XX 18-MAR-2003; 2003JP-00074312.  
XX  
XX (OKAD/) OKADA H.  
XX  
XX (OKAD/) OKADA N.  
XX  
XX Okada H, Okada N;  
PI WPI; 2004-083055/08.  
XX  
XX Human IgM monoclonal antibody against activated human lymphocytes or HIV  
PT infected cells for treatment of HIV.  
XX  
XX Claim 4; SEQ ID NO 2; 27pp; Japanese.  
XX  
XX The present invention describes a human immunoglobulin M (IgM) monoclonal  
CC antibody (I) against activated human lymphocytes or HIV infected cells,  
CC mediated by homologous complement. Also described: (1) an  
CC immunosuppressing agent and HIV treatment containing the antibody; and  
CC (2) cells PERM PB-8379 that produce the antibody. (I) has anti-HIV  
CC activity, and can be used in the treatment of HIV. The present sequence  
CC represents the variable region of the human 9F11 antibody k-chain  
CC nucleotide sequence, which is used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 401 BP; 92 A; 110 C; 105 G; 94 T; 0 U; 0 Other;  
Query Match 89.2%; Score 283.6; DB 12; Length 401;  
Best Local Similarity 93.9%; Pred. No. 1.5e-81;  
Matches 295; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGTCTCATCTTCCGTCGATCTGTAGAGACAGAGTCAACATTAATT 61  
DB 8 AGATGACCCAGTCTTCATCTTCCGTCGATCTGTAGAGACAGAGTCAACATTAATT 147  
QY 62 GTCCGGCGAGTCAAGGATTAAGAGTTGGTAGCTGTATCAGAGAAACAGGAAAG 121  
DB 148 GTCCGGCGAGTCAAGGATTAAGAGTTGGTAGCTGTATCAGAGAAACAGGAAAG 207  
QY 122 CCCCTAACTCTGATCTATTCTGATCCAGTTTGCAAAAGTGGGGTCCCGTCAAGTTCA 181  
DB 128 CCCCTAACTCTGATCTATTCTGATCCAGTTTGCAAAAGTGGGGTCCCGTCAAGTTCA 267  
QY 182 GCGGAGTGAATCTGGGACAGATTTCACTCACCATCAGAGCCTGAGGCTGAAGATT 241  
DB 208 GCGGAGTGAATCTGGGACAGATTTCACTCACCATCAGAGCCTGAGGCTGAAGATT 327  
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGTACACTTTTGGCCAGGGAGCA 301  
DB 248 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGTACACTTTTGGCCAGGGAGCA 387  
QY 302 AGGTGGAATCAAA 315  
DB 388 AGGTGAGATCAAA 401  
RESULT 11  
AAT73445  
ID AAT73445 standard; DNA; 420 BP.  
XX  
XX AAT73445;  
XX  
XX



DT 03-DEC-1997 (first entry)  
XX  
DE Human immunoglobulin light chain variable region partial transcript.  
XX  
KM Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;  
KM transgenic; mouse; CD4; antibody; autoimmune; inflammatory;  
KM transplant rejection; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO9713852-A1.  
XX  
PD 17-APR-1997.  
XX  
PF 10-OCT-1996; 96WO-US016433.  
XX  
PR 10-OCT-1995; 95US-00544404.  
XX  
PA (GENP-) GENPHARM INT INC.  
XX  
PI Lonberg N, Kay RM;  
XX  
DR WPI; 1997-235888/21.  
XX  
PT Novel anti-CD4 antibody produced by transgenic mice - used in the  
PT treatment of auto-immune disease etc.  
XX  
PS Claim 45; Page 272-273; 396pp; English.  
XX  
CC A novel composition has been developed which comprises an immunoglobulin  
CC (Ig) having an affinity constant (Ka) of at least 2 multiply 1000000000 M  
CC -1 for binding to a predetermined human antigen. The present sequence  
CC represents a human light chain variable region partial nucleotide  
CC sequence, LC6G5, which encodes an amino acid sequence from a claimed  
CC immunoglobulin that specifically binds human CD4. The anti-CD4 antibodies  
CC may be used in therapeutic and diagnostic applications, especially for  
CC the treatment of human diseases. These antibodies reduce activity of CD4  
CC cells and reduce undesirable autoimmune reactions, inflammatory response  
CC and transplant rejection. Transgenic animals are capable of producing  
CC heterologous antibodies of multiple isotypes by undergoing isotype  
CC switching. These animals produce a first Ig type that is necessary for  
CC antigen-stimulated B-cell maturation and can switch to encode and produce  
CC one or more subsequent heterologous isotypes  
XX  
SQ Sequence 420 BP; 98 A; 116 C; 98 G; 108 T; 0 U; 0 Other;  
Query Match 89.1%; Score 283.4; DB 2; Length 420;  
Best Local Similarity 93.4%; Pred. No. 1.8e-81;  
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGCTTCATCTTCCGTCTGCATCTGTAGAGACAGACAGTCAACCATTA 61  
DB 80 AGATGACCCAGCTTCATCTTCCGTCTGCATCTGTAGAGACAGACAGTCAACCATTA 139  
QY 62 GTGGGGGAGCAGAGGATTTAGAGTTGGTACCTGTATCAGAGAAACAGAGAAAG 121  
DB 140 GTCCGGGCGAGTCAGATATTTAGACAGCTGGTAACTGTATCAGATTAACAGAGTAAAG 199  
QY 122 CCCCTAAACTCTGATCTATCTGCATCCAGTTTGCAAGTGGGTCCCGTCAAGTTCA 181  
DB 200 CACTTAAGCTCTATCTATCTATCTGCATCAGTTTGCAAGTGGTCCCATCAAGTTCA 259  
QY 182 GCGGCACTGATCTGGGACAGATTTCACTTCAACATCAGAGAGCTTGAGGCTTGAAGTT 241  
DB 260 GCGGAAAGTATCTGGGACAGATTTCACTTCAACATCAGAGAGCTTGAGGCTTGAAGTT 319  
QY 242 CTGCAACTTACTATTTGTCAACAGGTTAAGTTTCCGTTAAGCTTTGGCCAGGGAGCA 301  
DB 320 TTGGAACCTACTATTTGTCAACAGGTTAAGTTTCCGTTAAGCTTTGGCCAGGGAGCA 379  
QY 302 AGGTGAAATCAACGA 318  
DB 380 AGCTGAGATCAACGA 396

RESULT 12  
AAV39293  
ID AAV39293 standard; DNA; 420 BP.  
XX  
AC AAV39293;  
XX  
DT 18-DEC-1998 (first entry)  
XX  
DE Synthetic kappa light chain sequence LC6G5.  
XX  
KM Transgenic animal; human heterologous antibody; transgene;  
KM isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;  
KM autoimmune reaction; inflammatory response; transplant rejection;  
KM acid induced lung injury; acute adult respiratory distress syndrome;  
KM ARDS; vasculitis; septic shock; allergic reaction; asthma;  
KM cystic fibrosis; ss.  
XX  
OS Synthetic.  
XX  
OS Homo sapiens.  
XX  
PN MO9824884-A1.  
XX  
PD 11-JUN-1998.  
XX  
PF 01-DEC-1997; 97WO-US021803.  
XX  
PR 02-DEC-1996; 96US-00758417.  
XX  
PA (GENP-) GENPHARM INT.  
XX  
PI Lonberg N, Kay RM;  
XX  
DR WPI; 1998-333306/29.  
XX  
PT Hybridoma producing antibody specific for interleukin-8 - used to prevent  
PT efflux of neutrophils from vasculature, and treat reperfusion injury.  
XX  
PS Example 42; Page 324-325; 452pp; English.  
XX  
CC The present sequence represents a synthetic kappa light sequence (created  
CC using oligonucleotides AAV39267-78). This synthetic sequence differs from  
CC natural sequences in that strings of repeated oligonucleotides are  
CC interrupted (to facilitate oligonucleotide synthesis and PCR  
CC amplification), optimal translation initiation sites are incorporated and  
CC HindIII sites were engineered upstream of the translation initiation  
CC sites. The sequence is used to make plasmid pHC6G5, which is used in the  
CC construction of minigenes for expression of Igkappa anti-CD4 antibodies,  
CC in the transgenic mouse of the invention. The specification describes  
CC transgenic non-human animals, especially a mouse, which are capable of  
CC producing a human heterologous antibodies of multiple isotypes by  
CC undergoing isotype switching. The transgenic animals have human heavy and  
CC light chain transgenes. The transgenes are capable of functionally  
CC rearranging a heterologous diversity (D) gene in a variable-diversity-  
CC junction (V-D-J) recombination. The transgenes include a heavy chain  
CC transgene comprising at least one V, D and J gene segment, and one  
CC constant region gene segment. The immunoglobulin (Ig) light chain  
CC transgene comprises at least one V and J gene segment and one constant  
CC region gene segment. The gene segments are heterologous to the transgenic  
CC animal. The antibody can be used to prevent efflux of neutrophils from  
CC vasculature. It can also be used to treat reperfusion injury. CD4 binding  
CC antibodies are used to reduce undesirable autoimmune reactions,  
CC inflammatory responses and rejection of transplanted organs. The anti-IL-  
CC 8 antibodies can reduce tissue damage and prolong survival in animal  
CC models of acute adult respiratory distress syndrome (ARDS) and acid  
CC induced lung injury. The anti-IL-8 antibodies can also be used for the  
CC treatment of vasculitis, septic shock, allergic reactions (e.g. asthma)  
CC and cystic fibrosis  
XX  
SQ Sequence 420 BP; 98 A; 116 C; 98 G; 108 T; 0 U; 0 Other;  
Query Match 89.1%; Score 283.4; DB 2; Length 420;



Best Local Similarity 93.4%; Pred. No. 1.8e-81;  
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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QY 2 AGCTCAGCAGCTCTCCGCTGTCATCTGTGAGAGACAGAGTACCATTAATT 61
DB 80 AGATGACCCAGCTCTCCGCTGTCATCTGTGAGAGACAGAGTACCATTAATT 139
QY 62 GTGCGGAGTCTGAGGATTTAGCAGTTGGTTAGCTGGTATCAGCAAAACAGGAAAG 121
DB 140 GTGCGGAGTCTGAGGATTTAGCAGTTGGTTAGCTGGTATCAGCAAAACAGGAAAG 199
QY 122 CCCCTAACTCTGATCTATCTGATCAGTTGGCAAAAGGGGTCCCGTCAAGTTCA 181
DB 200 CACCTAAGCTCTGATCTATCTGATCAGTTGGCAAAAGGGGTCCCGTCAAGTTCA 259
QY 182 GCGGAGTCTGAGGATTTAGCAGTTGGTTAGCTGGTATCAGCAAAACAGGAAAG 241
DB 260 GTGCGGAGTCTGAGGATTTAGCAGTTGGTTAGCTGGTATCAGCAAAACAGGAAAG 319
QY 242 CTGCAACTTACTATTTGTCACAGGCTTAACAGTTTCCGTCACATTTGGCCAGGAAAC 301
DB 320 TTGCAACTTACTATTTGTCACAGGCTTAACAGTTTCCGTCACATTTGGCCAGGAAAC 379
QY 302 AGTGAATCAACGA 318
DB 380 AGCTGAGATCAACGA 396
```

## RESULT 13

AAZ22047  
ID AAZ22047 standard; DNA; 420 BP.

AC AAZ22047;

DT 24-NOV-1999 (first entry)

DE Nucleotide sequence of LC6G5.

XX Transgenic animal; heterologous antibody; hybridoma; B cell;

KW transgenic mouse; human heavy chain transgene; digoxin;

KW human light chain transgene; immortalized cell; immunoglobulin;

KW Shiga-like toxin; autoimmune disease; cancer; infectious disease;

KW transplant rejection; blood disorder; coagulation disorder; ss.

XX Synthetic.

OS

XX WO9945962-A1.

PN

XX 16-SEP-1999.

PD

XX 12-MAR-1999; 99WO-US005535.

PF

XX 13-MAR-1998; 98US-00042353.

PR

XX (GENP-) GENPHARM INT INC.

XX PA

XX Lonberg N, Fishwild DM, Ball WJ;

PI

XX WPI; 1999-551219/46.

DR

XX Novel transgenic non-human animals used to produce heterologous

PT antibodies.

XX

XX Example 42; Page 325-326; 484pp; English.

XX

CC The specification describes transgenic animals that are capable of

CC producing a heterologous antibody. The antibodies are isolated from a

CC hybridoma, comprising B cells, that is obtained from a transgenic mouse

CC having a genome comprising a human heavy chain transgene and a human

CC light chain transgene. The B cells are fused to immortalized cells

CC suitable for generating a hybridoma, which produces a detectable amount

CC of an immunoglobulin that specifically binds digoxin or Shiga-like

CC toxin. B cells from transgenic animals can be used to generate hybridomas

CC expressing monoclonal high affinity human sequence antibodies. Antibodies  
CC produced from the transgenic animals of the invention can be used to  
CC treat human diseases, e.g. autoimmune diseases, cancer, infectious  
CC disease, transplant rejection, blood disorders such as coagulation  
CC disorders and other diseases. The present sequence is used in the course  
CC of the invention

XX Sequence 420 BP; 98 A; 116 C; 98 G; 108 T; 0 U; 0 Other;

SQ

Query Match 89.1%; Score 283.4; DB 2; Length 420;

Best Local Similarity 93.4%; Pred. No. 1.8e-81;

Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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QY 2 AGCTCAGCAGCTCTCCGCTGTCATCTGTGAGAGACAGAGTACCATTAATT 61
DB 80 AGATGACCCAGCTCTCCGCTGTCATCTGTGAGAGACAGAGTACCATTAATT 139
QY 62 GTGCGGAGTCTGAGGATTTAGCAGTTGGTTAGCTGGTATCAGCAAAACAGGAAAG 121
DB 140 GTGCGGAGTCTGAGGATTTAGCAGTTGGTTAGCTGGTATCAGCAAAACAGGAAAG 199
QY 122 CCCCTAACTCTGATCTATCTGATCAGTTGGCAAAAGGGGTCCCGTCAAGTTCA 181
DB 200 CACCTAAGCTCTGATCTATCTGATCAGTTGGCAAAAGGGGTCCCGTCAAGTTCA 259
QY 182 GCGGAGTCTGAGGATTTAGCAGTTGGTTAGCTGGTATCAGCAAAACAGGAAAG 241
DB 260 GTGCGGAGTCTGAGGATTTAGCAGTTGGTTAGCTGGTATCAGCAAAACAGGAAAG 319
QY 242 CTGCAACTTACTATTTGTCACAGGCTTAACAGTTTCCGTCACATTTGGCCAGGAAAC 301
DB 320 TTGCAACTTACTATTTGTCACAGGCTTAACAGTTTCCGTCACATTTGGCCAGGAAAC 379
QY 302 AGTGAATCAACGA 318
DB 380 AGCTGAGATCAACGA 396
```

## RESULT 14

AAZ78825  
ID AAT78825 standard; DNA; 3819 BP.

AC AAT78825;

DT 23-JAN-1998 (first entry)

DE Kappa light chain plasmid pLC65.

XX Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;

KW transgenic; mouse; CD4; antibody; autoimmune; inflammatory;

KW transplant rejection; immunoglobulin; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9713852-A1.

PN

XX 17-APR-1997.

PD

XX 10-OCT-1996; 96WO-US016433.

PF

XX 10-OCT-1995; 95US-00544404.

PR

XX (GENP-) GENPHARM INT INC.

XX PA

XX Lonberg N, Kay RM;

PI

XX WPI; 1997-235886/21.

DR

XX Novel anti-CD4 antibody produced by transgenic mice - used in the

PT treatment of auto-immune disease etc.

XX

XX Example 42; Page 266-268; 396pp; English.

XX

XX A novel composition has been developed which comprises an immunoglobulin  
CC (Ig) having an affinity constant (Ka) of at least 2 multiply 1000000000 M<sup>-1</sup>  
CC -1 for binding to a predetermined human antigen. The present sequence  
CC represents the kappa light chain plasmid pKCG5 which includes the kappa  
CC constant region and polyadenylation site. Anti- CD4 antibodies may be  
CC used in therapeutic and diagnostic applications, especially for the  
CC treatment of human diseases. These antibodies reduce activity of CD4  
CC cells and reduce undesirable autoimmune reactions, inflammatory response  
CC and transplant rejection. Transgenic animals are capable of producing  
CC heterologous antibodies of multiple isotypes by undergoing isotype  
CC switching. These animals produce a first Ig type that is necessary for  
CC antigen-stimulated B-cell maturation and can switch to encode and produce  
CC one or more subsequent heterologous isotypes.  
XX  
XX Sequence 3819 BP, 947 A, 1015 C, 912 G, 945 T, 0 U, 0 Other;

Query Match	89.1%	Score 283.4	DB 2	Length 3819
Best Local Similarity	93.4%	Pred. No. 4.3e-81		
Matches 296	Conservative 0	Mismatches 21	Indels 0	Gaps 0

QY	2	AGCTCAGCCAGATCTCACTCTCCGGTCTGCACTGTGAGAGACAGATGACATTAAGTT	61
Db	2513	AGATGACCAGTCTCATCTTCCGGTCTGCATCTGTGAGAGACAGATGACATTAAGTT	2572
QY	62	GTCCGGCGCAGTCAGGGATTATAGCACTGGTTAGCTGGTATTACGAGAAACCGAGGAAG	121
Db	2573	GTCCGGCGCAGTCAGGATATATAGCACTGGTATTAGCTGGTATTCAGGATAAACCGAGTAAAG	2633
QY	122	CCCCATAAATCTCTGATCTATTTCTGCATCCAGTTTGCAAAAGTGGGTCCCGTCAAGTTTCA	181
Db	2633	CACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGTGTCCCATCAAGTTTCA	2692
QY	182	GCGGCAGTGGATCTGGGACAAATTTCACTCTACCATACGACGCTGCAGCTGAAAGTT	241
Db	2693	GCGGAAGTGGATCTGGGACAAATTTCACTCTACCATACGACGCTGCAGCTGAAAGTT	2755
QY	242	CTGCAACTACTATATTGTCAACAGGCTAAACAGTTTCCGTACACTTTTGGCCAGGAGACCA	301
Db	2753	TTGCAACTTATCTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTACGAGACCA	2812
QY	302	AGGTGGAATCAAAACA 318	
Db	2813	AGCTGAGATCAAAACA 2829	

RESULT 15	
AAV39266	
ID	AAV39266 standard; DNA; 3819 BP.
XX	
AC	AAV39266;
XX	
DT	18-DEC-1998 (first entry)
XX	
DE	Plasmid pLC6G5 nucleotide sequence.
XX	
KW	Transgenic animal; human heterologous antibody; transgene;
KW	isotype switching; neutrophil efflux; reperfusion injury; CD4 binding
KW	autoimmune response; inflammatory response; transplant rejection;
KW	acid induced lung injury; acute adult respiratory distress syndrome;
KW	ARDS; vasculitis; septic shock; allergic reaction; asthma;
XX	cystic fibrosis; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
FN	W09824884-A1.
XX	
PD	11-JUN-1998.
XX	
PE	01-DEC-1997; 97MO-US021803.
XX	
PR	02-DEC-1996; 96US-00758417.

XX (GENP-) GENPHARM INT.  
PA  
XX  
XX  
PI Lonberg N, Kay RM;  
XX  
DR WPI; 1998-333306/29.

PT Hybridoma producing antibody specific for interleukin-8 - used to prevent  
PT efflux of neutrophils from vasculature, and treat reperfusion injury.  
XX  
PS Example 42, Page 317-319; 452pp; English.

The present sequence represents a plasmid, pLC665, which contains a synthetic kappa light chain sequence (created using oligonucleotide AA939244-65). This synthetic sequence differs from natural sequences in that strings of repeated oligonucleotides are interrupted (to facilitate oligonucleotide synthesis and PCR amplification), optimal translation initiation sites are incorporated and HindIII sites were engineered upstream of the translation initiation sites. The plasmid is used in the construction of minigenes for expression of Igkappa anti-CD4 antibodies, in the transgenic mouse of the invention. The specification describes transgenic non-human animals, especially a mouse, which are capable of producing a human heterologous antibodies of multiple isotypes by undergoing isotype switching. The transgenic animals have human heavy and light chain transgenes. The transgenes are capable of functionally rearranging a heterologous diversity (D) gene in a variable-diversity-junction (V-D-J) recombination. The transgenes include a heavy chain transgene comprising at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (Ig) light chain transgene comprises at least one V and J gene segment and one constant region gene segment. The gene segments are heterologous to the transgenic animal. The antibody can be used to prevent efflux of neutrophils from vasculature. It can also be used to treat reperfusion injury. CD4 binding antibodies are used to reduce undesirable autoimmune reactions, inflammatory responses and rejection of transplanted organs. The, anti-IL-8 antibodies can reduce tissue damage and prolong survival in animal models of acute adult respiratory distress syndrome (ARDS) and acid induced lung injury. The anti-IL-8 antibodies can also be used for the treatment of vasculitis, septic shock, allergic reactions (e.g. asthma) and cystic fibrosis

Sequence	3819 BP,	947 A,	1015 C,	912 G,	945 T,	0 U,	0 Other,
Query Match	89.1%,	Score 283.4,	DB 2,	Length 3819,			
Best Local Similarity	93.4%,	Pred. No. 4.3e-81,					
Matches 296,	Conservative 0,	Mismatches 21,	Indels 0,	Gaps 0,			

QY	2	AGCTCAGCACTCTCCACTCTTCGCGTCTGGATCTGTAGGAGACAGAGTCAACATTACTT	61
Db	2513	AGATGACCCCACTCTCCACTCTTCGCGTCTGGATCTGTAGGAGACAGAGTCAACATTACTT	2572
QY	62	GTCCGGCGAGTCCAGGGATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACGAGGAAAG	121
Db	2573	GTCCGGCGCAGTCCAGGATTATTAGCAGCTGGTTAGCCTGGTATCAGCAGTAAACGAGGTTAAAG	2632
QY	122	CCCCTAATCTCTGATCTATTCTGATCAGATTGCAAAAGGGGTCCCGTCAAGGTCA	181
Db	2633	CACCTTAGCTCTCTGATCTATTCTGATCAGATTGCAAAAGGGGTGCCCATCAAGTTCA	2692
QY	182	GCGCAGTGGATCTGGGACAGATTTCACTTCACCATCAGCAGCGCTGCAGCTGAAGTT	241
Db	2693	GCGGAAAGTGGATCTGGGACAGATTTCACTTCACCATCAGCAGCGCTGCAGCTGAAGTT	2752
QY	242	CTGCACATTAATATTGTTCAACAGGCTTAACAGTTTCCCGTACACTTTTGCCAGGGGACCA	301
Db	2753	TTGCACTTAATATTGTTCAACAGGCTTAATATTTCCTGACACTTTTGCTCAGGGAACA	2812
QY	302	AGGTGGAAATCAAAACA	318
Db	2813	AGCTGAGATCAAAACA	2829

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	291.4	91.6	974	22	US-10-800-250-29
5	288.2	90.6	711	21	US-10-910-901-11
6	286.8	90.2	321	21	US-10-727-155-121
7	286.4	90.1	632	21	US-10-714-079C-4

8	286.2	90.0	322	17	US-10-309-762-224	Sequence 224, App
9	284.6	89.5	322	21	US-10-638-265-75	Sequence 75, Appl
10	284.6	89.5	711	21	US-10-910-901-3	Sequence 3, Appl
11	283.6	89.2	387	21	US-10-893-576-1	Sequence 1, Appl
12	281.8	88.6	705	17	US-10-292-088-23	Sequence 23, Appl
13	280.8	88.3	728	9	US-09-844-684-15	Sequence 15, Appl
14	280.8	88.3	728	14	US-10-040-244-15	Sequence 15, Appl
15	280.8	88.3	728	19	US-10-693-629-63	Sequence 63, Appl
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17	280.2	88.1	705	17	US-10-292-088-47	Sequence 47, Appl
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35	275.6	86.7	321	20	US-10-482-630-84	Sequence 84, Appl
36	275.4	86.6	384	20	US-10-723-860-2996	Sequence 2996, Ap
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38	275	86.5	322	17	US-10-309-762-215	Sequence 215, Ap
39	275	86.5	322	17	US-10-309-762-228	Sequence 228, Ap
40	275	86.5	322	17	US-10-309-762-238	Sequence 238, Ap
41	275	86.5	322	18	US-10-269-711-8	Sequence 8, Appl
42	275	86.5	322	19	US-10-684-109-8	Sequence 8, Appl
43	274	86.2	321	19	US-10-703-714-7	Sequence 7, Appl
44	274	86.2	321	19	US-10-703-714-7	Sequence 7, Appl
45	274	86.2	321	19	US-10-703-714-15	Sequence 15, Appl

## ALIGNMENTS

RESULT 1  
US-10-027-725a-6  
; Sequence 6, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027, 725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259, 436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 318  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-027-725a-6

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RESULT 2  
US-09-859-053-29  
; Sequence 29, Application US/09859053  
; Patent No. US20020102658A1  
; GENERAL INFORMATION:  
; APPLICANT: Tezuka, Takashi  
; APPLICANT: Tezuka, Katsunari  
; APPLICANT: Hori, No. US20020102658A1uaki  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND  
; FILE REFERENCE: 06501-079001  
; CURRENT APPLICATION NUMBER: US/09/859,053  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: JP 2001-99508  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-147116  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 4.0  
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; TYPE: DNA  
; ORGANISM: Homo sapiens  
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; LOCATION: (39)...(746)  
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; LOCATION: (750)...(974)  
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; LOCATION: (39)...(104)  
US-09-859-053-29

Query Match 91.6%; Score 291.4; DB 9; Length 974;  
Best Local Similarity 95.0%; Pred. No. 2.7e-85;  
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
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Db 112 AGATGACCCAGATCTTCATCTTCCGTCTGCATCTGTGAGAGACAGAGTACCATTAATCTT 171  
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Qy 122 CCCCTTAACCTCTGATCTATTTCTGCATCCAGTTTGCAAGTGGGGTCCGTCAGAGTTCA 181  
Db 232 CCCCTTAACCTCTGATCTATTTCTGCATCCAGTTTGCAAGTGGGGTCCGTCAGAGTTCA 291  
Qy 182 GCGGAGTGGATCTGGGAGCAGATTTCAGTCTCAGATCAGCAGAGCTGAGAGCTGAAGATT 241  
Db 292 GCGGAGTGGATCTGGGAGCAGATTTCAGTCTCAGATCAGCAGAGCTGAGAGCTGAAGATT 351

Qy 242 CTGCACTTACTATTTGTCACAGGCTTACAGTTTCCGTCACATTTTGGCCAGGGGACC 301  
Db 352 TTGCACTTACTATTTGTCACAGGCTTACAGTTTCCGTCACATTTTGGCCAGGGGACC 411  
Qy 302 AAGGTGAATCAACGA 318  
Db 412 AAGGTGAATCAACGA 428

RESULT 3  
US-10-625-105-29  
; Sequence 29, Application US/10625105  
; Publication No. US20040180052A1  
; GENERAL INFORMATION:  
; APPLICANT: Tezuka, Takashi  
; APPLICANT: Tezuka, Katsunari  
; APPLICANT: Hori, Nobuaki  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND  
; FILE REFERENCE: 06501-079001  
; CURRENT APPLICATION NUMBER: US/10/625,105  
; CURRENT FILING DATE: 2003-07-22  
; PRIOR APPLICATION NUMBER: US/09/859,053  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: JP 2001-99508  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-147116  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 974  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (1)...(38)  
; NAME/KEY: CDS  
; LOCATION: (39)...(746)  
; NAME/KEY: 3'UTR  
; LOCATION: (750)...(974)  
; NAME/KEY: sig\_peptide  
; LOCATION: (39)...(104)  
US-10-625-105-29

Query Match 91.6%; Score 291.4; DB 19; Length 974;  
Best Local Similarity 95.0%; Pred. No. 2.7e-85;  
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
Qy 2 AGCTCAGCAGATCTTCATCTTCCGTCTGCATCTGTGAGAGACAGAGTACCATTAATCTT 61  
Db 112 AGATGACCCAGATCTTCATCTTCCGTCTGCATCTGTGAGAGACAGAGTACCATTAATCTT 171  
Qy 62 GTGGGGAGTCAGGGATTATAGCAGTTGATTAGCTGTGATCAGCAGAAACAGGGAAG 121  
Db 172 GTGGGGAGTCAGGGATTATAGCAGTTGATTAGCTGTGATCAGCAGAAACAGGGAAG 231  
Qy 122 CCCCTTAACCTCTGATCTATTTCTGCATCCAGTTTGCAAGTGGGGTCCGTCAGAGTTCA 181  
Db 232 CCCCTTAACCTCTGATCTATTTCTGCATCCAGTTTGCAAGTGGGGTCCGTCAGAGTTCA 291  
Qy 182 GCGGAGTGGATCTGGGAGCAGATTTCAGTCTCAGATCAGCAGAGCTGAGAGCTGAAGATT 241  
Db 292 GCGGAGTGGATCTGGGAGCAGATTTCAGTCTCAGATCAGCAGAGCTGAGAGCTGAAGATT 351  
Qy 242 CTGCACTTACTATTTGTCACAGGCTTACAGTTTCCGTCACATTTTGGCCAGGGGACC 301  
Db 352 TTGCACTTACTATTTGTCACAGGCTTACAGTTTCCGTCACATTTTGGCCAGGGGACC 411

OY 302 AGGTGAAATCAACGA 318  
Db 412 AGGTGAAATCAACGA 428

## RESULT 4

US-10-800-250-29  
; Sequence 29, Application US/10800250  
; Publication No. US20040146991A1  
; GENERAL INFORMATION:  
; APPLICANT: Tsuji, Takashi  
; APPLICANT: Tezuka, Katsunari  
; APPLICANT: Hori, Nobuaki  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALIUM AND  
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF  
; FILE REFERENCE: 06501-079001  
; CURRENT APPLICATION NUMBER: US/10/800,250  
; PRIOR FILING DATE: 2004-03-10  
; PRIOR APPLICATION NUMBER: US/09/859,053  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: JP 2001-99508  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-147116  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 974  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (1)...(38)  
; NAME/KEY: CDS  
; LOCATION: (39)...(746)  
; FEATURE:  
; NAME/KEY: 3'UTR  
; LOCATION: (750)...(974)  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: (39)...(104)  
US-10-800-250-29

Query Match 91.6%; Score 291.4; DB 22; Length 974;  
Best Local Similarity 95.0%; Pred. No. 2.7e-85;  
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 2 AGCTCAAGCAGTCTTCATCTTCCGTCTGCATCTGTGAGAGACAGAGTCAACATTAATT 61  
Db 112 AGATGACCCAGTCTTCATCTTCCGTCTGCATCTGTGAGAGACAGAGTCAACATTAATT 171  
OY 62 GTCCGGGAGTCAAGGAGTATTAAGCAGTGTAGCTGTATCAGAGAGAACCAAGGAAAG 121  
Db 172 GTCCGGGAGTCAAGGAGTATTAAGCAGTGTATTAAGCAGTGTATCAGAGAGAACCAAGGAAAG 231  
OY 122 CCCCTAACTCTGATCTATTTCTGATCAGTTTGCAAGTGGGGTCCCGTCAAGTTCA 181  
Db 232 CCCCTAACTCTGATCTATGTTGATCAAGTTTGCAAGTGGGGTCCCGTCAAGTTCA 291  
OY 182 GCGGAGTGTATCTGGGACAGATTTGATCTCAATCAGCAGGCTGCAAGCTGAAGTT 241  
Db 292 GCGGAGTGTATCTGGGACAGATTTGATCTCAATCAGCAGGCTGCAAGCTGAAGTT 351  
OY 242 CTGCAACTTACTATGTCAACAGGCTAAAGTTTCCCGTCAAGTTTGCCGAGGAGCA 301  
Db 352 TTGCAACTTACTATGTCAACAGGCTAAAGTTTCCCGTCAAGTTTGCCGAGGAGCA 411  
OY 302 AGGTGAAATCAACGA 318  
Db 412 AGGTGAAATCAACGA 428

## RESULT 5

US-10-910-901-11  
; Sequence 11, Application US/10910901  
; Publication No. US20050054019A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHAUD, NEIL R., et al.  
; TITLE OF INVENTION: ANTIBODIES TO C-MET  
; FILE REFERENCE: ABX-PP5  
; CURRENT APPLICATION NUMBER: US/10/910,901  
; PRIOR FILING DATE: 2004-08-03  
; PRIOR APPLICATION NUMBER: US 60/492,432  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 11  
; LENGTH: 711  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-910-901-11

Query Match 90.6%; Score 288.2; DB 21; Length 711;  
Best Local Similarity 94.3%; Pred. No. 2.8e-84;  
Matches 299; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 2 AGCTCAAGCAGTCTTCATCTTCCGTCTGCATCTGTGAGAGACAGAGTCAACATTAATT 61  
Db 74 AGATGACCCAGTCTTCATCTTCCGTCTGCATCTGTGAGAGACAGAGTCAACATTAATT 133  
OY 62 GTCCGGGAGTCAAGGAGTATTAAGCAGTGTAGCTGTATCAGAGAGAACCAAGGAAAG 121  
Db 134 GTCCGGGAGTCAAGGAGTATTAAGCAGTGTAGCTGTATCAGAGAGAACCAAGGAAAG 193  
OY 122 CCCCTAACTCTGATCTATTTCTGATCAGTTTGCAAGTGGGGTCCCGTCAAGTTCA 181  
Db 194 CCCCTAACTCTGATCTATGTTGATCAAGTTTGCAAGTGGGGTCCCGTCAAGTTCA 253  
OY 182 GCGGAGTGTATCTGGGACAGATTTGATCTCAATCAGCAGGCTGCAAGCTGAAGTT 241  
Db 254 GCGGAGTGTATCTGGGACAGATTTGATCTCAATCAGCAGGCTGCAAGCTGAAGTT 313  
OY 242 CTGCAACTTACTATGTCAACAGGCTAAAGTTTCCCGTCAAGTTTGCCGAGGAGCA 301  
Db 314 TTGCAACTTACTATGTCAACAGGCTAAAGTTTCCCGTCAAGTTTGCCGAGGAGCA 373  
OY 302 AGGTGAAATCAACGA 318  
Db 374 AGGTGAAATCAACGA 390

## RESULT 6

US-10-727-155-121  
; Sequence 121, Application US/10727155  
; Publication No. US20050049402A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. Babcock  
; APPLICANT: Jaepal S. Kang  
; APPLICANT: Orlit Foord  
; APPLICANT: Larry Green  
; APPLICANT: Xiao Feng  
; APPLICANT: Scott Klakamp  
; APPLICANT: Mary Haak-Frendescho  
; APPLICANT: Palaniswami Rathanaswami  
; APPLICANT: Craig Pigott  
; APPLICANT: Meina Liang  
; APPLICANT: Rozanne Lee  
; APPLICANT: Kathy Manchulenko  
; APPLICANT: Raffaella Paggioli  
; APPLICANT: Giorgio Senaldi  
; APPLICANT: Qiaojuan Jane Su  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
; FACTOR AND USES THEREOF

FILE REFERENCE: AGENIX 073A  
CURRENT APPLICATION NUMBER: US/10/727,155  
CURRENT FILING DATE: 2003-12-02  
PRIOR APPLICATION NUMBER: 60/430729  
PRIOR FILING DATE: 2002-12-02  
NUMBER OF SEQ ID NOS: 320  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 121  
LENGTH: 321  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-727-155-121

Query Match 90.2%; Score 286.8; DB 21; Length 321;  
Best Local Similarity 94.6%; Pred. No. 6.7e-84;  
Matches 297; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTCCGGTCTGCATCTGTGAGAGACAGAGTCAACATTAATT 61  
DB 8 AGATGACCCAGTCTCCATCTCCGGTCTGCATCTGTGAGAGACAGAGTCAACATTAATT 67  
QY 62 GTCGGGCGAGTCAAGGATTAAGAGTTGTTAGCTGTATCAGAGAAACAGGGAAG 121  
DB 68 GTCGGGCGAGTCAAGGATTAAGAGTTGTTAGCTGTATCAGAGAAACAGGGAAG 127  
QY 122 CCCCCTAACTCTGATCTATCTGATCAGATTGGCAAGTGGGGTCCCTCAAGTTCA 181  
DB 128 CCCCCTAACTCTGATCTATCTGATCAGATTGGCAAGTGGGGTCCCTCAAGTTCA 187  
QY 182 GCGGAGTGTATCTGGGACAGATTTCAGTCTCACCATCAGAGCCTGAGCCTGAAGTT 241  
DB 188 GCGGAGTGTATCTGGGACAGATTTCAGTCTCACCATCAGAGCCTGAGCCTGAAGTT 247  
QY 242 CTGCAACTTACTATGTCAACAGGCTAACAGTTCCCTGACACTTTTGGCCAGGGGACCA 301  
DB 248 TTGCAAGTACTATTTGTCAACAGGCTAACAGTTCCCTGAGCCTGAGCCTGAAGTTCA 307  
QY 302 AGGTGGAATCAAA 315  
DB 308 AGGTGGAATCAAA 321

RESULT 7  
US-10-714-079C-4  
Sequence 4, Application US/10714079C  
Publication No. US20050014931A1  
GENERAL INFORMATION:  
APPLICANT: PIROFSKI, LISE-ANNE  
APPLICANT: ZHONG, ZHAOJING  
TITLE OF INVENTION: HUMAN ANTIPNEUMOCOCCAL ANTIBODIES FROM NON-HUMAN  
FILE REFERENCE: ABX-AEI CON  
CURRENT APPLICATION NUMBER: US/10/714,079C  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: PCT/US02/18363  
PRIOR FILING DATE: 2002-05-16  
PRIOR APPLICATION NUMBER: 60/291,492  
PRIOR FILING DATE: 2001-05-16  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 632  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-714-079C-4

Query Match 90.1%; Score 286.4; DB 21; Length 632;  
Best Local Similarity 94.9%; Pred. No. 1.1e-83;  
Matches 296; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 7 ACGAGTCTCCATCTCCGTCGTCTGCATCTGTGAGAGACAGAGTCAACATTAATTGTGG 66  
DB 7 ACGAGTCTCCATCTCCGTCGTCTGCATCTGTGAGAGACAGAGTCAACATTAATTGTGG 66

DB 12 ACGAGTCTCCATCTCCGTCGTCTGCATCTGTGAGAGACAGAGTCAACATTAATTGTGG 71  
QY 67 GCGAGTCAAGGATTAAGAGTTGTTAGCTGTATCAGAGAAACAGGGAAGCCCTT 126  
DB 72 GCGAGTCAAGGATTAAGAGTTGTTAGCTGTATCAGAGAAACAGGGAAGCCCTT 131  
QY 127 AAACCTCGATCTATTTGTGATCAGATTGGCAAGTGGGGTCCCGTCAAGGTTAGGGGC 186  
DB 132 AAGCTCTGATCTATGTTGATCCGTTGCAAGTGGGGTCCCATCAAGGTTAGCGGC 191  
QY 187 AGTGAATCTGGGACAGATTTCAGTCTCACCATCAGAGCCTGAGCCTGAAGATTCTGCA 246  
DB 192 AGTGAATCTGGGACAGATTTCAGTCTCACCATCAGAGCCTGAGCCTGAAGATTCTGCA 251  
QY 247 ACTTACTATTTGTCAACAGGCTTAACAGTTTCCCTGACACTTTTGGCCAGGGGACCAAGTGG 306  
DB 252 ACTTACTATTTGTCAACAGGCTTAACAGTTTCCCTGACAGTTCGCGCCAAAGGACCAAGTGG 311  
QY 307 GAATCAACGA 318  
DB 312 GAATCAACGA 323

RESULT 8  
US-10-309-762-224  
Sequence 224, Application US/10309762  
Publication No. US20040018198A1  
GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Polt, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX  
FILE REFERENCE: AGENIX .027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 224  
LENGTH: 322  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-309-762-224

Query Match 90.0%; Score 286.2; DB 17; Length 322;  
Best Local Similarity 94.3%; Pred. No. 1.1e-83;  
Matches 297; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTCCGGTCTGCATCTGTGAGAGACAGAGTCAACATTAATT 61  
DB 8 AGATGACCCAGTCTCCATCTCCGGTCTGCATCTGTGAGAGACAGAGTCAACATTAATT 67  
QY 62 GTCGGGCGAGTCAAGGATTAAGAGTTGTTAGCTGTATCAGAGAAACAGGGAAG 121  
DB 68 GTCGGGCGAGTCAAGGATTAAGAGTTGTTAGCTGTATCAGAGAAACAGGGAAG 127  
QY 122 CCCCCTAACTCTGATCTATCTGATCAGATTGGCAAGTGGGGTCCCTCAAGTTCA 181  
DB 128 CCCCCTAACTCTGATCTATCTGATCAGATTGGCAAGTGGGGTCCCTCAAGTTCA 187  
QY 182 GCGGAGTGTATCTGGGACAGATTTCAGTCTCACCATCAGAGCCTGAGCCTGAAGTT 241  
DB 188 GCGGAGTGTATCTGGGACAGATTTCAGTCTCACCATCAGAGCCTGAGCCTGAAGTT 247  
QY 242 CTGCAACTTACTATGTCAACAGGCTTAACAGTTTCCCTGACACTTTTGGCCAGGGGACCA 301  
DB 248 TTGCAAGTACTATTTGTCAACAGGCTTAACAGTTTCCCTGACACTTTGCGCCCTGAAGTTCA 307  
QY 302 AGGTGGAATCAAA 316  
DB 302 AGGTGGAATCAAA 316



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Db          308 AAGTGATATCAAC 322

RESULT 9
US-10-638-265-75
; Sequence 75, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Poltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; TITLE OF INVENTION: HORMONE (PTH) AND USES THEREOF
; FILE REFERENCE: ABGENIX.092A
; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-638-265-75

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Query Match	89.5%;	Score 284.6;	DB 21;	Length 322;
Best Local Similarity	94.0%;	Pred. No. 3.5e-83;		
Matches 296;	Conservative	0;	Mismatches 19;	Indels 0;
				Gaps 0;

Oy	2	AGCTCAGCAGAGCTCCATCTTCCGATGTCGATCTGTAGGAGACAGAGTACCATTA	61
Db	8	AGATACCCAGATCTCCATCTTCCGATCTGTAGGAGACAGAGTACCATTA	67
Oy	62	GTCCGGCCGATCAGGGTATTATAGCAGTTGGTGTAGCCTGTATCAGCAGAAAC	121
Db	68	GTCCGGCCGATCAGGGTATTATAGCAGTTGGTGTAGCCTGTATCAGCAGAAAC	127
Oy	122	CCCCTAACTCCTGATCTATTCTGCATCCAGTTTGAAAGTGGGGTCCCGTCAAGTTCA	181
Db	128	CCCCTAAAGTCTGTATCTATGCTGCATCATTTTAAAGTGGGGTCCCGTCAAGTTCA	187
Oy	182	GGCGCAGTGTGATCTGGGACAGATTTAAGTCTCACCATCAGCAGCCTGCAGCTGAA	241
Db	188	GGCGCAGTGTGATCTGGGACAGATTTAAGTCTCACCATCAGCAGCCTGCAGCTGAA	247
Oy	242	CTGCACCTTACTATTTGTCAACAGGCTTAAACAGTTTCCCGTACATTTTGGCAGGGACCA	301
Db	248	TTGCAACTTACTATTTGTCAACAGGCTTAAACAGTTTCCCGTACATTTTGGCAGGGACCA	307
Oy	302	AGTGGAAATCAAAAC	316
Db	308	AAGTGATATCAAAAC	322

```

US-10-910-901-3
RESULT 10
US-10-910-901-3
; Sequence 3, Application US/10910901
; Publication NO. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO C-WET
; FILE REFERENCE: ABX-PFS
; CURRENT APPLICATION NUMBER: US/10/910,901
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-910-901-3

```

	Query Match	Best Local Similarity	89.5%: Score 284.6; DB 21; Length 711;
	Matches 296; Conservative 1;	Mismatches 20; Indels 0; Gaps 0;	
QY	2 AGCTCAGCAGCTCTCATCTTCCGTGCTCGATCTGAGAGACAGATCCATACCTT	61	
DB	74 AGATGACCAAGTCTCCATCTTCCGTGCTCGATCTGAGAGACAGATCCATACCTT	133	
QY	62 GTGCGGCGAGTCAGGGTATTAGCAGTTGGTTAGCTGGTATCAGCAGAAACAGAGGAAG	121	
DB	134 GTGCGGCGAGTCAGGGTATTAAACCTGGTTAGCTGGTATCAGCAGAAACAGAGGAAG	193	
QY	122 CCCCTAAACTCTGATCTATTCTGCATCCAGTTTGCAAAAGTGGGTCCCGTCAAGTTCA	181	
DB	194 CCCCTAAACTCTGATCTATTCTGCATCCAGTTTGCAAAAGTGGGTCCCGTCAAGTTCA	253	
QY	182 GCGGCAGTGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGAGCCTGGAAGTT	241	
DB	254 GCGGCAGTGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGAGCCTGGAAGTT	313	
QY	242 CTGCAACTTACTATTGTGCAAGGCTAACAGTTTCCGTACACTTTTGGCCAGGGAGACA	301	
DB	314 TTGCAACTTACTATTGTGCAAGGCTAACAGATTTCCCTCACTTTGGCGGAGGGAGACA	373	
QY	302 AGGTGAATCAACGA 318		
DB	374 AGGTGAATCAACGA 390		

RESULT 11  
US-10-893-576-1

```

/ Sequence 1, Application US/10893576
/ Publication No. US20050118643A1
/ GENERAL INFORMATION:
/ APPLICANT: BURGESS, TERESA L.
/ APPLICANT: COXON, ANGELA
/ APPLICANT: GREEN, LARRY L.
/ APPLICANT: ZHANG, KE
/ TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCTE GROWTH FACTOR
/ FILE REFERENCE: 06843.0051-00000
/ CURRENT APPLICATION NUMBER: US/10/893.576
/ CURRENT FILING DATE: 2004-07-16
/ PRIOR APPLICATION NUMBER: US 60/488,661
/ PRIOR FILING DATE: 2003-07-18
/ NUMBER OF SEQ ID NOS: 194
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 1
/
/ LENGTH: 387
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic HGF 1.24.1 Light
/ US-10-893-576-1

```

Query Match	89.2%;	Score 283.6;	DB 21;	Length 387;
Best Local Similarity	93.9%;	Pred. No. 7.9e-83;		
Matches 295; Conservative	0;	Mismatches 19;	Indels 0;	Gaps 0

QY	2	AGCTCAGCAGCTCCATCTTCCGTCGTGCATCTGTAGAGACAGATCCACATACCT	61
Db	74	AGATACCCAGTCTTCATCTTCCGTCTGCATCTGTAGAGACAGATCACCATCATCTT	133
QY	62	GTCCGGCAGTCAGGGTATTAGCAATTGTTAGCTGTATCAGCAGAAACGAGGAAG	121
Db	134	GTCCGGCAGTCAGGGTATTAGCAGCTGTTAGCTGTATCAGCAGAAACGAGGAAG	193
QY	122	CCCTTAACTCTGATCTATTCTGATCTCACTTTGCAAAAGTGGTCCCGTTAAAGTTCA	181
Db	194	CCCTTAACTCTGATCTATTGATGAGCATCAGTTTGCAAAAGTGGTCCCATCAAGTTCTG	253
QY	162	GCGGAGTGTCTGGGACAGATTTCACTTCACATCAGCAGCTTGACCTGAAGATT	241

Db 254 GCGGACGTGATCTGGACAGATTTCACCTCCACATCAGACGCTGACGCTGAAGATT 313  
Qy 242 CTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCGCTACATTTTGGCCAGGGAAACA 301  
Db 314 TTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCGCTACATTTTGGCCAGGGAAACA 373  
Qy 302 AGGTGAATCAAA 315  
Db 374 AGGTGAATCAAA 387

## RESULT 12

US-10-292-088-23  
; Sequence 23, Application US/10292088  
; Publication No. US200321100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 705  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-292-088-23

Query Match 88.6%; Score 281.8; DB 17; Length 705;  
Best Local Similarity 93.1%; Pred. No. 3.6e-82;  
Matches 295; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 2 AGCTCAGCAGTCTCCATCTTCCGTCTGTCATCTGAGAGACAGAGTCAACATACTT 61  
Db 68 AGATGACCCAGTCTCCATCTTCCGTCTGTCATCTGAGAGAGAGATCAACATACTT 127  
Qy 62 GTCGGGAGAGTCAAGGATTTAGCAGTTGCTTGGTATTCAGCAAAACAGGAAAG 121  
Db 128 GTCGGGAGAGTCAAGGATTTAGCAGTTGCTTGGTATTCAGCAAAACAGGAAAG 187  
Qy 122 CCCCTAACTCCTGATCTATCTGCATCAGTTTGCAGAGTGGGGTCCGCTCAAGTTCA 181  
Db 188 CCCCTAACTCCTGATCTATCTGCATCAGTTTGCAGAGTGGGGTCCGCTCAAGTTCA 247  
Qy 182 GCGGACGTGATCTGGACAGATTTCAGTTCACCATCAGACGCTGACGCTGAAGATT 241  
Db 248 GCGGACGTGATCTGGACAGATTTCAGTTCACCATCAGACGCTGACGCTGAAGATT 307  
Qy 242 CTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCGCTACATTTTGGCCAGGGAAACA 301  
Db 308 TTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCGCTACATTTTGGCCAGGGAAACA 367  
Qy 302 AGGTGAATCAAA 318  
Db 368 AGGTGAATCAAA 384

## RESULT 13

US-09-844-684-15  
; Sequence 15, Application US/09844684  
; Patent No. US20020142358A1  
; GENERAL INFORMATION:  
; APPLICANT: GEMINI SCIENCE, INC.  
; APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY  
; TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME  
; FILE REFERENCE: 21286/0276339

; CURRENT APPLICATION NUMBER: US/09/844,684  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,601  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 728  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-844-684-15

Query Match 88.3%; Score 280.8; DB 9; Length 728;  
Best Local Similarity 93.0%; Pred. No. 7.8e-82;  
Matches 294; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 2 AGCTCAGCAGTCTCCATCTTCCGTCTGTCATCTGAGAGACAGAGTCAACATACTT 61  
Db 132 AGATGACCCAGTCTCCATCTTCCGTCTGTCATCTGAGAGAGAGATCAACATACTT 191  
Qy 62 GTCGGGAGAGTCAAGGATTTAGCAGTTGCTTGGTATTCAGCAAAACAGGAAAG 121  
Db 192 GTCGGGAGAGTCAAGGATTTAGCAGTTGCTTGGTATTCAGCAAAACAGGAAAG 251  
Qy 122 CCCCTAACTCCTGATCTATCTGCATCAGTTTGCAGAGTGGGGTCCGCTCAAGTTCA 181  
Db 252 CCCCTAACTCCTGATCTATCTGCATCAGTTTGCAGAGTGGGGTCCGCTCAAGTTCA 311  
Qy 182 GCGGACGTGATCTGGACAGATTTCAGTTCACCATCAGACGCTGACGCTGAAGATT 241  
Db 312 GCGGACGTGATCTGGACAGATTTCAGTTCACCATCAGACGCTGACGCTGAAGATT 371  
Qy 242 CTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCGCTACATTTTGGCCAGGGAAACA 301  
Db 372 TTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCGCTACATTTTGGCCAGGGAAACA 431  
Qy 302 AGGTGAATCAAA 317  
Db 432 AGGTGAATCAAA 447

## RESULT 14

US-10-040-244-15  
; Sequence 15, Application US/10040244  
; Publication No. US20030059427A1  
; GENERAL INFORMATION:  
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
; APPLICANT: FORCE, WALKER F.  
; APPLICANT: TAKAHASHI, NOBUAKI  
; APPLICANT: MIYAYAMA, TOSHITOMI  
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBODIES  
; FILE REFERENCE: 021286/0272501  
; CURRENT APPLICATION NUMBER: US/10/040,244  
; PRIOR FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: 60/200,601  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: PCT/US01/13672  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: 09/844,684  
; PRIOR FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent In Ver. 3.0  
; SEQ ID NO 15  
; LENGTH: 728  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-040-244-15

Query Match 88.3%; Score 280.8; DB 14; Length 728;  
Best Local Similarity 93.0%; Pred. No. 7.8e-82;  
Matches 294; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 2 AGCTCAGCAGTCTCCATCTTCCGTCTGTCATCTGAGAGACAGAGTCAACATACTT 61



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:42:26 ; Search time 88.6545 Seconds  
(without alignment)  
5869.253 Million cell updates/sec

Title: US-10-027-725A-5  
Perfect score: 318  
Sequence: 1 gagctcaccagctccatc.....ccaactgagatcaacga 318

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 240568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	276.4	86.9	321	US-09-240-274-102	Sequence 102, App
2	276.4	86.9	321	US-09-240-274-199	Sequence 109, App
3	273.2	85.9	321	US-09-240-274-107	Sequence 107, App
4	273.2	85.9	321	US-09-240-274-113	Sequence 113, App
5	273.2	85.9	321	US-09-240-274-201	Sequence 201, App
6	273.2	85.9	321	US-09-240-274-211	Sequence 211, App
7	273.2	85.9	321	US-09-240-274-218	Sequence 218, App
8	271.6	85.4	321	US-09-240-274-106	Sequence 106, App
9	271.6	85.4	321	US-09-240-274-205	Sequence 205, App
10	271.6	85.4	321	US-09-240-274-221	Sequence 221, App
11	271.6	85.4	321	US-09-240-274-222	Sequence 222, App
12	271.2	85.3	720	US-09-192-854-1	Sequence 1, App11
13	270	84.9	321	US-09-240-274-215	Sequence 215, App
14	270	84.9	321	US-09-240-274-217	Sequence 217, App
15	268.4	84.4	321	US-09-240-274-105	Sequence 105, App
16	268.4	84.4	714	US-09-472-087-62	Sequence 62, App1
17	265.2	83.4	321	US-09-240-274-109	Sequence 109, App
18	265.2	83.4	321	US-09-240-274-216	Sequence 216, App
19	263.6	82.8	321	US-09-240-274-207	Sequence 207, App
20	263.4	82.8	324	US-09-240-274-101	Sequence 101, App
21	263.4	82.8	324	US-09-240-274-112	Sequence 112, App
22	263.4	82.8	324	US-09-240-274-210	Sequence 210, App
23	262.4	82.5	451	US-09-472-087-50	Sequence 50, App1
24	262	82.3	321	US-09-240-274-104	Sequence 104, App
25	261.8	82.3	324	US-09-240-274-110	Sequence 110, App
26	261.8	82.3	324	US-09-240-274-206	Sequence 206, App
27	261.4	82.2	402	US-09-472-087-49	Sequence 49, App1

28	261.2	82.1	321	US-08-378-939-13	Sequence 13, App1
29	260.4	81.9	321	US-09-240-274-103	Sequence 103, App
30	260	81.8	672	US-09-456-090A-47	Sequence 47, App1
31	260	81.8	672	US-09-453-234-47	Sequence 47, App1
32	256.6	80.7	417	US-09-472-087-48	Sequence 48, App1
33	256.2	80.6	458	US-09-472-087-44	Sequence 44, App1
34	255.4	80.3	324	US-09-240-274-224	Sequence 224, App
35	254.8	80.1	318	US-08-844-215-20	Sequence 20, App
36	254	79.9	321	US-09-240-274-200	Sequence 200, App
37	254	79.9	321	US-09-240-274-213	Sequence 213, App
38	252.4	79.4	318	US-09-240-274-202	Sequence 202, App
39	250.8	78.9	318	US-09-240-274-208	Sequence 208, App
40	250.8	78.9	321	US-09-240-274-108	Sequence 108, App
41	250.8	78.9	321	US-09-240-274-114	Sequence 114, App
42	250.8	78.9	321	US-09-240-274-203	Sequence 203, App
43	247.2	77.7	705	US-08-488-376-16	Sequence 16, App1
44	247.2	77.7	705	US-08-634-223-16	Sequence 16, App1
45	247.2	77.7	705	US-08-634-224-16	Sequence 16, App1

## ALIGNMENTS

RESULT 1					
US-09-240-274-102					
Sequence 102, Application US/09240274					
Patent No. 6255455					
GENERAL INFORMATION:					
APPLICANT: Siegel, Donald L.					
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL					
FILE REFERENCE: 09596-4202					
CURRENT FILING DATE: 1999-01-29					
EARLIER APPLICATION NUMBER: 60/081,380					
EARLIER FILING DATE: 1998-04-10					
EARLIER APPLICATION NUMBER: 60/028,550					
EARLIER FILING DATE: 1996-10-11					
NUMBER OF SEQ ID NOS: 224					
SOFTWARE: PatentIn Ver. 2.0					
SEQ ID NO: 102					
LENGTH: 321					
TYPE: DNA					
ORGANISM: Homo sapiens					
FEATURE:					
OTHER INFORMATION: anti-Rh(D) chain 102					
US-09-240-274-102					
Query Match					
Best Local Similarity 91.8%; Pred. No. 1.5e-85;					
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;					
QY	1	GAGCTACCCAGTCTCCATCTCTCTGCTGTGAGAGACAGTACATCACT	60		
DB	4	GAGCTACCCAGTCTCCATCTCTCTGCTGTGAGAGACAGTACATCACT	63		
QY	61	TGCGGGCACTGAGATTAAGCACTTAATTAATGATTCGCGGAACCGGGAG	120		
DB	64	TGCGGGCACTGAGATTAAGCACTTAATTAATGATTCGCGGAACCGGGAA	123		
QY	121	GCCCTAAGCTCTGATCTGATGATTCATTCATTTGCAAGTGGGGTCCATCAG	180		
DB	124	GCCCTAAGCTCTGATCTGATGATTCATTCATTTGCAAGTGGGGTCCATCAG	183		
QY	181	AGTGGAGTGTGATTCGAGACAGTTCATCTTCACCAATCTGCAACTGAGAC	240		
DB	184	AGTGGAGTGTGATTCGAGACAGTTCATCTTCACCAATCTGCAACTGAGAT	243		
QY	241	TTTGCAAGTACTGATCTGCAAGTTCATCTTATTAACCTTGGCGCTGGGAGC	300		
DB	244	TTTGCAAGTACTGATCTGCAAGTTCATCTTATTAACCTTGGCGCTGGGAGC	303		
QY	301	AACTGAGATCAACGA 318			

Db 304 AAGCTGGAATCAACGA 321

## RESULT 2

US-09-240-274-199  
Sequence 199, Application US/09240274  
Patent No. 6255455

GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEROF

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 199

LENGTH: 321

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH13

US-09-240-274-199

Query Match 85.9%; Score 276.4; DB 3; Length 321;  
Best Local Similarity 91.8%; Pred. No. 1.5e-85;

Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 GAGCTACCCAGTCTCCATCTCTGCTGCTCTGTGAGAGACAGAGTCCATCACT 60  
Db 4 GAGCTACCCAGTCTCCATCTCTGCTGCTCTGTGAGAGACAGAGTCCATCACT 63

Qy 61 TGCCTGGCAGCTCAGAGTATTAGCACTATTAAATTGATATCAGCAGAAACCGGGAG 120  
Db 64 TGCCTGGCAGCTCAGAGTATTAGCACTATTAAATTGATATCAGCAGAAACCGGGAG 123

Qy 121 GCCCTAAGCTCCGATCTGTAGTGCATCCAAATTTGCAAGTGGGTCCTCCATCGAGTTC 180  
Db 124 GCCCTAAGCTCCGATCTGTAGTGCATCCAAATTTGCAAGTGGGTCCTCCATCGAGTTC 183

Qy 181 AGTGGCAGTGTATGGGACAGAGTTCACTCTCAACATTCGCAACTGGAAGAC 240  
Db 184 AGTGGCAGTGTATGGGACAGAGTTCACTCTCAACATTCGCAACTGGAAGAT 243

Qy 241 TTTCGAAGTTACTGTCTGCAAGAGTTACCTTATATACCTTGGCCCTGGGACC 300  
Db 244 TTTCGAAGTTACTGTCTGCAAGAGTTACCTTATATACCTTGGCCCTGGGACC 303

Qy 301 AAAGTGAGATCAACGA 318  
Db 304 AAGCTGAGATCAACGA 321

## RESULT 3

US-09-240-274-107  
Sequence 107, Application US/09240274  
Patent No. 6255455

GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEROF

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 107  
LENGTH: 321  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain 107

## US-09-240-274-107

Query Match 85.9%; Score 273.2; DB 3; Length 321;  
Best Local Similarity 91.2%; Pred. No. 2e-84;

Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 GAGCTACCCAGTCTCCATCTCTGCTGCTCTGTGAGAGACAGAGTCCATCACT 60  
Db 4 GAGCTACCCAGTCTCCATCTCTGCTGCTCTGTGAGAGACAGAGTCCATCACT 63

Qy 61 TGCCTGGCAGCTCAGAGTATTAGCACTATTAAATTGATATCAGCAGAAACCGGGAG 120  
Db 64 TGCCTGGCAGCTCAGAGTATTAGCACTATTAAATTGATATCAGCAGAAACCGGGAG 123

Qy 121 GCCCTAAGCTCCGATCTGTAGTGCATCCAAATTTGCAAGTGGGTCCTCCATCGAGTTC 180  
Db 124 GCCCTAAGCTCCGATCTGTAGTGCATCCAAATTTGCAAGTGGGTCCTCCATCGAGTTC 183

Qy 181 AGTGGCAGTGTATGGGACAGAGTTCACTCTCAACATTCGCAACTGGAAGAC 240  
Db 184 AGTGGCAGTGTATGGGACAGAGTTCACTCTCAACATTCGCAACTGGAAGAT 243

Qy 241 TTTCGAAGTTACTGTCTGCAAGAGTTACCTTATATACCTTGGCCCTGGGACC 300  
Db 244 TTTCGAAGTTACTGTCTGCAAGAGTTACCTTATATACCTTGGCCCTGGGACC 303

Qy 301 AAAGTGAGATCAACGA 318  
Db 304 AAGCTGAGATCAACGA 321

## RESULT 4

US-09-240-274-113  
Sequence 113, Application US/09240274  
Patent No. 6255455

GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEROF

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 113

LENGTH: 321

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain 113

US-09-240-274-113

Query Match 85.9%; Score 273.2; DB 3; Length 321;  
Best Local Similarity 91.2%; Pred. No. 2e-84;

Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 GAGCTACCCAGTCTCCATCTCTGCTGCTCTGTGAGAGACAGAGTCCATCACT 60  
Db 4 GAGCTACCCAGTCTCCATCTCTGCTGCTCTGTGAGAGACAGAGTCCATCACT 63

Qy 61 TGCCTGGCAGCTCAGAGTATTAGCACTATTAAATTGATATCAGCAGAAACCGGGAG 120

```
Db      64 TCCGGGCAAGTCAGAGCATTTAGCAGGATTTAAATTGATTCAGCAGAAACCGAGGAAA 123
Qy      121 GCGCCCTAAGCTCCGATCTGTAGTCATTCATTCATTCGAAAGTGGGTCCTCATCAGGTTTC 180
Db      124 GCGCCCTAAGCTCCGATCTGTAGTCATTCATTCGAAAGTGGGTCCTCATCAGGTTTC 183
Qy      181 AGTGGCAGTGGATCTGGGACAGATTCATCTCAACATCAGCAATCTGCAACTGAAAGAC 240
Db      184 AGTGGCAGTGGATCTGGGACAGATTCATCTCAACATCAGCAAGTCTGCAACTGAAAGAT 243
Qy      241 TTTCGAAGTACTACTGTCAACAGAGTTACACTTATATACCTTGCGCCCTGGGAGCC 300
Db      244 TTTCGAAGTACTACTGTCAACAGAGTTACCGTACCCCTCAGAGTTTGGCGGGGAGACC 303
Qy      301 AAAGTGAGATCAACGA 318
Db      304 AAGCTGAGATCAACGA 321
```

## RESULT 5

```
US-09-240-274-201
; Sequence 201, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 201
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-240-274-201
```

```
Query Match      85.9%; Score 273.2; DB 3; Length 321;
Best Local Similarity 91.2%; Pred. No. 2e-84;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
```

```
Qy      1 GAGCTCAACCCAGTCTCCATCTCCCTGCTGCTGTAGAGAGACAGATCCATCACT 60
Db      4 GAGCTCAACCCAGTCTCCATCTCCCTGCTGCTGTAGAGAGACAGATCCATCACT 63
Qy      61 TCCCGGCAAGTCAGAGTATTAGCACTATTAAATTGATTCAGCAGAAACCGGGGAAG 120
Db      64 TCCCGGCAAGTCAGAGATTTAGCAGCTATTAAATTGATTCAGCAGAAACCGGGGAAA 123
Qy      121 GCGCCCTAAGCTCCGATCTGTAGTCATTCATTCGAAAGTGGGTCCTCATCAGGTTTC 180
Db      124 GCGCCCTAAGCTCCGATCTGTAGTCATTCGAAAGTGGGTCCTCATCAGGTTTC 183
Qy      181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCAACATCAGCAATCTGCAACTGAAAGAC 240
Db      184 AGTGGCAGTGGATCTGGGACAGATTTCACTCAACATCAGCAAGTCTGCAACTGAAAGAT 243
Qy      241 TTTCGAAGTACTACTGTCAACAGAGTTACACTTATATACCTTGCGCCCTGGGAGCC 300
Db      244 TTTCGAAGTACTACTGTCAACAGAGTTACAGTACCCCTCAGAGTTTGGCGGGGAGACC 303
Qy      301 AAAGTGAGATCAACGA 318
Db      304 AAGCTGAGATCAACGA 321
```

## RESULT 6

```
US-09-240-274-211
; Sequence 211, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-240-274-211
```

```
Query Match      85.9%; Score 273.2; DB 3; Length 321;
Best Local Similarity 91.2%; Pred. No. 2e-84;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
```

```
Qy      1 GAGCTCAACCCAGTCTCCATCTCCCTGCTGCTGTAGAGAGACAGATCCATCACT 60
Db      4 GAGCTCAACCCAGTCTCCATCTCCCTGCTGCTGTAGAGAGACAGATCCATCACT 63
Qy      61 TCCCGGCAAGTCAGAGTATTAGCACTATTAAATTGATTCAGCAGAAACCGGGGAAG 120
Db      64 TCCCGGCAAGTCAGAGATTTAGCAGCTATTAAATTGATTCAGCAGAAACCGGGGAAA 123
Qy      121 GCGCCCTAAGCTCCGATCTGTAGTCATTCATTCGAAAGTGGGTCCTCATCAGGTTTC 180
Db      124 TCCCTAAGCTCCGATCTGTAGTCATTCGAAAGTGGGTCCTCATCAGGTTTC 183
Qy      181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCAACATCAGCAATCTGCAACTGAAAGAC 240
Db      184 AGTGGCAGTGGATCTGGGACAGATTTCACTCAACATCAGCAAGTCTGCAACTGAAAGAT 243
Qy      241 TTTCGAAGTACTACTGTCAACAGAGTTACACTTATATACCTTGCGCCCTGGGAGCC 300
Db      244 TTTCGAAGTACTACTGTCAACAGAGTTACAGTACCCCTCAGAGTTTGGCGGGGAGACC 303
Qy      301 AAAGTGAGATCAACGA 318
Db      304 AAGCTGAGATCAACGA 321
```

## RESULT 7

```
US-09-240-274-218
; Sequence 218, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
```





```
; Sequence 221, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-221

Query Match      85.4%; Score 271.6; DB 3; Length 321;
Best Local Similarity 90.9%; Pred. No. 7e-84;
Matches 289; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 GAGCTCACCAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 60
   |||||
DB 4 GAGCTCACCAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 63
   |||||

QY 61 TGCCGGGACAGTCTGAGTATTAGACCTATTAAATTGGATACAGAGAAACCGGGGAG 120
   |||||
DB 64 TGCCGGGACAGTCTGAGTATTAGACCTATTAAATTGGATACAGAGAAACCGGGGAA 123
   |||||

QY 121 GCCCTTAAGCTCTGATCTGTAGTCAATTTGGCAAATGGGGTCCCATCCAGTTTC 180
   |||||
DB 124 GCCCTTAAGCTCTGATCTGTAGTCAATTTGGCAAATGGGGTCCCATCCAGTTTC 183
   |||||

QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCACTGAAGAC 240
   |||||
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCACTGAAGAT 243
   |||||

QY 241 TTTCGAAGTCTACTCTGTCAACAGAGTTACACTTATATACCTTGGGCTGGGAGCC 300
   |||||
DB 244 TTTCGAAGTCTACTCTGTCAACAGAGTTACACTTATATACCTTGGGCTGGGAGCC 303
   |||||

QY 301 AAAGTGAATCAACGA 318
   |||||
DB 304 AAAGTGAATCAACGA 321
   |||||

RESULT 11
US-09-240-274-222
; Sequence 222, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-222

Query Match      85.4%; Score 271.6; DB 3; Length 321;
Best Local Similarity 90.9%; Pred. No. 7e-84;
Matches 289; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 GAGCTCACCAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 60
   |||||
DB 4 GAGCTCACCAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 63
   |||||

QY 61 TGCCGGGACAGTCTGAGTATTAGACCTATTAAATTGGATACAGAGAAACCGGGGAG 120
   |||||
DB 64 TGCCGGGACAGTCTGAGTATTAGACCTATTAAATTGGATACAGAGAAACCGGGGAA 123
   |||||

QY 121 GCCCTTAAGCTCTGATCTGTAGTCAATTTGGCAAATGGGGTCCCATCCAGTTTC 180
   |||||
DB 124 GCCCTTAAGCTCTGATCTGTAGTCAATTTGGCAAATGGGGTCCCATCCAGTTTC 183
   |||||

QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCACTGAAGAC 240
   |||||
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCACTGAAGAT 243
   |||||

QY 241 TTTCGAAGTCTACTCTGTCAACAGAGTTACACTTATATACCTTGGGCTGGGAGCC 300
   |||||
DB 244 TTTCGAAGTCTACTCTGTCAACAGAGTTACACTTATATACCTTGGGCTGGGAGCC 303
   |||||

QY 301 AAAGTGAATCAACGA 318
   |||||
DB 304 AAAGTGAATCAACGA 321
   |||||

RESULT 12
US-09-192-854-1
; Sequence 1, Application US/09192854
; Patent No. 6698245
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian
; APPLICANT: Winter, Greg
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; EARLIER FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-192-854-1

Query Match      85.3%; Score 271.2; DB 4; Length 720;
Best Local Similarity 91.1%; Pred. No. 1.4e-83;
Matches 288; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2 AGCTCACCAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACTT 61
   |||||
DB 404 AGATGACCAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACTT 463
   |||||

QY 62 GCCGGGACAGTCTGAGTATTAGACCTATTAAATTGGTATCAGAGAAACCGGGGAGG 121
   |||||
DB 464 GCCGGGACAGTCTGAGTATTAGACCTATTAAATTGGTATCAGAGAAACCGGGGAGG 523
   |||||

QY 122 CCCCTTAAGCTCTGATCTGTAGTCAATTTGGCAAATGGGGTCCCATCCAGTTTC 181
   |||||
DB 524 CCCCTTAAGCTCTGATCTGTAGTCAATTTGGCAAATGGGGTCCCATCCAGTTTC 583
   |||||

QY 182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCACTGAAGCT 241
   |||||
DB 584 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCACTGAAGCT 643
   |||||
```

QY	Db	QY	Db
24	TTTCAAGTACTACTCTGTCACAGAGTTACACTACCTTATATACCTTGGGCCCCGGAGCA	302	AACGTGAGATCTAAACG 317
644	TTTCAACTACTACTCTGTCACAGAGTTACAGTACCCTTATACCTTCCGCGCAAGGACCA	704	AGGTGGAATCTAAACG 719

**RESULT 13**  
US-09-240-274-215  
; Sequence 215, Application US/09240274  
; Data: No. CCEFAE

```

1 TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
2
3 TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
4
5 FILE REFERENCE: 09596-4202
6
7 CURRENT APPLICATION NUMBER: US/09/240,274
8
9 CURRENT FILING DATE: 1999-01-29
10
11 EARLIER APPLICATION NUMBER: 60/081,380
12
13 EARLIER FILING DATE: 1998-04-10
14
15 EARLIER APPLICATION NUMBER: 60/028,550
16
17 EARLIER FILING DATE: 1996-10-11
18
19 NUMBER OF SEQ ID NOS: 224
20
21 SOFTWARE: PatentIn Ver. 2.0
22
23 SEQ ID NO 215
24
25 LENGTH: 321
26
27 TYPE: DNA
28
29 ORGANISM: Homo sapiens
30
31 FEATURE:
32
33 OTHER INFORMATION: anti-Rh(D) antibody clone SH46
34
35 US-09-240-274-215

```

Query Match	84.9%;	Score 270;	DB 3;	Length 321;
Best Local Similarity	90.6%;	Pred. No. 2.5e-83;		
Matches 288; Conservative	0;	Mismatches 30;	Indels 0;	Gaps 0;

OY	GAGGTACCCAGTCTCATCTCCGTCTGGCTCTGAGGAGACAGAGTACATCACT	60
Db	GAGCTACCCAGTCTCATCTCTCTGTGTGATCTGAGGAGACAGAGTACATCACT	63
OY	TGCGGGCAGCTCAGAGTATTAGCAGCTATTTAAATGGTATCAGCAAAAACGGGGAG	120
Db	TGCGGGCAGCTCAGTACATATTAGCAGCTATTTAAATGGTATCAGCAAAAACGGGGAAA	122
OY	GCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGTGGGTCCCATCAGGTTT	180
Db	GCCCTTAATCTCGATCTATGTGTGATTCAGTTGGCAAAAGTGGGTCCCATCAAGGTTT	183
OY	AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTTACCATCAGCATCTGCAACTTGAAGAC	240
Db	AGTGGCAGTGGATCTGGGACAGATTTCACTTCAACCATCAGCAGTCTGCAACTGTAAGAT	242
OY	TTTGGCAAGTTACTACTGTCAACAGAGTTACACTTAATATATCTTGGGCCCTGGGACC	300
Db	TTTGGCAACTACTACTGTCAACAGACTTACAGTTCCCTTACAGCATTTGGGCCCTGGGACC	303
OY	AAACTGGAGATCAAAACA 318	
Db	AAAGTGATATCAAAACA 321	

RESULT 14  
 US-09-240-274-217  
 : Sequence 217, Application US/09240274  
 : Patent No. 625545  
 : GENERAL INFORMATION:  
 : APPLICANT: Siegel, Donald L.  
 : TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLULOSE  
 : TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
 : FILE REFERENCE: 09596-4202

```

CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 217
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH48
US-09-240-274-217

Query Match      84.9%   Score 270:   DB 3:   Length 321,
Best Local Similarity 90.6%:   Pred No. 2.5e-83:
Matches 288: Conservative 0: Mismatches 30, Indels 0: Gaps 0:

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OTHER INFORMATION: anti-Rh(D) antibody clone SH48  
US-09-240-274-217

[illegible]

RESULT 15  
US-09-240-274-105  
; Sequence 105, Application US/09240274

; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
;

```

: CURRENT APPLICATION NUMBER: US/09/240,274
: CURRENT FILING DATE: 1999-01-29
: EARLIER APPLICATION NUMBER: 60/061,380
: EARLIER FILING DATE: 1998-04-10
: EARLIER APPLICATION NUMBER: 60/028,550
: EARLIER FILING DATE: 1996-10-11
: NUMBER OF SEQ ID NOS: 224
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 105
: LENGTH: 321
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: anti-Rh(D) chain I05
US-09-240-274-I05

```

Query Match 84.4%; Score 268.4; DB 3; Length 321;  
 Best Local Similarity 90.3%; Pred. No. 9e-83;  
 Matches 287; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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QY      1 GAGTCACCCAGTCTCCATCTCCCTGTCTGCTGTAGAGACAGAGTCAACCATCACT 60
      |||||||
Db      4 GAGTCACCCAGTCTCCATCTCCCTGTCTGCTGTAGAGACAGAGTCAACCATCACT 63
      |||||||
QY      61 TGCCTGGGACAGTCTGAGTATTAGACCTATTAAATTGATCAGAGAAAACCGGGAG 120
      |||||||
Db      64 TGCCTGGGACAGTCTGAGTATTAGACCTATTAAATTGATCAGAGAAAACCGGGAA 123
      |||||||
QY      121 GCCCTTAAGCTCCTGATCTGTAGTCAATCCAAATTGCAAAAGTGGGTCCCATCCAGGTTT 180
      |||||||
Db      124 GCCCTTAAGCTCCTGATCTGTAGTCAATCCAAATTGCAAAAGTGGGTCCCATCAAGGTTT 183
      |||||||
QY      181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCAATCTGCAACTGAAAGAC 240
      |||||||
Db      184 ACTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCAATCTGCAACTGAAAGAT 243
      |||||||
QY      241 TTGCAAGTACTACTGTCAACAGAGTTACACTTATATACCTTCGGGCTGGGACC 300
      |||||||
Db      244 TTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCAACGTTTCGGGCAAGGACC 303
      |||||||
QY      301 AAACGTGAGATCAACGA 318
      |||||||
Db      304 AAGTGAATCAACGA 321
      |||||||
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Search completed: July 27, 2005, 12:41:22  
Job time : 89.6545 secs

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## OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:15:56 ; Search time 1958.75 Seconds

(without alignments)  
6179.670 Million cell updates/sec

Title: US-10-027-725A-5

Perfect score: 318  
Sequence: 1 gagctcaccagctctcctc...ccaactggagatcaacgca 318Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hnc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	270.6	85.1	422	2	AM407904 UI-HF-BLO
2	270.6	85.1	1084	6	CB986592 AGENCOURT
3	269	84.6	493	2	AM405753 UI-HF-BLO
4	269	84.6	624	6	CD690145 EST6668 h
5	269	84.6	770	4	BG685444 602637305
6	269	84.6	797	6	CB987347 AGENCOURT
7	267.4	84.1	525	6	CD705928 EST22455
8	267.4	84.1	750	6	CB985395 AGENCOURT
9	265.8	83.6	431	2	AM406886 UI-HF-BLO
10	265.8	83.6	693	6	CD684441 EST1961 hu
11	265.8	83.6	799	6	CB984750 AGENCOURT
12	265.8	83.6	819	6	CB985931 AGENCOURT
13	265.8	83.6	864	4	BG548281 602575248
14	265.8	83.6	933	4	BQ899146 AGENCOURT
15	265.8	83.6	992	5	BQ708832 AGENCOURT
16	264.2	83.1	391	2	AM404992 UI-HF-BLO
17	264.2	83.1	447	2	AM405752 UI-HF-BLO
18	264.2	83.1	487	2	AM405301 UI-HF-BLO
19	264.2	83.1	498	6	CD684450 EST970 hu
20	264.2	83.1	499	6	CD685478 EST1998 h
21	264.2	83.1	608	2	AM404714 UI-HF-BLO
22	264.2	83.1	619	6	CD693603 EST10126
23	264.2	83.1	724	6	CB959008 AGENCOURT
24	264.2	83.1	745	6	CB958128 AGENCOURT

25	264.2	83.1	748	6	CB956867	CB956867 AGENCOURT
26	262.8	82.6	471	2	AM406294	AM406294 UI-HF-BLO
27	262.6	82.6	550	6	CD709957	EST26484
28	262.6	82.6	708	6	CB956923	CB956923 AGENCOURT
29	262.6	82.6	725	6	CB987519	CB987519 AGENCOURT
30	262.6	82.6	742	6	CB984723	CB984723 AGENCOURT
31	262.6	82.6	923	5	BQ882857	BQ882857 AGENCOURT
32	261.8	82.3	921	4	BG341239	BG341239 602463904
33	261.2	82.1	854	5	BX397739	BX397739
34	261	82.1	598	6	CD692150	EST8689 h
35	261	82.1	671	4	BM830977	BM830977 K-EST0104
36	261	82.1	684	4	BM769909	BM769909 K-EST0053
37	261	82.1	753	6	CB955708	CB955708 AGENCOURT
38	261	82.1	855	6	CB995312	CB995312 AGENCOURT
39	259.4	81.6	460	2	AM405906	AM405906 UI-HF-BLO
40	259.4	81.6	532	2	BM823145	BM823145 K-EST0094
41	259.4	81.6	566	2	AM406081	AM406081 UI-HF-BLO
42	259.4	81.6	743	6	CB957909	CB957909 AGENCOURT
43	259.4	81.6	754	6	CB986767	CB986767 AGENCOURT
44	259.4	81.6	762	6	CB958057	CB958057 AGENCOURT
45	259.4	81.6	793	6	CB987506	CB987506 AGENCOURT

## ALIGNMENTS

RESULT 1  
AM407904  
LOCUS  
DEFINITION  
UI-HF-BLO-add-a-01-0-UI.r2 NIH MGC\_37 Homo sapiens cDNA clone  
IMAGE:3061128 5', mRNA sequence.  
ACCESSION  
AM407904  
VERSION  
AM407904.1 GI:6926961  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 422)  
NIH-MGC http://mgs.nci.nih.gov/.  
NATIONAL INSTITUTE OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)  
UNPUBLISHED (1999)  
CONTACT: ROBERT STRAUSBERG, Ph.D.  
EMAIL: rgs@bbs-remail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNI at:  
www-bio.llnl.gov/bdip/image/image.html  
Seq primer: M13 Forward.  
Location/Qualifiers  
1..422  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3061128"  
/cistype="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LTI)"  
/clone\_id="NIH\_MGC\_37"  
/note="Vector: pRT3-Pac; Site 1: NotI; Site 2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonafido, Ph.D. and M. Bento Soares, Ph.D."

## FEATURES

source

ORIGIN  
Query Match 85.1%, Score 270.6; DB 2; Length 422;  
Best Local Similarity 90.9%; Pred. No. 9.2e-75;

Matches 288; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 2 AGCTACCCAGTCTCCATCTCCTCTGCTGTAAGAGACAGAGTCCATCACTT 61  
 Db AGATGACCCAGTCTCCATCTCCTCTGCTGTAAGAGAGAGTCCATCACTT 89  
 QY 62 GCGGGGACGTCAGAGTATAGACCTATTTAAATGGTATCAGCAGAAACCGGGGAAG 121  
 Db GCGGGGACGTCAGAGTATAGACCTATTTAAATGGTATCAGCAGAAACCGGGGAAG 149  
 QY 122 CCCCTAAGCTCTGATCTGATGATCAATTCATTTGCAAGTGGGGTCCCATCAGTTCA 181  
 Db CCCCTAAGCTCTGATCTGATGATCAATTCATTTGCAAGTGGGGTCCCATCAGTTCA 209  
 QY 182 GTGCACTGATCTGGGACAGAGTTCACCTCCATCAGCAATCTGCACTGAAGACT 241  
 Db GTGCACTGATCTGGGACAGAGTTCACCTCCATCAGCAATCTGCACTGAAGACT 269  
 QY 242 TTGCAATTAACCTGTCAGAGTTACCTATACCTTGGGCGCTGGAGCA 301  
 Db TTGCAATTAACCTGTCAGAGTTACCTATACCTTGGGCGCTGGAGCA 329  
 QY 302 AACTGAGATCAAAACA 318  
 Db 330 AGTGGAATCAAAACA 346

RESULT 2  
 LOCUS CB986592 1084 bp mRNA linear EST 01-MAY-2003  
 DEFINITION AGENCOURT 13567591 NIH\_MGC\_184 Homo sapiens cDNA clone  
 IMAGE:30326813 5', mRNA sequence.

ACCESSION CB986592  
 VERSION CB986592.1 GI:30281112  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1084)  
 NIH-MGC http://img.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov  
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.lnl.gov  
 Plate: NDCM134 row: n column: 06  
 High quality sequence stop: 330.

#### FEATURES

SOURCE

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 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:30326813"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_184"  
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site\_1:  
 SfiI (ggccatattggc); Site\_2: SfiI (ggccggccggc);  
 Library is oligo-dr primed and directionally cloned. cDNA  
 was prepared from a glandular pool of tissues from thyroid,  
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'  
 adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGCCATTATGCGC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCGGCGCGCATGCTG-3' (30) BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.38  
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones

ORIGIN  
 Query Match 85.1%; Score 270.6; DB 6; Length 1084;  
 Best Local Similarity 90.9%; Pred. No. 1.2e-74;  
 Matches 288; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

QY 2 AGCTACCCAGTCTCCATCTCCTCTGCTGTAAGAGACAGAGTCCATCACTT 61  
 Db AGATGACCCAGTCTCCATCTCCTCTGCTGTAAGAGAGAGTCCATCACTT 156  
 QY 62 GCGGGGACGTCAGAGTATAGACCTATTTAAATGGTATCAGCAGAAACCGGGGAAG 121  
 Db GCGGGGACGTCAGAGTATAGACCTATTTAAATGGTATCAGCAGAAACCGGGGAAG 216  
 QY 122 CCCCTAAGCTCTGATCTGATGATCAATTCATTTGCAAGTGGGGTCCCATCAGTTCA 181  
 Db CCCCTAAGCTCTGATCTGATGATCAATTCATTTGCAAGTGGGGTCCCATCAGTTCA 276  
 QY 182 GTGCACTGATCTGGGACAGAGTTCACCTCCATCAGCAATCTGCACTGAAGACT 241  
 Db GTGCACTGATCTGGGACAGAGTTCACCTCCATCAGCAATCTGCACTGAAGACT 336  
 QY 242 TTGCAATTAACCTGTCAGAGTTACCTATACCTTGGGCGCTGGAGCA 301  
 Db TTGCAATTAACCTGTCAGAGTTACCTATACCTTGGGCGCTGGAGCA 396  
 QY 302 AACTGAGATCAAAACA 318  
 Db 397 AACTGAGATCAAAACA 413

RESULT 3  
 LOCUS AM405753 493 bp mRNA linear EST 16-FEB-2000  
 DEFINITION UT-HF-B10-abp-a-02-0-UI.r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
 IMAGE:3057290 5', mRNA sequence.

ACCESSION AM405753  
 VERSION AM405753.1 GI:6924810  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 493)  
 NIH-MGC http://img.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: M.B. Soares Lab  
 cDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 www-bio.lnl.gov/bbrp/image/image.html  
 Seq primer: M13 forward

#### FEATURES

SOURCE

1..493  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3057290"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="lymph"  
 /issue\_type="lymph"  
 /cell\_type="germinal center B cells"  
 /cell\_line="MGC85"  
 /lab\_host="DH10B (LTI)"  
 /clone\_lib="NIH\_MGC\_37"  
 /note="Vector: p773-Pac; Site\_1: NotI; Site\_2: Eco RI;  
 Constructed from size fractionated cytoplasmic mRNA

(1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staedt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "

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Best Local Similarity 90.5%; Pred: No. 3.1e-14;
Matches 287: Conservative 0: Mismatches 30: Indels 0: Gaps 0:

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79 AGATGACCACTTCCATCTGTCATGAGAGACAGTCCATCACTT 13

Db 139 GCCGGCAAGTCAGAGCATTTAAATTGGTATCAGCAGAAACAGGGAAG 19

Db 199 CCCTAGCTCCTGATCTATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGTTCA 25

100

302 AACTGGAGATCAACGA 318

ACCESSION	CB690145
VERSION	CD690145.1
GT	GT:32210615

SOURCE	Homo sapiens (human)
1. <i>Chimpanzee</i>	
2. <i>Orangutan</i>	
3. <i>Gorilla</i>	
4. <i>Human</i>	

REFERENCE	1 (bases 1 to 624)
AUTHORS	Liu X -O    Zhou Y    Zhang L -I    Xu H    Chen H -K    Pan Z -G and

Cancer Center  
Sun Yat-sen University

FEATURES	Location/Qualifiers
source	1 62A

## ORIGIN

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62 GCCGGCAGTCAAGTATTAGCACCTATTTTAAATTGGTATCAGCAGAAACCGGGGAAAGG 121

QY 122 CCCCTAAGCTCCTGATCTGTAGTGCATCCAAATTGCAAGTGGGTCCTCATCCAGTTCA 181

182 GTGCAGTGGATCTGGGACAGAGTTCACCTCTCACCATCAGCAATCTGCCAACCTGAAGACT 241

1. The first part of the document is a list of 10 items, each consisting of a number followed by a description of a task or activity. The items are numbered 1 through 10.

421 AGCTGGAGATCAACGA 437

**DEFINITION** 602637305F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4765129 5',

ORGANISM Homo sapiens

**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

FEATURES	Location/Qualifiers
source	1-770

## ORIGIN

[illegible]

	Matches	287	Conservative	0	Mismatches	30	Indels	0	Gaps	0
QY	2	AGCTCA	CCCCAATCTTC	CACTCTCCCTGTCTGCTCTGTATG	AGACACAGAGTCA	CACATCACTT	61			
Db	80	AGATGACCCCACTTCC	CAACCTCCCTGTCTGTATG	AGAGACAGAGTCA	CCATCACTT	139				
QY	62	GCCGGGACGCTCAGAGTATTA	TGACCCATTTAAATTG	TATTCAGAGAAACCGGGGAAG	121					
Db	140	GCCGGACAGTCAAGAGAA	TTAGCACTATTTCAATTTG	TATTCAGAGAAACCGGGGAAG	199					
QY	122	CCCTTAAGCTCCTGATCTGT	AGTGATCCAAATTTG	CAAGTGGGGTCCCATCAAGTTCA	181					
Db	200	CCCTTAAGCTCCTGATCTGT	CTGTGATCCAAATTTG	CAAGTGGGGTCCCATCAAGTTCA	259					
QY	182	GTGSCAGTGATCTTGGGA	CAGAGTTCACTTTC	ACCATCAGCAATCTGCAACCTGAAAGCT	241					
Db	260	GTGSCAGTGATCTTGGGA	CAGAGTTTCACTTTC	ACCATCAGCAAGTCTGCAACCTGAAAGTT	319					
QY	242	TTTGCAAGTACTACTGTCA	CAGAGTTCACTACTT	TATATCTTTGGGCTTGGGACCA	301					
Db	320	TTTGCAACTTACTACTGTCA	CAGAGTTCAATTA	CCCTCCCACTTTGGGCTTGGGACCA	379					
QY	302	AACTGAGATCAAAACGA	318							
Db	380	AACTGAGATCAAAACGA	396							

RESULT	6
LOCUS	CB987347
DEFINITION	797 bp mRNA linear EST 01-MAY-2001
ACCESSION	CB987347
VERSION	CB987347
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 797) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaab@remail.nih.gov Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
AUTHORS	CNDA Library Preparation: CLONTECH Laboratories, Inc.
JOURNAL	CNDA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
COMMENT	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> Plate: NDGM13 row: h column: 21 High quality sequence stop: 437.

## FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30326300"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1db="NIH MGC 184"
/name="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggcgcatctggcc); Site_2: SfiI (ggcgccctggccg);
Library is oligo-dT primed and directionally cloned. cDNA
library was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCGCATATGGCC-3' and 3' adaptor sequence:
5'-ATTTCAGAGCGCGGGCGGCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones

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and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

[illegible]

RESULT 7	CD705928	525 bp	mRNA, linear	EST 25-JUN-2001
LOCUS	CD705928			
DEFINITION	EST224255 human nasopharynx Homo sapiens cDNA, mRNA sequence.			
ACCESSION	CD705928			
VERSION	CD705928.1	GI:32236558		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniota; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
AUTHORS	1 (bases 1 to 525) Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-X., Pan, Z.-G. and Zeng, Y.-X.			
TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Yixin Zeng Cancer Center Sun Yat-sen University 651 Dongfeng Road East, GuangZhou 510060, China Tel: 86-1380-9770-743 Fax: 86-20-8775-4506 Email: yxzeng@gzsums.edu.cn			
FEATURES	Location/Qualifiers			
Source	1..525			

FEATURES	SOURCE
Location/Qualifiers	1. 525
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/tissue_type="normal nasopharynx"
	/clone_lib="human nasopharynx"
	/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

Query Match	84.1%	Score 267.4;	DB 6;	Length 525;
Best Local Similarity	90.2%;	Pred. No. 1e-73;		
Matches 286;	Conservative 0;	Mismatches 31;	Indels 0;	Gaps 0.

QY 2 AGCTACCCCACTTCCATCTCTCCCTGTGTGCTCTGTAGAGACAGAGTCACCATCACTT 61

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Db 124 AGATGACCCAGTCTCCATCCCTGCTGTCATCTGTAGAGACAGATCAACATCACTT 183  
 Qy 62 GCCGGGACGCTCAGAGATTATGACACCTATTAAATTTGATACAGAAAACCGGGGAAG 121  
 Db 184 GCCGGGACGCTCAGAGATTATGACACCTATTAAATTTGATACAGAAAACCGGGGAAG 243  
 Qy 122 CCCCTAAGCTCCGATCTGTAGTGCATCCAAATTTGCAAGTGGGGTCCCATCCAGTTCA 181  
 Db 244 CCCCTAAGCTCCGATCTGTAGTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTCA 303  
 Qy 182 GTGCGATGATCTGGGACAGAGTTTCACTCTCACCATCAGCAATCTGCACCTGAAGACT 241  
 Db 304 GTGCGATGATCTGGGACAGAGTTTCACTCTCACCATCAGCAATCTGCACCTGAAGACT 363  
 Qy 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTGGGCGCTGGACCA 301  
 Db 364 TTGCAAGTTACTACTGTCAACAGAGTTACAGTTACAGTCCGTTACACTTTGGCCAGGACCA 423  
 Qy 302 AACTGAGATCAAAACA 318  
 Db 424 AACTGAGATCAAAACA 440

RESULT 8  
 LOCUS CB985395  
 DEFINITION AGENCOURT 13643437 NIH\_MGC\_184 Homo sapiens cDNA clone  
 IMAGE:3028513 5', mRNA sequence.

ACCESSION CB985395  
 VERSION CB985395.1 GI:30279919  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: NDCM139 row: e column: 02  
 High quality sequence stop: 555.

# FEATURES

Location/Qualifiers  
 1..750  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3028513"  
 /lab\_host="DH10B (TI phage-resistant)"  
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site\_1: SfiI (ggccataggc); Site\_2: SfiI (ggccggccggc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 84.1%; Score 267.4; DB 6; Length 750;  
 Best Local Similarity 90.2%; Pred. No. 1.1e-73;  
 Matches 286; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
 Qy 2 AGCTACCCAGTCTCCATCCCTGCTGTCATCTGTAGAGACAGATCAACATCACTT 61  
 Db 104 AGATGACCCAGTCTCCATCCCTGCTGTCATCTGTAGAGACAGATCAACATCACTT 163  
 Qy 62 GCCGGGACGCTCAGAGATTATGACACCTATTAAATTTGATACAGAAAACCGGGGAAG 121  
 Db 164 GCCGGGACGCTCAGAGATTATGACACCTATTAAATTTGATACAGAAAACCGGGGAAG 223  
 Qy 122 CCCCTAAGCTCCGATCTGTAGTGCATCCAAATTTGCAAGTGGGGTCCCATCCAGTTCA 181  
 Db 244 CCCCTAAGCTCCGATCTGTAGTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTCA 283  
 Qy 182 GTGCGATGATCTGGGACAGAGTTTCACTCTCACCATCAGCAATCTGCACCTGAAGACT 241  
 Db 284 GTGCGATGATCTGGGACAGAGTTTCACTCTCACCATCAGCAATCTGCACCTGAAGACT 343  
 Qy 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTGGGCGCTGGACCA 301  
 Db 344 TTGCAAGTTACTACTGTCAACAGAGTTACAGTTACAGTCCGTTACACTTTGGCCAGGACCA 403  
 Qy 302 AACTGAGATCAAAACA 318  
 Db 404 AACTGAGATCAAAACA 420

RESULT 9  
 LOCUS AM406886  
 DEFINITION UT-HF-BLD-ady-b-06-0-UT\_r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
 IMAGE:3061499 5', mRNA sequence.

ACCESSION AM406886  
 VERSION AM406886.1 GI:6925943  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Eco RI site shown at the beginning of the sequence.  
 Tissue Procurement: Louis M. Staedt, M.D., Ph.D.  
 CDNA Library Preparation: M.B. Soares Lab  
 CDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
 www-bio.llnl.gov/bdrrp/image/image.html  
 Seq primer: M13 Forward.

# FEATURES

Location/Qualifiers  
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 /organism="Homo sapiens"  
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 /clone="IMAGE:3061499"  
 /tissue\_type="lymph"  
 /cell\_type="germinal center B cells"  
 /lab\_host="DH10B (LTI)"  
 /clone\_1bp="NIH\_MGC\_37"  
 /note="Vector: pT7T3-Pac; Site\_1: NotI; Site\_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staedt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 83.6%; Score 265.8; DB 2; Length 431;  
Best Local Similarity 89.9%; Pred. No. 3.1e-73;  
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGCTCACCAGCTCCCATCCCTCCCTGCTGCTGATAGAGACAGATCCATCACTT 61  
DB 67 AGATGACCCAGCTCCCATCCCTCCCTGCTGCTGATAGAGACAGATCCATCACTT 126  
QY 62 GCCGGGACGTCAGAGTATTAGACCTATTAAATGGTATCAGAGAAACCGGGGAAG 121  
DB 127 GCCGGGACGTCAGAGTATTAGAGCTTTTAAATGGTATCAGAGAAACCGGGGAAG 186  
QY 122 CCCCTAAGCTCTGATCTGATAGTCATCAATTTTGAAAGTGGGGTCCCATCAGTTCA 181  
DB 187 CCCCTAAGCTCTGATCTGATAGTCATCAATTTTGAAAGTGGGGTCCCATCAGTTCA 246  
QY 182 GTGGCAGTGTATCTGGGACAGAGTTCATCTCAGCATACAGATCTGCAACTGTAAGACT 241  
DB 247 GTGGCAGTGTATCTGGGACAGAGTTCATCTCAGCATACAGATCTGCAACTGTAAGACT 306  
QY 242 TTGCAAGTATTACTGTGCAAGAGTTACACTACCTTATATACCTTGGCCCTGGAGCA 301  
DB 307 TTGCAAGTATTACTGTGCAAGAGTTACACTACCTTATATACCTTGGCCCTGGAGCA 366  
QY 302 AACTGAGATCAACGA 318  
DB 367 AGGTGAGATCAACGA 383

RESULT 10  
CD684441 693 bp mRNA linear EST 25-JUN-2003  
LOCUS E87961 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD684441  
VERSION CD684441.1 GI:32199435  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and  
Zeng,Y.-X.  
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gzsun.edu.cn.

FEATURES  
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library from southern Chinese"

ORIGIN  
Query Match 83.6%; Score 265.8; DB 6; Length 693;  
Best Local Similarity 89.9%; Pred. No. 3.6e-73;  
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGCTCACCAGCTCCCATCCCTCCCTGCTGCTGATAGAGACAGATCCATCACTT 61  
DB 127 AGATGACCCAGCTCCCATCCCTCCCTGCTGCTGATAGAGACAGATCCATCACTT 186  
QY 62 GCCGGGACGTCAGAGTATTAGACCTATTAAATGGTATCAGAGAAACCGGGGAAG 121

DB 187 GCCGGGACCCAGAGATTAGCCGCTATTAAATGGTATCAGAGAAACCGGGGAAG 246  
QY 122 CCCCTAAGCTCTGATCTGATAGTCATCAATTTTGAAAGTGGGGTCCCATCAGTTCA 181  
DB 247 CCCCTAAGCTCTGATCTGATAGTCATCAATTTTGAAAGTGGGGTCCCATCAGTTCA 306  
QY 182 GTGGCAGTGTATCTGGGACAGAGTTCATCTCAGCATACAGATCTGCAACTGTAAGACT 241  
DB 307 GTGGCAGTGTATCTGGGACAGAGTTCATCTCAGCATACAGATCTGCAACTGTAAGACT 366  
QY 242 TTGCAAGTATTACTGTGCAAGAGTTACACTACCTTATATACCTTGGCCCTGGAGCA 301  
DB 367 TTGCAAGTATTACTGTGCAAGAGTTACACTACCTTATATACCTTGGCCCTGGAGCA 426  
QY 302 AACTGAGATCAACGA 318  
DB 427 AGGTGAGATCAACGA 443

RESULT 11  
CB984750 799 bp mRNA linear EST 01-MAY-2003  
LOCUS AGENCOURT\_13574990 NIH\_MGC\_184 Homo sapiens cDNA clone  
DEFINITION IMAGE:30326373 5', mRNA sequence.  
ACCESSION CB984750  
VERSION CB984750.1 GI:30279274  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NIH-MGC http://mgc.ncl.nih.gov/  
TITLE NIH-MGC  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-rc@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palokovits  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: NDCM133 row: k column: 22  
High quality sequence stop: 412.

FEATURES  
source  
1..799  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30326373"  
/lab\_host="DH10B (TI phage-resistant)"  
/clone\_lib="NIH\_MGC\_184"  
/note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site 1:  
SfiI (ggccatcatgccc); Site 2: SfiI (ggccctccggcc);  
Library is oligo-dT primed and directionally cloned. cDNA  
was prepared from a glandular pool of tissues from thyroid,  
parathyroid, adrenal, cortex and pineal gland. 5' adaptor  
adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTATAGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCCGCGCGCCGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.38  
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 83.6%; Score 265.8; DB 6; Length 799;  
Best Local Similarity 89.9%; Pred. No. 3.8e-73;  
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

ORIGIN	CA. Note: this is a NIH_MGC Library."
Query Match	83.6%; Score 265.8; DB 6; Length 819;
Best Local Similarity	89.9%; Pred. No. 3.8e-73;
Matches 285; Conservative	0; Mismatches 32; Indels 0; Gaps 0;
Db	104 AGATGACCCGAGTCTCCATCTCCCTGCTCTGATGAGGAGACAGATCACTACTT 61
Qy	2 AGCTCACCCGAGTCTCCATCTCCCTGCTCTGATGAGGAGACAGATCACTACTT 61
Db	104 AGATGACCCGAGTCTCCATCTCCCTGCTCTGATGAGGAGACAGATCACTACTT 163
Qy	62 GCCGGGCACTCAGATGATTAGCAACCTATTAAATTGGTATCAGCAAAAACGGGGAAG 121
Db	164 GCCGGGCACTCAGATGATTAGCAACCTATTAAATTGGTATCAGCAAAAACGGGGAAG 223
Qy	122 CCCCTAAGCTCTGATCTGATGATCAATCAATTTGGCAAAGTGGGCTCCCATCAGTTCA 181
Db	224 CCCCTAAGCTCTGATCTGATGATCAATCAATTTGGCAAAGTGGGCTCCCATCAGTTCA 283
Qy	182 GTGGCAATGATCTGGGACAGATTCCTCTCAACCATCAGCAAACTTCGAACCTGAAGCT 241
Db	284 GTGGCAATGATCTGGGACAGATTCCTCTCAACCATCAGCAAACTTCGAACCTGAAGCT 343
Qy	242 TTGCAAGTACTCTGTCACACAGATGATCACTACTATATACCTTGGGCTGGGACCA 301
Db	344 TTGCAAGTACTCTGTCACACAGATGATCACTACTATATACCTTGGGCTGGGACCA 403
Qy	302 AACTGAGATCAAAACA 318
Db	404 AGGTGAAATCAAAACA 420
RESULT 13	
BG548281	864 bp mRNA linear EST 04-APR-2001
LOCUS	602575248F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4703483 5',
DEFINITION	mRNA sequence.
ACCESSION	BG548281
VERSION	BG548281.1 GI:13546946
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Bukacinski, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 864)
TITLE	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.
	Email: cgabds-remail.nih.gov
	Tissue Procurement: CLONTECH Laboratories, Inc.
	cDNA Library Preparation: CLONTECH Laboratories, Inc.
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LNLN at:
	http://image.lnl.gov
	Plate: L1CM1541 row: p column: 12
	High quality sequence stop: 726.
FEATURES	Location/Qualifiers
Source	1..864
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAGE:4703483"
	/lab_host="DH10B (TI phage-resistant)"
	/clone_id="NIH_MGC_77"
	/note="Organ: Lung; Vector: pDNR-LIB (Clontech); Site: 1;
	SfiI (ggcgccctcgagc); Site 2: SfiI (ggccatctggcc); 5' and
	3' adaptors were used in cloning as follows: 5' adaptor
	sequence: 5'-CACGGCATTATGCGC-3' and 3' adaptor sequence
	5'-ATTGTAGAGCGCGGCGCGCGCATG-3' (30) BN-3' (where B = A,
	C, or G and N = A, C, G, or T). Average insert size 1.9

kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 83.6%; Score 265.8; DB 4; Length 864;  
Best Local Similarity 89.9%; Pred. No. 3.9e-73;  
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGCTACCCAGTCTCCATCCCTGCTGCTGTGAGAGACAGATCCATCACTT 61  
DB 100 AGATGACCCAGTCTCCATCCCTGCTGCTGTGAGAGACAGATCCATCACTT 159  
QY 62 GCCGGGACGTCAGAGATTAGACCTATTAAATGGTATCAGAGAAACCGGGGAAG 121  
DB 160 GCCGGGACGTCAGAGATTAGACCTATTAAATGGTATCAGAGAAACCGGGGAAG 219  
QY 122 CCCCTAAGCTCTGATCTGTAGTCATCAATTTGGCAAGTGGGGTCCCATCCAGTTCA 181  
DB 220 CCCCTAAGCTCTGATCTGTAGTCATCAATTTGGCAAGTGGGGTCCCATCCAGTTCA 279  
QY 182 GTGCGAGTGAATCTGGGACAGAGTTCACTCTCAGCATCAGCAATCTGCACCTGAAGACT 241  
DB 280 GTGCGAGTGAATCTGGGACAGATTTCACTCTCAGCATCAGCAATCTGCACCTGAAGACT 339  
QY 242 TTGCAAGTTACTACTGTCAACAGATTACCTACTTATATACCTTGCGCCCTGGGACCA 301  
DB 340 TTGCAAGTTACTACTGTCAACAGATTACCTACTTATATACCTTGCGCCCTGGGACCA 399  
QY 302 AACTGAGATCAACGA 318  
DB 400 CGGTGAGATCAACGA 416

RESULT 14  
LOCUS B0899146 933 bp mRNA linear EST 16-AUG-2002  
DEFINITION AGENCOURT\_8585624 NIH\_MGC\_113 Homo sapiens CDNA clone IMAGE:6302530  
5', mRNA sequence.  
ACCESSION B0899146  
VERSION B0899146.1 GI:22291160  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 933)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: LNCM2520 row: c column: 11  
High quality sequence start: 9  
High quality sequence stop: 589.  
Location/Qualifiers  
1..933  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6302530"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_113"  
/note="Organ: spleen; Vector: pOT87; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned

FEATURES  
SOURCE

into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGAG(G). Library constructed by Ling Hong in the  
Laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

## ORIGIN

Query Match 83.6%; Score 265.8; DB 5; Length 933;  
Best Local Similarity 89.9%; Pred. No. 4e-73;  
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGCTACCCAGTCTCCATCCCTGCTGCTGTGAGAGACAGATCCATCACTT 61  
DB 101 AGATGACCCAGTCTCCATCCCTGCTGCTGTGAGAGACAGATCCATCACTT 160  
QY 62 GCCGGGACGTCAGAGATTAGACCTATTAAATGGTATCAGAGAAACCGGGGAAG 121  
DB 161 GCCGGGACGTCAGAGATTAGACCTATTAAATGGTATCAGAGAAACCGGGGAAG 220  
QY 122 CCCCTAAGCTCTGATCTGTAGTCATCAATTTGGCAAGTGGGGTCCCATCCAGTTCA 181  
DB 221 CCCCTAAGCTCTGATCTGTAGTCATCAATTTGGCAAGTGGGGTCCCATCCAGTTCA 280  
QY 182 GTGCGAGTGAATCTGGGACAGAGTTCACTCTCAGCATCAGCAATCTGCACCTGAAGACT 241  
DB 281 GTGCGAGTGAATCTGGGACAGAGTTCACTCTCAGCATCAGCAATCTGCACCTGAAGACT 340  
QY 242 TTGCAAGTTACTACTGTCAACAGATTACCTACTTATATACCTTGCGCCCTGGGACCA 301  
DB 341 TTGCAAGTTACTACTGTCAACAGATTACCTACTTATATACCTTGCGCCCTGGGACCA 400  
QY 302 AACTGAGATCAACGA 318  
DB 401 AGGTGAATCAACGA 417

RESULT 15  
LOCUS B0708832 992 bp mRNA linear EST 16-JUL-2002  
DEFINITION AGENCOURT\_8353479 NIH\_MGC\_113 Homo sapiens CDNA clone IMAGE:6279561  
5', mRNA sequence.  
ACCESSION B0708832  
VERSION B0708832.1 GI:21847731  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 992)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: LNCM2469 row: f column: 10  
High quality sequence start: 5  
High quality sequence stop: 696.  
Location/Qualifiers  
1..992  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6279561"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_113"

FEATURES  
SOURCE

/note="Organ: spleen; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

## ORIGIN

Query Match 83.6%; Score 265.8; DB 5; Length 992;

Best Local Similarity 89.9%; Pred. No. 4e-73; Mismatches 32; Indels 0; Gaps 0;

Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY	2	AGCTACCCAGTCTTCATCTCCCTGTCGCTCTGTAGAGACAGAGTCAACATCACTT	61
Db	105	AGATGACCCAGTCTTCATCTCCCTGTCGCTCTGTAGAGACAGAGTCAACATCACTT	164
QY	62	GCCGGGACGTCAGAGTATTAGCACCTATTAAATTGGTATCAGCAGAAACCGGGGAAG	121
Db	165	GCCGGGCAAGTCAGAGTATTAGCACTTTTAAATTGGTATCAGCAGAAACCGGGGAAG	224
QY	122	CCCTAAGCTCCTGATCTGTAGTGCATTCATTTGGCAAGTGGGGTCCCATCAGGTTCA	181
Db	225	CCCTACTCTGTGATCTTGTGTCATCCAAATTGCAAGTGGGGTCCCATCAGGTTCA	284
QY	182	GTGGCAGTGCATCTGGACAGAGTTCACTTCACCATCAGCAATCTGCAACTGAGACT	241
Db	285	GTGGCAGTGCATCTGGACAGAGTTCACTTCACCATCAGCCGCTGCAACTGAGAGTT	344
QY	242	TTGCAAGTACTACTGTCAACAGAGTTACACTTATATACCTTGGGCCCTGGACCA	301
Db	345	TTGCAACTTACTACTGTCAACAGAGTTACATTACCCCTGGACGTTTGGCCAAGGACCA	404
QY	302	AACTGGAGATCAAGCA	318
Db	405	AGTGGAAATCAACGA	421

Search completed: July 27, 2005, 12:32:12  
Job time : 1959.75 secs

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Query Match	99.5%	Score 316.4	DB 6	Length 318
Best Local Similarity	99.7%	Pred. No. 1,4e-91		
Matches 317	Conservative	0	Mismatches 1	Indels 0
			Gaps 0	
QY	1 GAGCTCACCACAGTCTCCATCCCTCGTCGCTCTGTAGAGAGACAGATCCATCACT	60		
DB	1 GAGCTCACCACAGTCTCCATCCCTCGTCGCTCTGTAGAGAGACAGATCCATCACT	60		
QY	61 TGCCGGGCAACGTCAGAGATTATGACACTATTTAAATGGTATCAGCAGAAACCGGGGAAG	120		
DB	61 TGCCGGGCAACGTCAGAGATTATGACACTATTTAAATGGTATCAGCAGAAACCGGGGAAG	120		
QY	121 GCCCTTAAGCTCTGATCTGTATGTGATCAATTTGGCAAAGTGGGGTCCCATCAGGTTTC	180		
DB	121 GCCCTTAAGCTCTGATCTGTATGTGATCAATTTGGCAAAGTGGGGTCCCATCAGGTTTC	180		
QY	181 AGTGCAGTGGATCTGGGACAGAGTTCATCTCCACATCAGCAATCTGCACCTGAAGAC	240		
DB	181 AGTGCAGTGGATCTGGGACAGAGTTCATCTCCACATCAGCAATCTGCACCTGAAGAC	240		
QY	241 TTTCGAGTTACTACTGTCAACAGAGTTACACTACTTATATATACCTTGGCCCTGGAGCC	300		
DB	241 TTTCGAGTTACTACTGTCAACAGAGTTACACTACTTATATATACCTTGGCCCTGGAGCC	300		
QY	301 AAACCTGAGATCAAAACA 318			
DB	301 AAACCTGAGATCAAAACA 318			

RESULT 2

AAH68647

ID AAH68647 standard; DNA; 321 BP.

AC AAH68647;

XX

DT 14-SEP-2001 (first entry)

XX

DE		Human anti-Rh(D) chain I02 nucleotide sequence.
KX		Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW		red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX		
OS	Homo sapiens.	
PV	US6255455-B1.	
PD	03-JUL-2001.	
XX		
PF	29-JAN-1999;	99US-00240274.
XX		
PR	11-OCT-1996;	96US-0028550P.
PR	27-JUN-1997;	97US-0088404S.
XX	10-APR-1998;	98US-0081380P.
PA	(TYPE-) UNIV PENNSYLVANIA.	
XX		
P1	Siegel DL;	
DR	WPI: 2001-388931/41.	
XX	P-PSDb; AAG93590.	
PT	New isolated protein, preferably a human anti-Rh(D) antibody for use in	
PT	diagnostics requiring a human instead of an animal antibody and in	
PT	therapeutic medicine.	
XX		
B5	Example 2; Col 54; 162pp; English.	
XX		
CC	The present invention describes an isolated Rh(D) binding protein,	
CC	preferably a human antibody, (I) having an amino acid sequence comprising	
CC	one of the sequences (S) given in AAG93558 to AAG93669. (I) has	
CC	immunostimulant activity, and can be used as an immune system stimulant.	
CC	(I) can be used in diagnostic and therapeutic medicine. The antibodies	
CC	are used in diagnostics that require human antibodies instead of animal	
CC	antibodies, such as determine the Rh phenotype of human red blood cells.	
CC	AAG68615 to AAH68726 represent the nucleotide sequence which encode	
CC	AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy	
CC	chain CDR3 amino acid sequences which are given in the exemplification of	
CC	the present invention	
XX		
SQ	Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;	
	Query Match	86.9%; Score 276.4; DB 5; Length 321;
	Best Local Similarity	91.8%; Pred. No. 1.le-78;
	Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0	
OY	1 GAGGTCAACCGAGTCTTCATCCTCCTGTCGCTCTGTAGAACAAGATCACATCACT	60
DB	4 GAGGTCAACCGAGTCTTCATCCTCCTGTCGCTCTGTAGAACAAGATCACATCACT	63
OY	61 TGCCGGGCAGCTCAGAGTTTAGCACTATTAAATGGTATCAGCAGAAAACGGGGANG	120
DB	64 TGCCGGGCAGAGTCAAGCATTAAGCAGCTATTAAATGGTATCAGCAGAAAACGGGAAA	123
OY	121 GCCCTTAAGCTCCGATCTGTAGTGCAATTCGAAGTGGGGGTCCCACCAAGTTTC	180
DB	124 GCCCTTAAGCTCCGATCTGTAGTGCGATCCAGTTTGCAAAGTGGGGTCCCACCAAGTTTC	183
OY	181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGAC	240
DB	184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACTGAAGAT	243
OY	241 TTTCGAACTTACTACTGTCAACAGAGTTTACCTAATTATACTTGGCCCTGGGACC	300
DB	244 TTTCGAACTTACTACTGTCAACAGAGTTTACCTAAGTACCTTGGCCTGAAGGACC	303
OY	301 AAACTGGAGATCAAAACGA 318	
DB	304 AAGGTGAAATCAAAACGA 321	



RESULT 3  
AAH68701  
ID AAH68701 standard; DNA; 321 BP.  
XX  
XX AAH68701;  
XX  
XX 14-SEP-2001 (first entry)  
XX  
XX Human anti-Rh(D) antibody clone SH13 nucleotide sequence.  
XX  
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
XX red blood cell; Rh phenotype; diagnosis; therapeutic; ds.  
XX  
XX Homo sapiens.  
XX OS  
XX US6255455-B1.  
XX PN  
XX 03-JUL-2001.  
XX PD  
XX 29-JAN-1999; 99US-00240274.  
XX PF  
XX 11-OCT-1996; 96US-0028550P.  
XX PR 27-JUN-1997; 97US-00884045.  
XX PR 10-APR-1998; 98US-0081380P.  
XX  
XX (TYPE-) UNIV PENNSYLVANIA.  
XX PA  
XX Siegel DL;  
XX PI  
XX WPI; 2001-388931/41.  
XX DR P-PSDB; AAG93644.  
XX  
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine.  
XX  
XX Example 3; Col 74; 162pp; English.  
XX  
XX The present invention describes an isolated Rh(D) binding protein,  
CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
CC immunostimulant activity, and can be used as an immune system stimulant.  
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
CC chain CDR3 amino acid sequences which are given in the exemplification of  
CC the present invention  
XX  
XX Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;  
SQ  
Query Match 86.9%; Score 276.4; DB 5; Length 321;  
Best Local Similarity 91.8%; Pred. No. 1.1e-78;  
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

DB 244 TTTGCAACTTACTGTCACAGAGATTACGATCCCTTCACTTTGGCAGGGAGCC 303  
OY 301 AAAGTGAGATCAACGA 318  
DB 304 AAGCTGAGATCAACGA 321  
RESULT 4  
ACD45311  
ID ACD45311 standard; DNA; 321 BP.  
XX  
XX ACD45311;  
XX AC  
XX 12-SEP-2003 (first entry)  
XX DT  
XX  
XX Anti-Rh(D) chain 102 DNA.  
XX DE  
XX Human; ds; gene; Rh(D) binding protein; blood typing; blood product;  
XX magnetically activated cell sorting.  
XX KW  
XX Homo sapiens.  
XX OS  
XX US2003040605-A1.  
XX PN  
XX 27-FEB-2003.  
XX PD  
XX 04-MAY-2001; 2001US-00848798.  
XX PF  
XX 11-OCT-1996; 96US-0028550P.  
XX PR 27-JUN-1997; 97US-00884045.  
XX PR 10-APR-1998; 98US-0081380P.  
XX PR 29-JAN-1999; 99US-00240274.  
XX  
XX (TYPE-) UNIV PENNSYLVANIA.  
XX PA  
XX Siegel DL;  
XX PI  
XX WPI; 2003-512273/48.  
XX DR P-PSDB; ABO27397.  
XX  
XX New human Rh(D)-binding protein useful for various diagnostic and  
PT therapeutic applications, including typing of blood or blood products.  
XX  
XX Claim 12; Page 39; 187pp; English.  
XX  
XX The invention relates to an isolated Rh(D) binding protein. The protein  
CC can be used for magnetically activated cell sorting. The protein is  
CC useful in various diagnostic and therapeutic applications in humans,  
CC including typing of blood or blood products. The present sequence  
CC represents DNA encoding a human anti-Rh(D) chain  
XX  
XX Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;  
SQ  
Query Match 86.9%; Score 276.4; DB 9; Length 321;  
Best Local Similarity 91.8%; Pred. No. 1.1e-78;  
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY	241	TTTTGAAGTTTCTACTGTGCAAGAGTTACACTACTATATACCTTGGCCCTGGAC	300
Db	244	TTTGCAACTTACTACTGTGCAAGAGTTACACTACTCTGTGGACGTTGGCCAAAGGACC	303
QY	301	AAACTGAGATCAACGCA	318
Db	304	AAGCTGGAATCAACGCA	321
RESULT 5			
ID	ACD45365	ACD45365 standard; DNA; 321 BP.	
XX	AC	ACD45365;	
XX	DT	12-SEP-2003 (first entry)	
XX	DE	Anti-Rh(D) light chain SH13 DNA.	
KW	XX	Human; ds; gene; RH(D) binding protein; blood typing; blood product;	
XX	XX	magnetically activated cell sorting.	
OS	XX	Homo sapiens.	
XX	PN	US2003040605-A1.	
XX	PD	27-FEB-2003.	
PF	XX	04-MAY-2001; 2001US-00848798.	
XX	PR	11-OCT-1996; 96US-0028550P.	
XX	PR	27-JUN-1997; 97US-0088404S.	
PR	XX	10-APR-1998; 98US-0081380P.	
XX	PR	29-JAN-1999; 99US-00240274.	
XX	PA	(UYPE-) UNIV PENNSYLVANIA.	
XX	PI	Siegel DL;	
XX	DR	MP1: 2003-512273/48.	
DR	XX	P-PSDB; ABO27451.	
XX	PT	New human Rh(D)-binding protein useful for various diagnostic and	
XX	XX	therapeutic applications, including typing of blood or blood products.	
PS	XX	Claim 12; Page 57; 187pp; English.	
XX	CC	The invention relates to an isolated Rh(D) binding protein. The protein	
XX	CC	can be used for magnetically activated cell sorting. The protein is	
CC	CC	useful in various diagnostic and therapeutic applications in humans,	
CC	CC	including typing of blood or blood products. The present sequence	
CC	XX	represents DNA encoding a human anti-Rh(D) chain	
XX	XX	Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;	
QY	Query Match	86.9%; Score 276.4; DB 9; Length 321;	
Db	Best Local Similarity	91.8%; Pred. No. 1,1e-78;	
XX	Matches	292; Conservative 0; Mismatches 26; Indels 0; Gaps 0	
QY	1	GAGCTCACCCAGTCTTCATCTCTCCCTGTGCTGTGTAAGACAGACTCACATCACT	60
Db	4	GAGCTCACCCAGTCTTCATCTCTCCCTGTGCTGTGTAAGACAGACTCACATCACT	63
QY	61	TGCCGGGACGTCAGAGTATAGCACTATTAAATGGTATCAGACGAAACCGGGGAAG	120
Db	64	TGCCGGGACGTCAGAGTATAGCACTATTAAATGGTATCAGACGAAACCGGGGAAG	123
QY	121	GCCCTTAAGCTCTGATCTGTAGTGATCCAAATTGGCAAGTGGGTCCTATCCAGTTTC	180
Db	124	GCCCTTAAGCTCTGATCTGTAGTGATCCAAATTGGCAAGTGGGTCCTATCCAGTTTC	183
QY	181	AGTGGCATGTGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCACCTTAAGAC	240

Db	184	AGTGCAGATGATGTGGACAGATTTCATCTTCAACATCAGAGCTGTGCAACCTGAAGAT	243
Qy	241	TTTGCAGATTACTCTGTCAACAGAGTTAACACTATTATATCCTTGGCCCTGGAC	300
Db	244	TTTGCAACTTACTACTGTCAACAGAGTTAAGTACCCCTTGTGCGCAGGGACC	303
Qy	301	AAACTGAGATCAACGA	318
Db	304	AAGCTGAGATCAACGA	321
RESULT 6			
AAV19761	AAV19761 standard; DNA, 315 BP.		
AC	AAV19761;		
XX	12-JUN-1998 (first entry)		
XX	Antibody LD2-20-VL chain coding sequence.		
XX	Antibody; variable heavy chain; VH chain; variable light chain; VL chain;		
XX	Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;		
XX	idiopathic thrombocytopenic purpura; haemolytic disease of the newborn;		
XX	ss.		
XX	Homo sapiens.		
XX	WO9749809-A1.		
XX	31-DEC-1997.		
XX	20-JUN-1997; 97WO-EP003253.		
XX	24-JUN-1996; 96EP-00810421.		
XX	(ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.		
XX	Miescher S, Vogel M, Stadler B, Morell A, Imboden M, Amstutz H;		
XX	WPI: 1998-077173/07.		
XX	P-ESDB; AAM52237.		
XX	New Rhesus D antigen binding polypeptide(s) - used to neutralise Rhesus		
XX	D antigen in therapy, e.g. for treating idiopathic thrombocytopenic		
XX	purpura.		
XX	Claim 6; Fig 13B; 68pp; English.		
XX	This sequence encodes the antibody LD2-20-VL chain sequence, which is a		
XX	polypeptide of the invention. The polypeptides are capable of forming		
XX	antigen binding structures with specificity for Rhesus D antigens which		
XX	include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of		
XX	variable heavy (VH) and variable light (VL) chain sequences. The		
XX	antibodies are active against the Rhesus D antigen. They can be used for		
XX	treating disorders which would benefit from anti-Rhesus D immunoglobulin,		
XX	e.g. idiopathic thrombocytopenic purpura. They can also be used for the		
XX	protection of Rhesus negative women before or immediately after the birth		
XX	of a Rhesus positive child to prevent haemolytic disease of the newborn		
XX	(HDN) in subsequent pregnancies. In addition, anti-Rhesus D		
XX	immunoglobulin can be used after transfusions of Rhesus positive blood		
XX	to Rhesus negative recipients in order to prevent sensitisation to the		
XX	Rhesus D antigen. The products can also be used as diagnostic reagents		
XX	Sequence 315 BP; 84 A; 83 C; 71 G; 77 T; 0 U; 0 Other;		
Query Match 86.0%; Score 273.4; DB 2; Length 315;			
Best Local Similarity 91.7%; Pred. No. 9.9e-78;			
Matches 289; Conservative 0; Mismatches 26; Indels 0; Gaps 0;			
Qy	1 GAGCTACCCAGTCTCCATCTCCCTGTGTGCTCTGTGAGACAGAGTACATCACTACT 60		

Db 1 GTGATGACCCAGTCTCCATCTCCCTGTCGTGATCTGTAGAGACAGAGTACCATCACT 60  
 QY 61 TGCCGGGACAGTCTGAGATATTAGACCTATTAAATTGATTCAGCAGAAACCGGGGAAG 120  
 Db 61 TGCCGGGACAGTCTGAGATATTAGACCTATTAAATTGATTCAGCAGAAACCGGGGAAG 120  
 QY 121 GCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAATGGGGTCCCTCAAGTTC 180  
 Db 121 GCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAATGGGGTCCCTCAAGTTC 180  
 QY 181 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCAACATCTGCAACCTGGAAGAC 240  
 Db 181 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCAACATCTGCAACCTGGAAGAT 240  
 QY 241 TTGCGAAGTTACTACTGTCAACAGAGTTTCACTCTTATTAACCTTGGGCTTGGGACC 300  
 Db 241 TTGCGAAGTTACTACTGTCAACAGAGTTTCACTCTTATTAACCTTGGGCTTGGGACC 300  
 QY 301 AAAGCTGAGATCAAA 315  
 Db 301 AAAGCTGAGATCAAA 315

RESULT 7  
 AAH68720  
 ID AAH68720 standard; DNA; 321 BP.  
 XX  
 AC AAH68720;  
 XX  
 DT 14-SEP-2001 (first entry)  
 XX  
 DE Human anti-Rh(D) antibody clone SH49 nucleotide sequence.  
 XX  
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KM red blood cell; Rh phenotype; diagnosis; therapeutic; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6255455-B1.  
 XX  
 PD 03-JUL-2001.  
 XX  
 PF 29-JAN-1999; 99US-00240274.  
 XX  
 PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 XX  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Siegel DL;  
 XX  
 DR WPI; 2001-388931/41.  
 DR P-PSDB; AAG93663.  
 XX  
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine.  
 XX  
 PS Example 3; Col 79; 162pp; English.  
 XX  
 CC The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification of  
 CC the present invention  
 CC  
 XX

SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;  
 Query Match 85.9%; Score 273.2; DB 5; Length 321;  
 Best Local Similarity 91.2%; Pred. No. 1.2e-77;  
 Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 GAGTCAACCCAGTCTCCATCTCCCTGTCGTGATCTGTAGAGACAGAGTACCATCACT 60  
 Db 4 GAGTCAACCCAGTCTCCATCTCCCTGTCGTGATCTGTAGAGACAGAGTACCATCACT 63  
 QY 61 TGCCGGGACAGTCTGAGATATTAGACCTATTAAATTGATTCAGCAGAAACCGGGGAAG 120  
 Db 64 TGCCGGGACAGTCTGAGATATTAGACCTATTAAATTGATTCAGCAGAAACCGGGGAAG 123  
 QY 121 GCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAATGGGGTCCCTCAAGTTC 180  
 Db 124 GCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAATGGGGTCCCTCAAGTTC 183  
 QY 181 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCAACATCTGCAACCTGGAAGAC 240  
 Db 184 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCAACATCTGCAACCTGGAAGAT 243  
 QY 241 TTGCGAAGTTACTACTGTCAACAGAGTTTCACTCTTATTAACCTTGGGCTTGGGACC 300  
 Db 244 TTGCGAAGTTACTACTGTCAACAGAGTTTCACTCTTATTAACCTTGGGCTTGGGACC 303  
 QY 301 AAAGCTGAGATCAAA 318  
 Db 304 AAAGCTGAGATCAAA 321

RESULT 8  
 AAH68658  
 ID AAH68658 standard; DNA; 321 BP.  
 XX  
 AC AAH68658;  
 XX  
 DT 14-SEP-2001 (first entry)  
 XX  
 DE Human anti-Rh(D) chain I13 nucleotide sequence.  
 XX  
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KM red blood cell; Rh phenotype; diagnosis; therapeutic; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6255455-B1.  
 XX  
 PD 03-JUL-2001.  
 XX  
 PF 29-JAN-1999; 99US-00240274.  
 XX  
 PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 XX  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Siegel DL;  
 XX  
 DR WPI; 2001-388931/41.  
 DR P-PSDB; AAG93601.  
 XX  
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine.  
 XX  
 PS Example 2; Col 57; 162pp; English.  
 XX  
 CC The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC  
 XX

CC	(I) can be used in diagnostic and therapeutic medicine. The antibodies
CC	are used in diagnostics that require human antibodies instead of animal
CC	antibodies, such as determine the Rh phenotype of human red blood cells.
CC	AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC	AAH93558 to AAH93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC	chain CDR3 amino acid sequences which are given in the exemplification of
CC	the present invention
XX	
XX	Sequence 321 BP; 82 A; 88 C; 77 G; 74 T; 0 U; 0 Other;
SQ	
Query Match	85.9%; Score 273.2; DB 5; Length 321;
Best Local Similarity	91.2%; Pred. No. 1.2e-77;
Matches	290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy	1 GAGCTCACCCAGTCTCATCTCCCTGCTGCTGTGAGAGACAGATCACATCACT 60
Db	4 GAGCTCACCCAGTCTCATCTCCCTGCTGCTGTGAGAGACAGATCACATCACT 63
Qy	61 TGCCGGGCACTCAAGATTAGCACTTATTAATTGATACAGCAAAACCGGGGAAG 120
Db	64 TGCCGGGCAAGTCAAGAGATTAGCGAGATTAAATTGGTATCAAGCAAAACCGGGGAAA 123
Qy	121 GCCCTTAAGCTCCTGATCTGTAGTGCATCATTTGGCAAAGGGGGTCCCATCCAGGTTTC 180
Db	124 GCCCTTAAGCTCCTGATCTGTAGTGCATCATTTGGCAAAGGGGGTCCCATCAAGGTTTC 183
Qy	181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGAC 240
Db	184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGAT 243
Qy	241 TTGGCAAGTACTACTGTCAACAGAGTTAACACTACTTATATCTTGGCCCTGGGACC 300
Db	244 TTGGCAAGTACTACTGTCAACAGAGTTAACAAGTATCGGTACCCCTCAAGTTTGGCCGGGGGACC 303
Qy	301 AAACGTGAGATCAAAACGA 318
Db	304 AAGCTGGAGATCAAAACGA 321
RESULT 9	
AAH68652	
ID	AAH68652 standard; DNA; 321 BP.
XX	
AC	AAH68652;
XX	
DT	14-SEP-2001 (first entry)
XX	
DE	Human anti-Rh(D) chain I07 nucleotide sequence.
XX	
KW	Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW	red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
OS	Homo sapiens.
XX	
PN	US6255455-B1.
PD	03-JUL-2001.
XX	
PF	29-JAN-1999; 99US-00240274.
XX	
PR	11-OCT-1996; 96US-0028550P.
PR	27-JUN-1997; 97US-00884045.
XX	
XX	10-APR-1998; 98US-0081380P.
PA	(UYPE-) UNIV PENNSYLVANIA.
XX	
PI	Siegel DL;
XX	
DR	WPI; 2001-388931/41.
DR	P-PSDB; AAG93595.
XX	
PT	New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT	diagnostics requiring a human instead of an animal antibody and in

PT		therapeutic medicine.
XX		
PS	Example 2; Col 55; 162pp; English.	
XX		
CC	The present invention describes an isolated Rh(D) binding protein,	
CC	preferably a human antibody, (I) having an amino acid sequence comprising	
CC	one of the sequences (S) given in AA93558 to AA93669. (I) has	
CC	immunostimulant activity, and can be used as an immune system stimulant.	
CC	(I) can be used in diagnostic and therapeutic medicine. The antibodies	
CC	are used in diagnostics that require human antibodies instead of animal	
CC	antibodies, such as determine the Rh phenotype of human red blood cells.	
CC	AAH6815 to AAH68726 represent the nucleotide sequence which encode	
CC	AA93558 to AA93669, AA93670 to AA93697 represent anti-Rh(D) heavy	
CC	chain CDR3 amino acid sequences which are given in the exemplification of	
CC	the present invention	
XX		
SQ	Sequence 321 BP; 85 A; 87 C; 76 G; 73 T; 0 U; 0 Other;	
Query Match	85.9%; Score 273.2, DB 5; Length 321;	
Best Local Similarity	91.2%; Pred.No. 1.2e-77;	
Matches 290; Conservative	0; Mismatches 28; Indels 0; Gaps 0	
OY	1 GAGCTCACCACGTCCTCCATCCCTCGTCTGCCTGTGAGAGACAGAGTCACCATCACT	60
Db	4 GAGCTCACCCAGCTCTCACTCCTCCTGTCGATCTGAGGACAGACTCACCATCACT	63
OY	61 TGCCGGGACGTCAGAGATTATGACCTATTATTAATTGGTATCAGCAGAAAACGGGGAAG	120
Db	64 TGCCGGGACAGTCAGAGCTTAGTGAGCTATTATTAATTGGTATCAGCAGAAAACGGGANA	123
OY	121 GCCCTTAAGCTCTGATCTGTAAGTCATCCAAATTGGCAAAGTGGGGTCCCATTCCAGTTTC	180
Db	124 GCCCTTAAGCTCTGATCTGTAAGTCATCCAAATTGGCAAAGTGGGGTCCCATTCCAGTTTC	183
OY	181 AGTGACAGTGCATCTGGGACAAGTCACTCCTCACATCAGCAATCTGCAACTGAGAAGAC	240
Db	184 AGTGACAGTGCATCTGGGACAAGTCACTCCTCACATCAGCAATCTGCAACTGAGAAGT	243
OY	241 TTTCGAAGTTACTACTGTCCAAGAGTTAACCTACTATATATACCTTCGCCCTTGGGACC	300
Db	244 TTTCGAAGTTACTACTGTCCAAGAGTTAACCTACTATATATACCTTCGCCCTTGGGAGACC	303
OY	301 AAACGTGAGATCAAAAGA 318	
Db	304 AAGGTGAGATCAAAAGA 321	
RESULT 10		
AAH68713		
ID	AAH68713 standard; DNA; 321 BP.	
XX		
AC	AAH68713;	
XX		
DT	14-SEP-2001 (first entry)	
XX		
XX		
DE	Human anti-Rh(D) antibody clone SH36 nucleotide sequence.	
XX		
PN	Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;	
KW	red blood cell; Rh phenotype; diagnosis; therapeutic; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	US6255455-B1.	
XX		
PD	03-JUL-2001.	
XX		
PF	29-JAN-1999; 99US-00240274.	
XX		
PR	11-OCT-1996; 96US-0028550P-	
PR	27-JUN-1997; 97US-0088404S.	
PR	10-APR-1996; 98US-0081380P.	
XX		
XX	(UYPE-) UNIV PENNSYLVANIA.	

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XX Siegel D.;
XX WPI; 2001-388931/41.
DR P-PSDB; AAG93656.
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX Example 3; Col 77; 162pp; English.
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93659. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAG93558 to AAG93659 represent the nucleotide sequence which encode
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX Sequence 321 BP; 83 A; 89 C; 72 G; 77 T; 0 U; 0 Other;
SQ
Query Match 85.9%; Score 273.2; DB 5; Length 321;
Best Local Similarity 91.2%; Pred. No. 1.2e-77;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1 GAGCTACCCAGTCTCCATCTCCCTGCTGCTGAGAGACAGAGTCAATCACT 60
DB 4 GAGCTCACTAGTCTCCATCTCCCTGCTGCTGAGAGACAGAGTCAATCACT 63
QY 61 TGCCTGGGACGTCAGAGTATTAGACCTATTAAATTGTTATCGCAGAAACCGGGAG 120
DB 64 TGCCTGGGACGTCAGAGTATTAGACCTATTAAATTGTTATCGCAGAAACCGGGAA 123
QY 121 GCCCTTAAGCTCTGATCTGTAGTGCATCCAAATTGCAAAAGTGGGGTCCCATCAAGTTTC 180
DB 124 TCCCTTAAGCTCTGATCTGTAGTGCATCCAAATTGCAAAAGTGGGGTCCCATCAAGTTTC 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCAATCTGCAACTGGAAGAC 240
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCAATCTGCAACTGGAAGAT 243
QY 241 TTTCGAAGTTACTACTGTGCAAGAGTTACACTACTTAATACCTTGCGCCCTGGGACC 300
DB 244 TTTCGAAGTTACTACTGTGCAAGAGTTACACTACTTAATACCTTGCGCCCTGGGACC 303
QY 301 AAAGTGGAGATCAACGA 318
DB 304 AAAGTGGAGATCAACGA 321
RESULT 11
AAH68703 standard; DNA; 321 BP.
ID AAH68703
XX AAH68703;
XX
XX 14-SEP-2001 (first entry)
XX Human anti-Rh(D) antibody clone SH16 nucleotide sequence.
XX
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KM red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
XX Homo sapiens.
XX
XX US6255455-B1.
XX
XX 03-JUL-2001.
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XX 29-JAN-1999; 99US-00240274.
XX
XX 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel D.;
XX WPI; 2001-388931/41.
DR P-PSDB; AAG93646.
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX Example 3; Col 75; 162pp; English.
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93659. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAG93558 to AAG93659 represent the nucleotide sequence which encode
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX Sequence 321 BP; 85 A; 89 C; 74 G; 73 T; 0 U; 0 Other;
SQ
Query Match 85.9%; Score 273.2; DB 5; Length 321;
Best Local Similarity 91.2%; Pred. No. 1.2e-77;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1 GAGCTACCCAGTCTCCATCTCCCTGCTGCTGAGAGACAGAGTCAATCACT 60
DB 4 GAGCTCACTAGTCTCCATCTCCCTGCTGCTGAGAGACAGAGTCAATCACT 63
QY 61 TGCCTGGGACGTCAGAGTATTAGACCTATTAAATTGTTATCGCAGAAACCGGGAG 120
DB 64 TGCCTGGGACGTCAGAGTATTAGACCTATTAAATTGTTATCGCAGAAACCGGGAA 123
QY 121 GCCCTTAAGCTCTGATCTGTAGTGCATCCAAATTGCAAAAGTGGGGTCCCATCAAGTTTC 180
DB 124 GCCCTTAAGCTCTGATCTGTAGTGCATCCAAATTGCAAAAGTGGGGTCCCATCAAGTTTC 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCAATCTGCAACTGGAAGAC 240
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCAATCTGCAACTGGAAGAT 243
QY 241 TTTCGAAGTTACTACTGTGCAAGAGTTACACTACTTAATACCTTGCGCCCTGGGACC 300
DB 244 TTTCGAAGTTACTACTGTGCAAGAGTTACACTACTTAATACCTTGCGCCCTGGGACC 303
QY 301 AAAGTGGAGATCAACGA 318
DB 304 AAAGTGGAGATCAACGA 321
RESULT 12
ACD45377 standard; DNA; 321 BP.
ID ACD45377
XX ACD45377;
XX
XX 12-SEP-2003 (first entry)
XX Anti-Rh(D) light chain SH36 DNA.
XX
XX
```

KM Human; ds; gene; RH(D) binding protein; blood typing; blood product;  
KW magnetically activated cell sorting.  
XX Homo sapiens.  
XX US2003040605-A1.  
XX PD 27-FEB-2003.  
XX PF 04-MAY-2001; 2001US-00848798.  
XX PR 11-OCT-1996; 96US-0028550P.  
XX PR 27-JUN-1997; 97US-00884045.  
XX PR 10-APR-1998; 98US-0081380P.  
XX PR 29-JAN-1999; 99US-00240274.  
XX PA (TYPE-) UNIV PENNSYLVANIA.  
XX PI Siegel DL;  
XX DR WPI; 2003-512273/48.  
XX DR P-PSDB; ABO27463.  
XX PT New human Rh(D)-binding protein useful for various diagnostic and  
XX therapeutic applications, including typing of blood or blood products.  
XX PS Claim 12; Page 60; 187P; English.  
XX CC The invention relates to an isolated Rh(D) binding protein. The protein  
XX can be used for magnetically activated cell sorting. The protein is  
XX useful in various diagnostic and therapeutic applications in humans,  
XX including typing of blood or blood products. The present sequence  
XX represents DNA encoding a human anti-Rh(D) chain  
SQ Sequence 321 BP; 83 A; 89 C; 72 G; 77 T; 0 U; 0 Other;  
Query Match 85.9%; Score 273.2; DB 9; Length 321;  
Best Local Similarity 91.2%; Pred. No. 1.2e-77;  
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
QY 1 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCACCATCACT 60  
DB 4 GAGCTACCTAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCACCATCACT 63  
QY 61 TGCCGGGCAAGTCAAGATTTAGCACTATTAAATTGGTATCAGAGAAACGGGGAAG 120  
DB 64 TGCCGGGCAAGTCAAGATTTAGCACTATTAAATTGGTATCAGAGAAACGGGGAAG 123  
QY 121 GCCCCTAAGCTCCTGATCTGTAGTCATCCAAATTGGAAAGTGGGTCCTCCATCCAGGTTT 180  
DB 124 TCCCTTAAGCTCCTGATCTGTAGTCATCCAAAGTGGGTCCTCCATCCAGGTTT 183  
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCAGCAATCTGCAACTGGAAGAC 240  
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCAGCAATCTGCAACTGGAAGAT 243  
QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTTCACTTATTAATCTTGGGCTTGGGAGCC 300  
DB 244 TTTCGAAGTTACTACTGTCAACAGAGTTTCACTTATTAATCTTGGGCTTGGGAGCC 303  
QY 301 AAAGTGAGATCAACGA 318  
DB 304 AAAGTGAGATCAACGA 321  
RESULT 13  
ACD45367  
ID ACD45367 standard; DNA; 321 BP.  
XX ACD45367;  
XX AC  
XX DT 12-SEP-2003 (first entry)  
XX

DE Anti-Rh(D) light chain SH16 DNA.  
XX  
XX KM Human; ds; gene; RH(D) binding protein; blood typing; blood product;  
KW magnetically activated cell sorting.  
XX Homo sapiens.  
XX US2003040605-A1.  
XX PD 27-FEB-2003.  
XX PF 04-MAY-2001; 2001US-00848798.  
XX PR 11-OCT-1996; 96US-0028550P.  
XX PR 27-JUN-1997; 97US-00884045.  
XX PR 10-APR-1998; 98US-0081380P.  
XX PR 29-JAN-1999; 99US-00240274.  
XX PA (TYPE-) UNIV PENNSYLVANIA.  
XX PI Siegel DL;  
XX DR WPI; 2003-512273/48.  
XX DR P-PSDB; ABO27453.  
XX PT New human Rh(D)-binding protein useful for various diagnostic and  
XX therapeutic applications, including typing of blood or blood products.  
XX PS Claim 12; Page 57; 187P; English.  
XX CC The invention relates to an isolated Rh(D) binding protein. The protein  
XX can be used for magnetically activated cell sorting. The protein is  
XX useful in various diagnostic and therapeutic applications in humans,  
XX including typing of blood or blood products. The present sequence  
XX represents DNA encoding a human anti-Rh(D) chain  
SQ Sequence 321 BP; 85 A; 89 C; 74 G; 73 T; 0 U; 0 Other;  
Query Match 85.9%; Score 273.2; DB 9; Length 321;  
Best Local Similarity 91.2%; Pred. No. 1.2e-77;  
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
QY 1 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCACCATCACT 60  
DB 4 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCACCATCACT 63  
QY 61 TGCCGGGCAAGTCAAGATTTAGCACTATTAAATTGGTATCAGAGAAACGGGGAAG 120  
DB 64 TGCCGGGCAAGTCAAGATTTAGCACTATTAAATTGGTATCAGAGAAACGGGGAAG 123  
QY 121 GCCCCTAAGCTCCTGATCTGTAGTCATCCAAATTGGAAAGTGGGTCCTCCATCCAGGTTT 180  
DB 124 GCCCCTAAGCTCCTGATCTGTAGTCATCCAAAGTGGGTCCTCCATCCAGGTTT 183  
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCAGCAATCTGCAACTGGAAGAC 240  
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCAGCAATCTGCAACTGGAAGAT 243  
QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTTCACTTATTAATCTTGGGCTTGGGAGCC 300  
DB 244 TTTCGAAGTTACTACTGTCAACAGAGTTTCACTTATTAATCTTGGGCTTGGGAGCC 303  
QY 301 AAAGTGAGATCAACGA 318  
DB 304 AAAGTGAGATCAACGA 321  
RESULT 14  
ACD45384  
ID ACD45384 standard; DNA; 321 BP.  
XX ACD45384;  
XX AC  
XX DT  
XX







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OM nucleic - nucleic search, using SW model

Run on: July 27, 2005, 09:08:49 ; Search time 476.839 Seconds

(without alignments)  
4312.305 Million cell updates/sec

Title: US-10-027-725a-5

Perfect score: 318  
Sequence: 1 gagctcaccgagctccatc.....ccaactggagatcaacga 318

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7277826 seqs, 3233139505 residues

Total number of hits satisfying chosen parameters: 1455652

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
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- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
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- 9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09C\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10I\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	100.0	318	14	US-10-027-725a-5
2	276.4	86.9	321	10	US-09-848-798-102
3	276.4	86.9	321	10	US-09-848-798-199
4	273.2	85.9	321	10	US-09-848-798-107
5	273.2	85.9	321	10	US-09-848-798-113
6	273.2	85.9	321	10	US-09-848-798-201
7	273.2	85.9	321	10	US-09-848-798-211

8	273.2	85.9	321	10	US-09-848-798-218	Sequence 218, App
9	272.2	85.6	384	17	US-10-309-762-115	Sequence 115, App
10	271.6	85.4	321	10	US-09-848-798-106	Sequence 106, App
11	271.6	85.4	321	10	US-09-848-798-205	Sequence 205, App
12	271.6	85.4	321	10	US-09-848-798-221	Sequence 221, App
13	271.6	85.4	321	10	US-09-848-798-222	Sequence 222, App
14	271.2	85.3	720	9	US-09-192-854-1	Sequence 1, App1
15	271.2	85.3	720	9	US-09-968-561a-1	Sequence 1, App1
16	271.2	85.3	720	11	US-09-968-561a-1	Sequence 1, App1
17	271.2	85.3	720	11	US-09-968-561a-1	Sequence 2, App1
18	271.2	85.3	720	20	US-10-744-774-2	Sequence 15, App1
19	270.6	85.1	405	21	US-10-783-311-15	Sequence 16, App1
20	270.6	85.1	405	21	US-10-783-311-16	Sequence 215, App
21	270.6	85.1	405	21	US-10-783-311-16	Sequence 217, App
22	270.6	85.1	405	21	US-10-783-311-16	Sequence 78, App1
23	269.2	84.7	729	15	US-10-216-484-125	Sequence 125, App
24	269.2	84.6	729	16	US-10-384-933-125	Sequence 125, App
25	269.2	84.6	729	16	US-10-384-933-125	Sequence 105, App
26	268.4	84.4	321	10	US-09-848-798-105	Sequence 3, App1
27	268.4	84.3	324	19	US-10-344-514-3	Sequence 4, App1
28	268.4	84.3	324	19	US-10-344-514-4	Sequence 7, App1
29	268.4	84.3	324	19	US-10-344-514-7	Sequence 8, App1
30	268.4	84.3	324	19	US-10-344-514-8	Sequence 35, App1
31	268.4	84.3	333	16	US-10-203-754a-60	Sequence 60, App1
32	268.4	84.3	900	16	US-10-203-754a-64	Sequence 64, App1
33	267.4	84.1	333	16	US-10-203-754a-61	Sequence 61, App1
34	267.4	84.1	472	21	US-10-805-177-19	Sequence 19, App1
35	267.4	84.1	702	21	US-10-938-353-3	Sequence 3, App1
36	267.4	84.1	702	21	US-10-938-353-7	Sequence 7, App1
37	267.4	84.1	708	21	US-10-938-353-35	Sequence 35, App1
38	267.4	84.1	714	14	US-10-153-882-18	Sequence 18, App1
39	267.4	84.1	714	20	US-10-612-497-62	Sequence 62, App1
40	267.4	84.1	714	20	US-10-776-649-62	Sequence 62, App1
41	267.4	84.1	900	16	US-10-203-754a-65	Sequence 65, App1
42	267.4	84.0	322	16	US-10-938-591-54	Sequence 54, App1
43	267.4	84.0	322	20	US-10-775-444a-54	Sequence 54, App1
44	265.2	83.4	321	10	US-09-848-798-109	Sequence 109, App
45	265.2	83.4	321	10	US-09-848-798-216	Sequence 216, App

## ALIGNMENTS

RESULT 1  
US-10-027-725a-5  
; Sequence 5, Application US/10027725a  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 318  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-027-725a-5

QY	1	GAGCTACCCGAGTCCATCTCCCTGCTGCTGAGGAGACAGTACCATCTACT	60
DB	1	GAGCTACCCGAGTCCATCTCCCTGCTGCTGAGGAGACAGTACCATCTACT	60
QY	61	TGCGGGGAGCTGAGTATTAGCACTATTAAATTGTATCAGCAGAAACGGGGAG	120

Db 61 TGGCGGCGACGTGACAGATATTAGACCTATTAAATTGTAATCAGCAAAAACCGGGAG 120  
QY 121 GCCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGTGGGTCCCATCCAGGTTTC 180  
Db 121 GCCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGTGGGTCCCATCCAGGTTTC 180  
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCCATCCAGCATCTGCAACCTGAAGAC 240  
Db 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCCATCCAGCATCTGCAACCTGAAGAC 240  
QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTCGGCCCTGGGACC 300  
Db 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTCGGCCCTGGGACC 300  
QY 301 AAATCGAGATCAACGCA 318  
Db 301 AAATCGAGATCAACGCA 318

RESULT 2  
US-09-848-798-102  
; Sequence 102, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 102  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain 102  
US-09-848-798-102

Query Match 86.9%; Score 276.4; DB 10; Length 321;  
Best Local Similarity 91.8%; Pred. No. 3.4e-84;  
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGGTACCCAGTCTCCATCTCCCTGTCGCTGTAGAGACAGATCCACATCACT 60  
Db 4 GAGGTACCCAGTCTCCATCTCCCTGTCGCTGTAGAGACAGATCCACATCACT 63  
QY 61 TGGCGGCGACGTGACAGATATTAGACCTATTAAATTGTAATCAGCAAAAACCGGGAG 120  
Db 64 TGGCGGCGACGTGACAGATATTAGACCTATTAAATTGTAATCAGCAAAAACCGGGAG 123  
QY 121 GCCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGTGGGTCCCATCCAGGTTTC 180  
Db 124 GCCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGTGGGTCCCATCCAGGTTTC 183  
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCCATCCAGCATCTGCAACCTGAAGAC 240  
Db 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCCATCCAGCATCTGCAACCTGAAGAT 243  
QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTCGGCCCTGGGACC 300  
Db 244 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTCGGCCCTGGGACC 303  
QY 301 AAATCGAGATCAACGCA 318  
Db 304 AAATCGAGATCAACGCA 321

RESULT 3  
US-09-848-798-199  
; Sequence 199, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 199  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13  
US-09-848-798-199

Query Match 86.9%; Score 276.4; DB 10; Length 321;  
Best Local Similarity 91.8%; Pred. No. 3.4e-84;  
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 1 GAGGTACCCAGTCTCCATCTCCCTGTCGCTGTAGAGACAGATCCACATCACT 60  
Db 4 GAGGTACCCAGTCTCCATCTCCCTGTCGCTGTAGAGACAGATCCACATCACT 63  
QY 61 TGGCGGCGACGTGACAGATATTAGACCTATTAAATTGTAATCAGCAAAAACCGGGAG 120  
Db 64 TGGCGGCGACGTGACAGATATTAGACCTATTAAATTGTAATCAGCAAAAACCGGGAG 123  
QY 121 GCCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGTGGGTCCCATCCAGGTTTC 180  
Db 124 GCCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGTGGGTCCCATCCAGGTTTC 183  
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCCATCCAGCATCTGCAACCTGAAGAC 240  
Db 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCCATCCAGCATCTGCAACCTGAAGAT 243  
QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTCGGCCCTGGGACC 300  
Db 244 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTCGGCCCTGGGACC 303  
QY 301 AAATCGAGATCAACGCA 318  
Db 304 AAATCGAGATCAACGCA 321

RESULT 4  
US-09-848-798-107  
; Sequence 107, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 107  
; LENGTH: 321



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; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: Rh(D)-BINDING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-848-798-211
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Query Match      85.9%; Score 273.2; DB 10; Length 321;
Best Local Similarity 91.2%; Pred. No. 4.2e-83;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
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QY 1 GAGCTACCCAGTCTCCATCTCTGCTGTGCTCTGTAGAGACAGAGTCACCATCACT 60
DB 4 GAGCTCACTAGTCTCCATCTCTGCTGTGCTCTGTAGAGACAGAGTCACCATCACT 63
QY 61 TGGCGGCGACGTGACAGATATTAGACACCTATTAAATGGTATGACGAAACCGGGGAG 120
DB 64 TGGCGGCGAAGTACAGACATTAGACAGCTATTAAATGGTATGACGAAACCGGGGAG 123
QY 121 GCCCTTAAGCTCTGATCTGTAGTGCATCCATTTGCAAGTGGGGTCCCATCCAGGTTTC 180
DB 124 TCCCTTAAGCTCTGATCTGTAGTGCATCCATTTGCAAGTGGGGTCCCATCCAGGTTTC 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACCTGAAGAC 240
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAACCTGCAACCTGAAGAT 243
QY 241 TTGGCAAGTTACTACTGTGACACAGAGTTACCTACTTATACCTTGGGCCCTGGGACC 300
DB 244 TTGGCAAGTTACTACTGTGACACAGAGTTACCTACTTATACCTTGGGCCCTGGGACC 303
QY 301 AAAGTGGAGATCAACGA 318
DB 304 AAAGTGGAGATCAACGA 321
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RESULT 8
US-09-848-798-218
; Sequence 218, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-218
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Query Match      85.9%; Score 273.2; DB 10; Length 321;
Best Local Similarity 91.2%; Pred. No. 4.2e-83;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
```

```
QY 1 GAGCTACCCAGTCTCCATCTCTGCTGTGCTCTGTAGAGACAGAGTCACCATCACT 60
DB 4 GAGCTCACTAGTCTCCATCTCTGCTGTGCTCTGTAGAGACAGAGTCACCATCACT 63
QY 61 TGGCGGCGACGTGACAGATATTAGACACCTATTAAATGGTATGACGAAACCGGGGAG 120
DB 64 TGGCGGCGAAGTACAGACATTAGACAGCTATTAAATGGTATGACGAAACCGGGGAG 123
QY 121 GCCCTTAAGCTCTGATCTGTAGTGCATCCATTTGCAAGTGGGGTCCCATCCAGGTTTC 180
DB 124 GCCCTTAAGCTCTGATCTGTAGTGCATCCATTTGCAAGTGGGGTCCCATCCAGGTTTC 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACCTGAAGAC 240
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACCTGAAGAT 243
QY 241 TTGGCAAGTTACTACTGTGACACAGAGTTACCTACTTATACCTTGGGCCCTGGGACC 300
DB 244 TTGGCAAGTTACTACTGTGACACAGAGTTACCTACTTATACCTTGGGCCCTGGGACC 303
QY 301 AAAGTGGAGATCAACGA 318
DB 304 AAAGTGGAGATCAACGA 321
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RESULT 9
US-10-309-762-115
; Sequence 115, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Folitz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYLIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX. 027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-115
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Query Match      85.6%; Score 272.2; DB 17; Length 384;
Best Local Similarity 91.2%; Pred. No. 1e-82;
Matches 289; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
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QY 2 AGCTACCCAGTCTCCATCTCTGCTGTGCTCTGTAGAGACAGAGTCACCATCACT 61
DB 68 AGATGACCCAGTCTCCATCTCTGCTGTGCTCTGTAGAGACAGAGTCACCATCACT 127
QY 62 GCGGGGCGACGTGACAGATATTAGACACCTATTAAATGGTATGACGAAACCGGGGAG 121
DB 128 GCGGGGCGAAGTACAGACATTAGACAGCTATTAAATGGTATGACGAAACCGGGGAG 187
QY 122 CCCCTTAAGCTCTGATCTGTAGTGCATCCATTTGCAAGTGGGGTCCCATCCAGGTTTC 181
DB 188 CCCCTTAAGCTCTGATCTGTAGTGCATCCATTTGCAAGTGGGGTCCCATCCAGGTTTC 247
QY 182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACCTGAAGACT 241
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D <sub>b</sub>	248	GTGGCAGTGGATCTGGGACAGATTTCACCTCTCACATCAGCGGTGTGGAACTTAAATT	307
O <sub>Y</sub>	242	TTGGCAATTACTACTGTCAAACAGATTACACTAATTATATACCTTGGGCCCTGGGACCA	301
D <sub>b</sub>	308	TTGGCAATTACTACTGTCAAACAGATTACAGTTCCTTAATCACTTGGGCCCTGGGACCA	367
O <sub>Y</sub>	302	AACGTGAGTATCAACGA	318
D <sub>b</sub>	368	AATGGATATCAACGA	384

RESULT 10  
 US-09-848-798-106  
 : Sequence 106, Application US/09848798  
 : Publication No. US2003004605A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Siegel, Donald L.  
 : TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
 : TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
 : FILE REFERENCE: 09596-42U2  
 : CURRENT APPLICATION NUMBER: US/09/848,798  
 : PRIOR FILING DATE: 2001-05-04  
 : PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
 : PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
 : PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
 : PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
 : NUMBER OF SEQ ID NOS: 224  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 106  
 : LENGTH: 321  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 : FEATURE:  
 : OTHER INFORMATION: anti-Rh(D) chain 106  
 US-09-848-798-106

Query Match	85.4%;	Score 271.6;	DB 10;	Length 321;
Best Local Similarity	90.9%;	Pred. No. 1,5e-82;		
Matches 289;	Conservative 0;	Mismatches 29;	Indels 0;	Gaps 0
Qy	1	GAGCTCACCCACATCTTCATCTCTCCCTGTCGCTCTGTGTGGAGACAGAGTCACCATCATCT	60	
Db	4	GAGCTCACCCAGTCTTCATCTCTCCCTGTCGCTCTGTGTGGAGACAGAGTCACCATCATCT	63	
Qy	61	TGCGGGGACGTCAGAGATTAGACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG	120	
Db	64	TGCGGGGACGTCAGAGATTAGACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG	123	
Qy	121	GCCCTTAAGCTCTGTATCTGTATGTATGATGATCCAAATTGGAAAGTGGGGTCCCATCAGGTTT	180	
Db	124	GCCCTTAAGCTCTGTATCTGTATGATGATGATCCAAATTGGAAAGTGGGGTCCCATCAGGTTT	183	
Qy	181	AGTGCAGTGCATCTGGGACAGAGTTCACTCTCAGCATCAGCAATGTCGCAACTGTAAGAC	240	
Db	184	AGTGCAGTGCATCTGGGACAGAGTTTCACTCTCAGCATCAGCAACTGTAAGAT	243	
Qy	241	TTTGCAGATTACTACTGTCAACAGAGTTACACTACCTTATATACCTTGGCCCTTGGGACC	300	
Db	244	TTTGCAGATTACTACTGTCAACAGAGTTACAGTACCCTGATCACTTTGGCCCAAGGACA	303	
Qy	301	AAACTGAGATCAAAACA 318		
Db	304	CGACTGAGATTTAAACA 321		

RESULT 11  
 US-09-848-798-205  
 ; Sequence 205. Application US/09848798  
 ; Publication No. US20030040605A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Siegel, Donald L.  
 ; TITLE OF INVENTION: Rn(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS

```

1  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
2
3  FILE REFERENCE: 09596-42KD
4
5  CURRENT APPLICATION NUMBER: US/09/848,798
6
7  PRIOR APPLICATION NUMBER: 2001-05-04
8
9  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
10
11 PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
12
13 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,555
14
15 PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
16
17 NUMBER OF SEQ ID NOS: 224
18
19 SOFTWARE: PatentIn Ver. 2.0
20
21 SEQ ID NO 205
22
23 LENGTH: 321
24
25 TYPE: DNA
26
27 ORGANISM: Homo sapiens
28
29 FEATURE:
30
31 OTHER INFORMATION: anti-Rh(D) antibody clone SH24
32
33 US-09-848-798-205

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	Query Match	Best Local Similarity	85.4%;	Score 271.6;	DB 10;	Length 321;	
			90.9%;	Pred. No. 1.5e-82;			
	Matches	289;	Conservative	0;	Mismatches	22;	Indels
							Gaps
							0
QY	1	GAGCTCACCCAGTCTCCATCCCTCGTCTGCTGCTCTGTAGGAGACAGAGTCCACATCACT					60
Db	4	GAGCTCACCCAGTCTCCATCCCTCGTCTGCTGCTGTAGGAGACAGAGTCCACATCACT					63
QY	61	TGCCCCGACGTCAGAGTTATGACACCTATTAAATTGGTATTCACAGAAACCGGGGGAAG					120
Db	64	TGCCCCGACAGTCAGAGATTGACACCTATTAAATTGGTATTCACAGAAACCGGGGGAAG					123
QY	121	GCCCCTAAGTCTCTGATCTGTAGTGCATCCATTTGCAAAAGTGGGGTCCCATCCAGGTTTC					180
Db	124	GCCCCTAAGTCTCTGATCTGTAGTGCATCCATTTGCAAAAGGGGGTCCCATCAAGGTTTC					183
QY	181	AGTGGCAGATGATCTGGGACAGAGTTCATCTCCACATCAGCAATCTGCAACCTGAAGAC					240
Db	184	ACTGGCAGATGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT					243
QY	241	TTTGGCAAGTACTACTGTCCACAGAGTTACACTACCTTATATACCTTGGCCCTGGGAGCC					300
Db	244	TTTGCACATTAATCTACTGTCCACAGAGTTACACTACCTTGTGGAGCCTTGGCCCAAGGAGCC					303
QY	301	AAACTGGAGATCAACGCA 318					
Db	304	AAAGATGCAATCAAGCA 321					

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RESULT 12
US-09-848-798-221
; Sequence 221, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL-
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; PTE REFERENCE: 09596-4302
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-221

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Query Match	85.4%;	Score 271.6;	DB 10;	Length 321;
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Best Local Similarity 90.9%; Pred. No. 1.5e-82;  
Matches 289; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 GAGCTCACCCAGTCTCCATCTCCCTGTCTGCTGTAGAGACAGAGTCCATCACT 60  
DB 4 GAGCTCACCCAGTCTCCATCTCCCTGTCTGCTGTAGAGACAGAGTCCATCACT 63  
QY 61 TGCCTGGGACAGTCTGAGTATTAGCACTATTAAATGGTATCAGCAAAACCGGGAG 120  
DB 64 TGCCTGGGACAGTCTGAGTATTAGCACTATTAAATGGTATCAGCAAAACCGGGAA 123  
QY 121 GCCCCTAAGCTCCGATCTGTAGTCACTCAATTGGCAAGTGGGGTCCCATCAGGTTC 180  
DB 124 GCCCCTAAGCTCCGATCTGTAGTCACTCAATTGGCAAGTGGGGTCCCATCAGGTTC 183  
QY 181 AGTGGCAGTGGATCTGGAGACAGATTCATCTCAACCAATCTGCAACTGGAAGAC 240  
DB 184 AGTGGCAGTGGATCTGGAGACAGATTCATCTCAACCAATCTGCAACTGGAAGAT 243  
QY 241 TTTCGAAGTTACTCTGTCAACAGAGTTACACTACCTTATACCTTGGCCCTGGGACC 300  
DB 244 TTTCGAAGTTACTCTGTCAACAGAGTTACACTACCTTATACCTTGGCCCAAGGACC 303  
QY 301 AAATGGAGATCAACGA 318  
DB 304 AAGGTGAATCAACGA 321

## RESULT 13

US-09-848-798-222  
; Sequence 222, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 222  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54  
US-09-848-798-222

Query Match 85.4%; Score 271.6; DB 10; Length 321;

Best Local Similarity 90.9%; Pred. No. 1.5e-82;  
Matches 289; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 GAGCTCACCCAGTCTCCATCTCCCTGTCTGCTGTAGAGACAGAGTCCATCACT 60  
DB 4 GAGCTCACCCAGTCTCCATCTCCCTGTCTGCTGTAGAGACAGAGTCCATCACT 63  
QY 61 TGCCTGGGACAGTCTGAGTATTAGCACTATTAAATGGTATCAGCAAAACCGGGAG 120  
DB 64 TGCCTGGGACAGTCTGAGTATTAGCACTATTAAATGGTATCAGCAAAACCGGGAA 123  
QY 121 GCCCCTAAGCTCCGATCTGTAGTCACTCAATTGGCAAGTGGGGTCCCATCAGGTTC 180  
DB 124 GCCCCTAAGCTCCGATCTGTAGTCACTCAATTGGCAAGTGGGGTCCCATCAGGTTC 183  
QY 181 AGTGGCAGTGGATCTGGAGACAGATTCATCTCAACCAATCTGCAACTGGAAGAC 240  
DB 184 AGTGGCAGTGGATCTGGAGACAGATTCATCTCAACCAATCTGCAACTGGAAGAT 243

QY 241 TTTCGAAGTTACTCTGTCAACAGAGTTACACTTATATACCTTGGCCCTGGGACC 300  
DB 244 TTTCGAAGTTACTCTGTCAACAGAGTTACACTTATATACCTTGGCCCAAGGACC 303  
QY 301 AAATGGAGATCAACGA 318  
DB 304 AAGGTGAATCAACGA 321

## RESULT 14

US-09-192-854-1  
; Sequence 1, Application US/09192854  
; Patent No. US20020068276A1  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Greg  
; APPLICANT: Tomlinson, Ian  
; TITLE OF INVENTION: Methods for Selecting Functional Peptides  
; FILE REFERENCE: 3789/72916  
; CURRENT APPLICATION NUMBER: US/09/192,854  
; CURRENT FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: 60/066,729  
; EARLIER FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-192-854-1

Query Match 85.3%; Score 271.2; DB 9; Length 720;  
Best Local Similarity 91.1%; Pred. No. 2.7e-82;  
Matches 288; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2 AGCTCACCCAGTCTCCATCTCCCTGTCTGCTGTAGAGACAGAGTCCATCACT 61  
DB 404 AGATGACCCAGTCTCCATCTCCCTGTCTGCTGTAGAGACAGAGTCCATCACT 463  
QY 62 GCCCGGACAGTCTGAGTATTAGCACTATTAAATGGTATCAGCAAAACCGGGAGG 121  
DB 464 GCCCGGACAGTCTGAGTATTAGCACTATTAAATGGTATCAGCAAAACCGGGAA 523  
QY 122 CCCCTAAGCTCCGATCTGTAGTCACTCAATTGGCAAGTGGGGTCCCATCAGGTTC 181  
DB 524 CCCCTAAGCTCCGATCTGTAGTCACTCAATTGGCAAGTGGGGTCCCATCAGGTTC 583  
QY 182 GTGGCAGTGGATCTGGAGACAGATTCATCTCAACCAATCTGCAACTGGAAGACT 241  
DB 584 GTGGCAGTGGATCTGGAGACAGATTCATCTCAACCAATCTGCAACTGGAAGATT 643  
QY 242 TTTCGAAGTTACTCTGTCAACAGAGTTACACTTATATACCTTGGCCCTGGGACCA 301  
DB 644 TTTCGAAGTTACTCTGTCAACAGAGTTACACTTATATACCTTGGCCCAAGGACCA 703  
QY 302 AACTGGAGATCAACG 317  
DB 704 AAGGTGAATCAACG 719

## RESULT 15

US-09-968-561A-1  
; Sequence 1, Application US/09968561A  
; Patent No. US20020164642A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands  
; FILE REFERENCE: 8039/1073B  
; CURRENT APPLICATION NUMBER: US/09/968,561A  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248

; PRIOR FILING DATE: 1997-11-13  
 ; PRIOR APPLICATION NUMBER: US 60/066,729  
 ; PRIOR FILING DATE: 1997-11-21  
 ; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
 ; PRIOR FILING DATE: 1998-10-20  
 ; PRIOR APPLICATION NUMBER: US 09/511,939  
 ; PRIOR FILING DATE: 2000-02-24  
 ; NUMBER OF SEQ ID NOS: 350  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 720  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-968-561A-1

Query Match 85.3%; Score 271.2; DB 9; Length 720;  
 Best Local Similarity 91.1%; Pred. No. 2.7e-82;  
 Matches 288; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Db	404	AGATGACCCAGTCTCATCTCCCTGCTGCTGAGAGACAGATCACCATCACTT	463
QY	62	GCCGGGCAAGTCAAGATTTAGCACTATTAAATTGGTATCAGCAGAAACCGGGAAAG	121
Db	464	GCCGGGCAAGTCAAGATTTAGCACTATTAAATTGGTATCAGCAGAAACCGGGAAAG	523
QY	122	CCCTTAGCTCCGATCTAGTATGATCCCAATTGGCAAGTGGGTCCTCCATCCAGGTTCA	181
Db	524	CCCTTAGCTCCGATCTAGTATGATCCCAATTGGCAAGTGGGTCCTCCATCCAGGTTCA	583
QY	182	GTGGCAGTGAATCGGAGAGATTCACTCTCACCATCAGCAATCTGCAACTGGAAGCT	241
Db	584	GTGGCAGTGAATCGGAGAGATTCACTCTCACCATCAGCAATCTGCAACTGGAAGCT	643
QY	242	TTGCAAGTACTACTGTCAACAGAGTTACACTTATATATACCTTGGCCCTGGAGCA	301
Db	644	TTGCAAGTACTACTGTCAACAGAGTTACACTTATATATACCTTGGCCCTGGAGCA	703
QY	302	AACGTGAGATCAACG 317	
Db	704	AGGTGAAATCAACG 719	

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Sequence: 1 gagctcacccagctccatc.....ccaactcgagatcaacga 318

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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4: gb\_cm:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	316.4	99.5	318	9	HS458380 Homo sapi
2	281.2	88.4	321	9	HS1GVK110
3	278	87.4	322	9	HUMIGHG
4	278	87.4	326	9	HUMIGHG
5	277	87.1	830	9	AB064095 Homo sapi
6	276.4	86.9	321	6	AR160973 Sequence
7	276.4	86.9	321	6	AR161027 Sequence
8	276.4	86.9	328	9	HUMIGHG
9	276.8	86.1	324	9	AB063929 Homo sapi
10	276.8	86.1	324	9	AR107245 Homo sapi
11	273.8	86.1	390	9	HS043773 Human immun
12	273.8	86.1	828	9	AB064098 Homo sapi
13	273.4	86.0	315	6	A68535 Sequence 51
14	273.4	86.0	315	9	HS1D220VL
15	273.4	86.0	318	12	AF044451
16	273.2	85.9	321	6	AR160978 Sequence
17	273.2	85.9	321	6	AR160984 Sequence
18	273.2	85.9	321	6	AR161029 Sequence
19	273.2	85.9	321	6	AR161039 Sequence

20	273.2	85.9	321	6	AR161046 Sequence
21	273.2	85.9	321	9	HS1GVK16F
22	273.2	85.9	796	9	AB064138 Homo sapi
23	272.6	85.7	311	9	HS98989
24	272.2	85.6	387	12	AF453148
25	272.2	85.6	429	9	HUMIGHG
26	272.2	85.6	735	6	CQ849413 Sequence
27	272.2	85.6	735	6	CQ849425 Sequence
28	272.2	85.6	735	6	CQ849427 Sequence
29	272.2	85.6	736	6	CQ758827 Sequence
30	272.2	85.6	738	6	CQ849415 Sequence
31	272.2	85.6	750	6	CQ849417 Sequence
32	272.2	85.6	750	6	CQ849421 Sequence
33	271.6	85.5	367	12	AF453190
34	271.6	85.4	321	6	AR160977
35	271.6	85.4	321	6	AR161033
36	271.6	85.4	321	6	AR161049
37	271.6	85.4	321	6	AR161050
38	271.6	85.4	324	9	AB063932
39	271.6	85.4	325	9	HUMIGHG
40	271.2	85.3	369	12	AF453186
41	271.2	85.3	720	6	CQ761230
42	271.2	85.3	720	6	CQ840583 Sequence
43	271.2	85.3	720	6	AR476229 Sequence
44	271.2	85.3	720	6	AR4740176
45	271.2	85.3	720	6	BD077368 Method of

#### ALIGNMENTS

RESULT 1	HS458380	318 bp	mRNA	linear	PRI 30-APR-2002
LOCUS	HS458380				
DEFINITION	Homo sapiens partial mRNA for immunoglobulin kappa light chain variable region (IGKV gene), clone 60.				
ACCESSION	AF458380				
VERSION	AF458380.1	GI:20387059			
KEYWORDS	IGKV gene; immunoglobulin kappa; light chain; variable region.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1. Flicker S., Steinberger P., Norderhaug L., Sperr W.R., Majlesi Y., Valent P., Kraft D. and Valenta R. Conversion of grass allergen-specific human IgE into a protective IgG1 antibody				
AUTHORS	Unpublished				
JOURNAL	2 (bases 1 to 318)				
REFERENCE	Flicker S.				
AUTHORS	Direct Submission				
TITLE	Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA				
JOURNAL					
FEATURES	source				
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Query Match 99.5%; Score 316.4; DB 9; Length 318;  
Best Local Similarity 99.7%; Pred. No. 5.5e-90;  
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGTAGAGAGACAGATCACCATCACT 60  
Db 1 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGTAGAGAGACAGATCACCATCACT 60  
QY 61 TGCGGGCAGCTGACAGTATTAGACCTATTAAATTGGATTCAGCAGAAACCGGGAG 120  
Db 61 TGCGGGCAGCTGACAGTATTAGACCTATTAAATTGGATTCAGCAGAAACCGGGAG 120  
QY 121 GCCCTTAAGCTCTGATCTGTAGTCATCCAAATTTGCAAAAGTGGGTCCTCCATCCAGTTTC 180  
Db 121 GCCCTTAAGCTCTGATCTGTAGTCATCCAAATTTGCAAAAGTGGGTCCTCCATCCAGTTTC 180  
QY 181 AGTGGCAGTGGATCTGGAGACAGATTCACTCAACATCAGCAATCTGCAACTGAAAGAC 240  
Db 181 AGTGGCAGTGGATCTGGAGACAGATTCACTCAACATCAGCAATCTGCAACTGAAAGAC 240  
QY 241 TTTCGAAGTACTACTGTCACAGAGTTACACTATATACCTTGGGCTTGGAGAC 300  
Db 241 TTTCGAAGTACTACTGTCACAGAGTTACACTATATACCTTGGGCTTGGAGAC 300  
QY 301 AAACCTGAGATCAACGA 318  
Db 301 AAACCTGAGATCAACGA 318

RESULT 2  
HSIGVK10 321 bp mRNA linear PRI 30-MAR-1995  
LOCUS H.sapiens mRNA for Ig kappa light chain variable region  
DEFINITION (V-J), subgroup 1 (clone 101).  
X73860  
ACCESSION X73860.1 GI:516249  
VERSION autoantibody; Ig J-segment; Ig kappa light chain; Ig subgroup I; Ig  
KEYWORDS variable region; Immunoglobulin.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Hexham,J.M., Furmaniak,J., Pegg,C., Burton,D.R. and Smith,B.R.  
TITLE Cloning of a human autoimmune response: preparation and sequencing  
of a human anti-thyroglobulin autoantibody using a combinatorial  
approach  
JOURNAL Autoimmunity 12 (2), 135-141 (1992)  
MEDLINE 92314301  
PUBMED 1617110  
REFERENCE 2 (bases 1 to 321)  
AUTHORS Hexham,J.M., Parttridge,L.J., Furmaniak,J., Petersen,V.B.,  
Colls,J.C., Pegg,C., Rees Smith,B. and Burton,D.R.  
TITLE Cloning and characterisation of TPO autoantibodies using  
combinatorial phage display libraries  
JOURNAL Autoimmunity 17 (3), 167-179 (1994)  
MEDLINE 95035699  
PUBMED 7524700  
REFERENCE 3 (bases 1 to 321)  
AUTHORS Hexham,J.M., Parttridge,L.J., Furmaniak,J., Petersen,V.B.,  
Colls,J.C., Pegg,C.A.S., Rees-Smith,B. and Burton,D.R.  
TITLE Probing the human anti-thyroid peroxidase repertoire of a  
Hashimoto's thyroiditis patient using combinatorial phage display  
libraries  
JOURNAL Unpublished  
REFERENCE 4 (bases 1 to 321)  
AUTHORS Hexham,J.

TITLE Direct Submission  
JOURNAL Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept. of  
Mol. Biology and Biotechnology, P. O. Box 594, Firth Court, Western  
Bank, Sheffield S10 2UH, UK  
FEATURES location/Qualifiers  
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/isolate="Hashimoto patient"  
/db\_xref="taxon:9606"  
/clone="101"  
/sex="female"  
/cell\_type="thyroid lymphocyte"  
/clone\_lib="pComb3 phagemid library"  
/note="rearranged"  
V\_region 1..321  
/product="Ig kappa light chain variable region, subgroup  
I"  
/note="Igk1/K anti-thyroid peroxidase autoantibody Fab"

ORIGIN

Query Match 88.4%; Score 281.2; DB 9; Length 321;  
Best Local Similarity 92.8%; Pred. No. 1e-78;  
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGTAGAGAGACAGATCACCATCACT 60  
Db 1 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGTAGAGAGACAGATCACCATCACT 60  
QY 61 TGCGGGCAGCTGACAGTATTAGACCTATTAAATTGGATTCAGCAGAAACCGGGAG 120  
Db 61 TGCGGGCAGCTGACAGTATTAGACCTATTAAATTGGATTCAGCAGAAACCGGGAG 120  
QY 121 GCCCTTAAGCTCTGATCTGTAGTCATCCAAATTTGCAAAAGTGGGTCCTCCATCCAGTTTC 180  
Db 121 GCCCTTAAGCTCTGATCTGTAGTCATCCAAATTTGCAAAAGTGGGTCCTCCATCCAGTTTC 180  
QY 181 AGTGGCAGTGGATCTGGAGACAGATTCACTCAACATCAGCAATCTGCAACTGAAAGAC 240  
Db 181 AGTGGCAGTGGATCTGGAGACAGATTCACTCAACATCAGCAATCTGCAACTGAAAGAC 240  
QY 241 TTTCGAAGTACTACTGTCACAGAGTTACACTATATACCTTGGGCTTGGAGAC 300  
Db 241 TTTCGAAGTACTACTGTCACAGAGTTACACTATATACCTTGGGCTTGGAGAC 300  
QY 301 AAACCTGAGATCAACGA 318  
Db 301 AAACCTGAGATCAACGA 318

RESULT 3  
HUMIGHGD 322 bp mRNA linear PRI 03-MAY-2000  
LOCUS Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region  
DEFINITION (IGHV6) mRNA, partial cds.  
L03142  
ACCESSION L03142.1 GI:185377  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 322)  
AUTHORS Collier,T.A., Roben,P., O'Kennedy,R., Barbas,C.F. III, Burton,D.R.  
and Lerner,R.A.  
TITLE A binary plasmid system for shuffling combinatorial antibody  
libraries  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)  
MEDLINE 93066172  
PUBMED 1438192  
FEATURES location/Qualifiers  
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ORIGIN
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Best Local Similarity 92.1%; Pred. No. 1.1e-77;
Matches 293; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 GAGCTACCCAGTCCATCTCCCTGTGCTCTGTAGAGACAGATCACCATCACT 60
DB 1 GAGCTACCCAGTCCATCTCCCTGTGCTCTGTAGAGACAGATCACCATCACT 60
QY 61 TGCCGGGCAAGTCAGAGATTAGACCACTTTAAATTGATTCAGCAAGAACCGGGGAAG 120
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QY 121 GCCCCTAAGCTCTGATCTGTAGTCATCCAAATTGGCAAGTGGGGTCCCATCAGGTTTC 180
DB 121 GCCCCTAAGCTCTGATCTGTAGTCATCCAAATTGGCAAGTGGGGTCCCATCAGGTTTC 180
QY 181 AGTGGCAGTGGATCTGGGACAGATTCTCACTCAACATCAGCACTGCAACCTGAAGAT 240
DB 181 AGTGGCAGTGGATCTGGGACAGATTCTCACTCAACATCAGCACTGCAACCTGAAGAT 240
QY 241 TTTCGAAGTTACTACTGTCAACAGATTACCTATTAACCTTGGGCCCTGGGAGCC 300
DB 241 TTTCGAAGTTACTACTGTCAACAGATTACCTATTAACCTTGGGCCCTGGGAGCC 300
QY 301 AAACCTGGAGATCAACGA 318
DB 301 AAACCTGGAGATCAACGA 318

RESULT 4
HUMIGHGY 326 bp mRNA linear PRI 03-MAY-2000
LOCUS Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region
DEFINITION (IGHV) mRNA, partial cds.
ACCESSION L03160
VERSION L03160.1 GI:185395
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 326)
Collier,T.A., Roben,P., O'Kennedy,R., Barbae,C.F. III, Burton,D.R.
and Lerner,R.A.
A binary plasmid system for shuffling combinatorial antibody
libraries
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
MEDLINE 93066172
PUBMED 1438192
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V_region

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Best Local Similarity 92.1%; Pred. No. 1.1e-77;
Matches 293; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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DB 1 GAGCTACCCAGTCCATCTCCCTGTGCTCTGTAGAGACAGATCACCATCACT 60
QY 61 TGCCGGGCAAGTCAGAGATTAGACCACTTTAAATTGATTCAGCAAGAACCGGGGAAG 120
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QY 121 GCCCCTAAGCTCTGATCTGTAGTCATCCAAATTGGCAAGTGGGGTCCCATCAGGTTTC 180
DB 121 GCCCCTAAGCTCTGATCTGTAGTCATCCAAATTGGCAAGTGGGGTCCCATCAGGTTTC 180
QY 181 AGTGGCAGTGGATCTGGGACAGATTCTCACTCAACATCAGCACTGCAACCTGAAGAT 240
DB 181 AGTGGCAGTGGATCTGGGACAGATTCTCACTCAACATCAGCACTGCAACCTGAAGAT 240
QY 241 TTTCGAAGTTACTACTGTCAACAGATTACCTATTAACCTTGGGCCCTGGGAGCC 300
DB 241 TTTCGAAGTTACTACTGTCAACAGATTACCTATTAACCTTGGGCCCTGGGAGCC 300
QY 301 AAACCTGGAGATCAACGA 318
DB 301 AAACCTGGAGATCAACGA 318

RESULT 5
AB064095 830 bp mRNA linear PRI 02-JUL-2002
LOCUS Homo sapiens IGH mRNA for immunoglobulin kappa 1 light chain VLJ
DEFINITION region, partial cde, clone:K54.
ACCESSION AB064095
VERSION AB064095.1 GI:21669396
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukal,Y., Honda,T., Katsumi,H., Okada,U.,
Miura,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation
```

of therapeutic human antibodies and application to functional genomics  
Unpublished  
2 (bases 1 to 830)  
Kurosawa, Y.  
Direct Submission  
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Kutsukake-cho, Toyake 470-1192, Japan  
E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)  
Please visit our web site  
URL: http://www.fujita-hu.ac.jp/immunity/.

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ORIGIN  
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Best Local Similarity 92.1%; Pred. No. 2,1e-77;  
Matches 292; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 2 AGCTACCCAGTCTCCATCTCTCCCTGTGCTCTGTAGAGAGACAGATCCATCACTT 61  
DB 74 AGATGACCCAGTCTCCATCTCTCCCTGTGCTCTGTAGAGAGACAGATCCATCACTT 133  
QY 62 GCCGGGACGTCAGAGATTAGACACTTTAAATTGGTATCAGACAGAAACCGGGGAAG 121  
DB 134 GCCGGGACGTCAGAGATTAGACACTTTAAATTGGTATCAGACAGAAACCGGGGAAG 193  
QY 122 CCCCTAAGCTCTGATCTGTAGTCATCCAAATTTGCAAAAGTGGGGTCCCATCAAGTTCA 181  
DB 194 CCCCTAAGCTCTGATCTGTAGTCATCCAAATTTGCAAAAGTGGGGTCCCATCAAGTTCA 253  
QY 182 GTGGCAGTGTCTGGGACAGAGTTCATCTCACCATCAGCAATCTGCAACCTGAAGACT 241  
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QY 242 TTGCAAGTTACTACTGTCTCAACAGAGTTACACTACTTATTAACCTTGGCCCTGGGACCA 301  
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QY 302 AACTGAGATCAACGA 318  
DB 374 AAGTGATATCAACGA 390

RESULT 6  
ARI60973 321 bp DNA linear PAT 17-OCT-2001  
LOCUS  
DEFINITION Sequence 102 from patent US 6255455.

ACCESSION ARI60973  
VERSION ARI60973.1 GI:16226189  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 321)  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
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ORIGIN  
Query Match 86.9%; Score 276.4; DB 6; Length 321;  
Best Local Similarity 91.8%; Pred. No. 3.6e-77;  
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGCTCACCCAGTCTCCATCTCTCCCTGTGCTCTGTAGAGAGACAGATCACCATCACT 60  
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QY 61 TGCCGGGACGTCAGAGATTAGACACTTATTAATTGGTATCGCAGAAACCGGGGAAG 120  
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QY 121 GCCCTAAGCTCTGATCTGTAGTCATCCAAATTTGCAAAAGTGGGGTCCCATCAAGTTTC 180  
DB 124 GCCCTAAGCTCTGATCTGTAGTCATCCAAATTTGCAAAAGTGGGGTCCCATCAAGTTTC 183  
QY 181 AGTGGCAGTGTCTGGGACAGAGTTCATCTCACCATCAGCAATCTGCAACCTGAAGAC 240  
DB 184 AGTGGCAGTGTCTGGGACAGAGTTCATCTCACCATCAGCAAGTCTGCAACCTGAAGAT 243  
QY 241 TTGCAAGTTACTACTGTCTCAACAGAGTTACACTACTTATTAATCTTGGCCCTGGGACC 300  
DB 244 TTGCAAGTTACTACTGTCTCAACAGAGTTACAGTACCCCATCACTTTCGGCCCTGGGACC 303  
QY 301 AACTGAGATCAACGA 318  
DB 304 AAGTGATATCAACGA 321

RESULT 7  
ARI61027  
LOCUS  
DEFINITION Sequence 199 from patent US 6255455.  
ACCESSION ARI61027  
VERSION ARI61027.1 GI:16226382  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 321)  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
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Best Local Similarity 91.8%; Pred. No. 3.6e-77;  
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QY 61 TGCCGGGACGTCAGAGATTAGACACTTATTAATTGGTATCGCAGAAACCGGGGAAG 120  
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DB 304 AAGTGATATCAACGA 321

Db 4 GAGCTCACCAGTCTCCATCTCCCTGTCGATCTGTAGAGACAGAGTCAACCATCACT 63  
 QY 61 TGCCGGGACGCTCAGAGTATTAGACCTATTAAATTGATTCAGACAGAAACCGGGGAAG 120  
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 QY 301 AAAGCTGAGATCAACGA 318  
 Db 304 AAAGCTGAGATCAACGA 321

RESULT 8  
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 LOCUS Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region  
 (IGHV6) mRNA, partial cds.  
 ACCESSION L03164  
 VERSION L03164.1 GI:185399  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 328)  
 AUTHORS Collier, T.A., Roben, P., O'Kennedy, R., Barbae, C.F. III, Burton, D.R.  
 and Lerner, R.A.  
 TITLE A binary plasmid system for shuffling combinatorial antibody  
 libraries  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)  
 MEDLINE 93066172  
 PUBMED 1438192  
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QY 1 GAGCTCACCAGTCTCCATCTCCCTGTCGATCTGTAGAGACAGAGTCAACCATCACT 60  
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 QY 301 AAAGCTGAGATCAACGA 318  
 Db 301 AAAGCTGAGATCAACGA 318

RESULT 9  
 AB063929 324 bp mRNA linear PRI 02-JUL-2002  
 LOCUS Homo sapiens IGH mRNA for immunoglobulin kappa light chain VLJ  
 region, partial cds, clone:K102.  
 ACCESSION AB063929  
 VERSION AB063929.1 GI:21669064  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1  
 AUTHORS Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirano, Y., Kakita, M.,  
 Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, T.,  
 Mura, K., and Kurosawa, Y.  
 TITLE Construction and characterization of antibody libraries: isolation  
 of therapeutic human antibodies and application to functional  
 genomics  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 324)  
 AUTHORS Kurosawa, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for  
 Comprehensive Medical Science, Fujita Health University;  
 Kutsukake-cho, Toyosake 470-1192, Japan  
 (E-mail:kurosawa@fujita-hu.ac.jp; Tel:81-562-93-9387)  
 Please visit our web site  
 URL: http://www.fujita-hu.ac.jp/immunity/.

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ORIGIN	Query Match	86.1%; Score 273.8; DB 9; Length 324;
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QY	2 AGCTCACCACATCTTCACATCCTCCTGTGTGCTCTGTGTGAGACAGAGTCACATCACTT	61
Db	8 AGATGACCCCAATCTCCATCTCCCTGTGTGATCTGTGTGAGACAGAGTCACATCACTT	67
QY	62 GCCGGGACGATCAGAGTATTTAGCAACCTATTTAAATTGGATTCAGCAAAACCGGGGAAG	121
Db	68 GCCGGGACGATCAGAGTATTTAGCAACCTATTTAAATTGGATTCAGCAAAACCGGGGAAG	127
QY	122 CCCCTAAGCTCTGTATCTGTAGTGATCCAAATTTGCCAAAGTGGGTCCCATTCAGTTC	181
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QY	182 GTGGCAGTGATCTGGGACAGAGTTCACTCTTCACCATAGCAANTGTCAACTGAAACT	241
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QY	242 TTGCAAGTTACTACGTCAACAAGATTCACACTTATATACCTTGGCCCTGGGACCA	301
Db	248 TTGCAAGTTACTACGTCAACAAGATTCACACTTATATACCTTGGCCCTGGGACCA	307
QY	302 AACTGAGANTCAACGA 318	
Db	308 AGCTGAGATCAACGA 324	
RESULT 10		
LOCUS	AF107245	324 bp mRNA linear PRI 13-JAN-2004
DEFINITION	Homo sapiens clone MD05 immunoglobulin kappa light chain variable	
ACCESSION	AF107245	region mRNA, partial cds.
VERSION	AF107245.1	GI:6492200
KEYWORDS		
SOURCE		
ORGANISM	Homo sapiens (human)	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
TITLE	1 (bases 1 to 324)	
JOURNAL	Perez, W.S., Moss, M.T. and Urbanik, S.J.	
MEDLINE	Transfusion 40 (7), 846-855 (2000)	
PUBMED	20385090	
REFERENCE	10924614	
AUTHORS	2 (bases 1 to 324)	
TITLE	Perez, W.S., Moss, M.T. and Urbanik, S.J.	
JOURNAL	Molecular Characterization Of Anti-RND Antibodies: Antibody	
REFERENCE	Repetoire, Affinity Maturation And Epitope Specificities	
AUTHORS	3 (bases 1 to 324)	
TITLE	Unpublished	
JOURNAL	Direct Submission	
REFERENCE	Submitted (18-NOV-1998) Academic Transfusion Medicine Unit,	
AUTHORS	Regional Transfusion Centre, Foresterhill Road, Foresterhill,	
TITLE	Aberdeen, Scotland AB25 2ZW, UK	
JOURNAL	Location/Qualifiers	
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Query Match	86.1%;	Score 273.8; DB 9; Length 324;		
Best Local Similarity	91.5%;	Pred. No. 2.5e-76;		
Matches 290; Conservative	0;	Mismatches 27; Indels 0; Gaps 0;		
Oy	2	AGTCACCCAGCTCTCCATCTCTCCCTGTGCTCTGTAGAGACAGAGTCACATCACTT 61		
Db	8	AGATGACCCAGCTCTCCATCTCTCCCTGTGCTCTGTAGAGACAGAGTCACATCACTT 67		
Oy	62	GCCGGGACCGTCAGAGTATTAGACCTATTAAATGGTATCAGACAGAAACCGGGGAAG 121		
Db	68	GCCGGGACGTCAGAGCATTAAGCATTAATTTAAATGGTATCAGACAGAAACCGGGAAG 127		
Oy	122	CCCTTAAGCTCTGATCTGTAGTCATCCAAATTTGGCAAAGTGGGTCCTCATCCAGTTCA 181		
Db	128	CCCTTAAGCTCTGATCTGTAGTCATCCAAATTTGGCAAAGTGGGTCCTCATCCAGTTCA 187		
Oy	182	GTGCGAGTGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTTAAGACT 241		
Db	188	GTGCGAGTGATCTGGGACAGAGTTCACTCTCACCATCAGCAAGTCTGCAACTTAAGACT 247		
Oy	242	TTGGAAGTATCTACTGTCAACAGAGTTACACTACTATATACCTTGGCCCTGGGACCA 301		
Db	248	TTGGAAGTATCTACTGTCAACAGAGTTACACTACTATATACCTTGGCCCAAGGACCA 307		
Oy	302	AACGTGAGATCAACGA 318		
Db	308	AGGTGGAATCAACGA 324		
RESULT 11				
HSU43773	390 bp	mRNA	Linear	PRI 05-JUN-1996
LOCUS	Human immunoglobulin light chain variable region mRNA, cell line			
DEFINITION	13d2, anti-RND, partial cds.			
ACCESSION	U43773			
VERSION	U43773.1 GI:1353831			
KEYWORDS	.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
AUTHORS	1 (bases 1 to 390) Boucher,G., Broly,H. and Lemieux,R.			
TITLE	Restricted Use of Cationic Germine VH Gene Segments in Human Rh(D) Red Cell Antibodies			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 390) Boucher,G.			
AUTHORS	Direct Submission			
TITLE	Submitted (21-DEC-1995) Gerard Boucher, Research and Development, The Canadian Red Cross Society, Transfusion Center of Quebec, 2535 Laurier Boulevard, Ste-Foy, Quebec G1V 4M3, Canada			
JOURNAL	Location/Qualifiers			
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DB 194 CCCCTAAGCTCTGATCTGATGATCATTTGGCAAGGGGTCCCATCCAGTTCA 253  
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DB 314 TTGCAAGTTACTACTGTCAACAGAGTTACACTTAAATTTGATCAGCAAAACCGGGAAAG 373  
QY 302 AACTGAGATCAACGA 318  
DB 374 AAGTGATATCAACGA 390

## RESULT 12

AB064098

LOCUS AB064098 828 bp mRNA linear PRI 02-JUL-2002  
DEFINITION Homo sapiens IGH mRNA for immunoglobulin kappa light chain VLJ  
region, partial cds, clone:K57.  
ACCESSION AB064098  
VERSION AB064098.1 GI:21669402  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

AUTHORS

1 Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirose, Y., Kakita, M.,  
Suzuki, K., Torii, H., Urali, Y., Honda, T., Katsunishi, H., Okada, U.,  
Mura, K., and Kurosawa, Y.  
Construction and characterization of antibody libraries: isolation  
of therapeutic human antibodies and application to functional

JOURNAL genomics  
REFERENCE Unpublished  
2 (bases 1 to 828)  
AUTHORS Kurosawa, Y.  
TITLE Direct Submission  
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for  
Comprehensive Medical Science, Fujita Health University;  
Kutsukake-cho, Toyoke 470-1192, Japan  
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)  
COMMENT Please visit our web site  
URL:http://www.fujita-hu.ac.jp/immunity/  
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DB 374 AAGTGATATCAACGA 390

## RESULT 13

A68535

LOCUS A68535 315 bp DNA linear PAT 06-MAY-1999  
DEFINITION Sequence 51 from Patent WO9749809.  
ACCESSION A68535



VERSION A68535.1 GI:4759587  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 315)  
AUTHORS Miescher, S., Vogel, M., Stadler, B., Morell, A., Imboden, M. and Amstutz, H.  
TITLE POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS, THE DNA ENCODING THEM AND THE PROCESS FOR THEIR PREPARATION AND USE  
JOURNAL Patent: WO 9749809-A 51-31-DEC-1997;  
ROTHERUSZSTIFTUNG ZENTRALLAB (CH)  
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DB 301 AAAGTGATATCAAA 315  
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LOCUS H.sapiens mRNA for variable region of immunoglobulin kappa light  
DEFINITION chain, clone LD2-20-VL.  
ACCESSION Y08251  
VERSION Y08251.1 GI:1561609

KEYWORDS Ig kappa chain; immunoglobulin; light chain; variable region.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Miescher, S.M.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 315)  
AUTHORS Miescher, S.M.  
TITLE Direct Submission  
JOURNAL Submitted (19-SEP-1996) S.M. Miescher, Institute of Immunology and Allergology, University of Bern, Sahli Haus 2, Inselspital, CH-3010 Bern, SWITZERLAND  
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DB 301 AAAGTGATATCAAA 315  
RESULT 15  
AF044451 318 bp mRNA linear SYN 31-OCT-2001  
LOCUS AF044451  
DEFINITION Synthetic construct from Homo sapiens clone 102 anti-Rh(D) antibody  
V kappa segment mRNA, partial cds.  
ACCESSION AF044451



VERSION AF044451.1 GI:3046473  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences: artificial sequences.  
REFERENCE  
AUTHORS Siegel,D.L., Chang,T.Y., Russell,S.L. and Bunya,V.Y.  
TITLE Isolation of cell surface-specific human monoclonal antibodies  
using phage display and magnetically-activated cell sorting:  
applications in immunohematology  
J. Immunol. Methods 206 (1-2), 73-85 (1997)  
JOURNAL MEDLINE 97469098  
PUBMED 9328570  
REFERENCE  
AUTHORS Chang,T.Y. and Siegel,D.L.  
TITLE Genetic and immunological properties of phage-displayed human  
anti-Rh(D) antibodies: implications for Rh(D) epitope topology  
Blood 91 (8), 3066-3078 (1998)  
JOURNAL MEDLINE 96200617  
PUBMED 9531621  
REFERENCE  
AUTHORS Chang,T.Y., Russell,S.L., Bunya,V.Y. and Siegel,D.L.  
TITLE Direct Submission  
JOURNAL Submitted (26-JAN-1998) Path & Lab Med, University of Pennsylvania,  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	287.6	90.4	321	US-09-240-274-199	Sequence 199, App
2	281.2	88.4	321	US-09-240-274-102	Sequence 102, App
3	281.2	88.4	321	US-09-240-274-109	Sequence 109, App
4	281.2	88.4	321	US-09-240-274-218	Sequence 218, App
5	279.6	87.9	321	US-09-240-274-107	Sequence 107, App
6	279.6	87.9	321	US-09-240-274-113	Sequence 113, App
7	279.6	87.9	321	US-09-240-274-221	Sequence 221, App
8	279.6	87.9	321	US-09-240-274-222	Sequence 222, App
9	276.4	86.9	321	US-09-240-274-201	Sequence 201, App
10	276.4	86.9	321	US-09-240-274-211	Sequence 211, App
11	276.2	86.9	324	US-09-240-274-101	Sequence 101, App
12	276.2	86.9	324	US-09-240-274-112	Sequence 112, App
13	276.2	86.9	324	US-09-240-274-210	Sequence 210, App
14	276	86.8	720	US-09-192-854-1	Sequence 1, Appl1
15	274.8	86.4	321	US-09-240-274-105	Sequence 105, App
16	274.8	86.4	321	US-09-240-274-216	Sequence 216, App
17	273.2	85.9	321	US-09-240-274-104	Sequence 104, App
18	273.2	85.9	321	US-09-240-274-106	Sequence 106, App
19	273.2	85.9	321	US-09-240-274-215	Sequence 215, App
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21	273	85.8	324	US-09-240-274-206	Sequence 206, App
22	271.4	85.3	324	US-09-240-274-110	Sequence 110, App
23	270.6	85.1	714	US-09-472-087-62	Sequence 62, Appl
24	270	84.9	321	US-09-240-274-205	Sequence 205, App
25	270	84.9	321	US-09-240-274-207	Sequence 207, App
26	268.2	84.3	324	US-09-240-274-224	Sequence 224, App
27	266.8	83.9	321	US-09-240-274-108	Sequence 108, App

28	266.8	83.9	321	US-09-240-274-203	Sequence 203, App
29	265.2	83.4	321	US-09-240-274-103	Sequence 103, App
30	261.6	82.3	672	US-09-456-090A-47	Sequence 47, Appl
31	261.6	82.3	672	US-09-453-234-47	Sequence 47, Appl
32	261.4	82.2	417	US-09-472-087-48	Sequence 48, Appl
33	261.2	82.1	321	US-08-378-939-13	Sequence 13, Appl
34	260.4	81.9	321	US-09-240-274-200	Sequence 200, App
35	260.4	81.9	321	US-09-240-274-213	Sequence 213, App
36	259.4	81.6	324	US-08-378-939-23	Sequence 23, Appl
37	259.4	81.6	458	US-09-472-087-44	Sequence 44, Appl
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39	259	81.4	388	US-09-042-353-358	Sequence 358, App
40	259	81.4	388	US-08-758-417A-206	Sequence 206, App
41	258.8	81.4	321	US-09-240-274-212	Sequence 212, App
42	258.2	81.2	402	US-09-472-087-49	Sequence 49, Appl
43	257.2	80.9	318	US-09-240-274-208	Sequence 208, App
44	256.4	80.6	318	US-08-844-215-20	Sequence 20, Appl
45	255.6	80.4	321	US-09-240-274-114	Sequence 114, App

# ALIGNMENTS

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RESULT 1
US-09-240-274-199
Sequence 199, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240, 274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 199
LENGTH: 321
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-199
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Best local similarity 94.0%; Pred. No. 9.2e-91;
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US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rn(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
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; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102

Query Match      88.4%; Score 281.2; DB 3; Length 321;
Best Local Similarity 92.8%; Pred. No. 1,6e-88;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0

QY      1 GAGCTCACTCAGCTCTCCATCTCTCCCTGCTGTCGATCTGTGGAGACAGAGTCCACATCAGT 60
Db      4 GAGCTCACCCAGCTCTCCATCTCTCCCTGCTGTCGATCTGTAGAGACAGAGTCCACATCAGT 63
|||||
QY      61 TGCCTGGGCAAGTCAGAGATTTAAACCTTTTAAATTGGATACGATTAACCAAGGAAA 120
Db      64 TGCCTGGGCAAGTCAGAGATTTAAACCTTTTAAATTGGATACGAGAAAACCAAGGAAA 123
|||||
QY      121 GCCCTTAAGCTCTCATCTATCTGTCGATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTTC 180
Db      124 GCCCTTAAGCTCTCATCTATCTGTCGATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTTC 183
|||||
QY      181 AGTGGCAGTGAATATGGGACAGACTTCACTTCCATCAGCAGAGTGCAGCTGAAGAT 240
Db      184 AGTGGCAGTGAATATGGGACAGACTTCACTTCCATCAGCAGAGTGCAGAACTGAAGAT 243
|||||
QY      241 TTGTGCAAGTACTACTGTGTAAGAGAGTCTCAGTGCTCGTACACTTTTGGCCAGGGAGCC 300
Db      244 TTGTGCAAGTACTACTGTGTAAGAGAGTCTCAGTACCTGTCGACGTTCCGCAAGGGAGCC 303
|||||
QY      301 AAGGTGAGATCAACGA 318
Db      304 AAGGTGAAATCAACGA 321
|||||

RESULT 3
US-09-240-274-109
; Sequence 109, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rn(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11

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: NUMBER OF SEQ ID NOS: 224
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 109
: LENGTH: 321
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: anti-Rh(D) chain I09
US-09-240-274-109

Query Match 88.4%; Score 281.2; DB 3; Length 321;
Best Local Similarity 92.8%; Pred. No. 1.6e-88;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGGTCACTAGTCTCATCTCTCCCTGTCTGCATCTGTGGAGACAGAGTCACATCACT 60
Db 4 GAGGTCAACCAAGTCTTCATCTCTCCCTGTCTGCATCTGTAGAGACAAGTCACATCACT 63
QY 61 TGCCGGGCAAGTCAGAGATTAAACCACTATTATTAATTGGTATCGACATTAACAGGAAA 120
Db 64 TGCCGGGCAAGTCAGAGACATTAGAGAGTATTTAATTGGTATCGACAGAAAACAGGAAA 123
QY 121 GCCCTTAAGTCTCTGATCTATGTCTGATTCAGTTGGAAAAGTGGGATCCCATCAAGGTT 180
Db 124 GCCCTTAAGTCTCTGATCTATGTCTGATTCAGTTGGAAAAGTGGGATCCCATCAAGGTT 183
QY 181 AGTGGCAGTGTGATTTGGGACAGACTTACCTTCACCATCAGACATCTGCAGCTCGAAGAT 240
Db 184 AGTGGCAGTGTGATTTGGGACAGACTTACCTTCACCATCAGACATCTGCAGCTCGAAGAT 243
QY 241 TTTCAGATTACTACTGTCAAGAGAGTCTAGTCTCTGATCACTTTTGGCAGGGAGC 300
Db 244 TTTCAGATTACTACTGTCAAGAGAGTCTAGTCTCTGATCACTTTTGGCAGGGAGC 303
QY 301 AAGGTGAGATCAACGA 318
Db 304 AAGGTGAGATCAACGA 321

RESULT 4
US-09-240-274-218
: Sequence 218; Application us/09240274
: Patent No. 6255455
: GENERAL INFORMATION:
: APPLICANT: Siegel, Donald L.
: TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
: FILE REFERENCE: 09596-42U2
: CURRENT APPLICATION NUMBER: US/09/240,274
: CURRENT FILING DATE: 1999-01-29
: EARLIER APPLICATION NUMBER: 60/081,380
: EARLIER FILING DATE: 1998-04-10
: EARLIER APPLICATION NUMBER: 60/028,550
: EARLIER FILING DATE: 1996-10-11
: NUMBER OF SEQ ID NOS: 224
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 218
: LENGTH: 321
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-218

Query Match 88.4%; Score 281.2; DB 3; Length 321;
Best Local Similarity 92.8%; Pred. No. 1.6e-88;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGGTCACTAGTCTCATCTCTCCCTGTCTGCATCTGTGGAGACAGAGTCACATCACT 60
Db 4 GAGGTCAACCAAGTCTTCATCTCTCCCTGTCTGCATCTGTAGAGACAAGTCACATCACT 63
QY 61 TGCCGGGCAAGTCAGAGATTAAACCACTATTATTAATTGGTATCGACATTAACAGGAAA 120
Db 64 TGCCGGGCAAGTCAGAGACATTAGAGAGTATTTAATTGGTATCGACAGAAAACAGGAAA 123
QY 121 GCCCTTAAGTCTCTGATCTATGTCTGATTCAGTTGGAAAAGTGGGATCCCATCAAGGTT 180
Db 124 GCCCTTAAGTCTCTGATCTATGTCTGATTCAGTTGGAAAAGTGGGATCCCATCAAGGTT 183
QY 181 AGTGGCAGTGTGATTTGGGACAGACTTACCTTCACCATCAGACATCTGCAGCTCGAAGAT 240
Db 184 AGTGGCAGTGTGATTTGGGACAGACTTACCTTCACCATCAGACATCTGCAGCTCGAAGAT 243
QY 241 TTTCAGATTACTACTGTCAAGAGAGTCTAGTCTCTGATCACTTTTGGCAGGGAGC 300
Db 244 TTTCAGATTACTACTGTCAAGAGAGTCTAGTCTCTGATCACTTTTGGCAGGGAGC 303
QY 301 AAGGTGAGATCAACGA 318
Db 304 AAGGTGAGATCAACGA 321

61 TGCCGGGCAAGTCAGAGATTAAACCACTATTATTAATTGGTATCGACATTAACAGGAAA 120

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Db      64 TCGCGGCAAGTCAGAGATTAGCAGCTATTAAATGGTATCAGCAAGAAACCGAGGAAA 123
Qy      121 GCCCCTAAGCTCCGATCTATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTC 180
Db      124 GCCCTTAAGCTCCGATCTATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTC 183
Qy      181 AGTGGCAGTGTATGGGACAGACTTCACTCTCAACATCAGACAGTCTGACCTGAAGAT 240
Db      184 AGTGGCAGTGTATGGGACAGATTTCATCTCTCAACATCAGACAGTCTGACCTGAAGAT 243
Qy      241 TTTCGAAGTACTACTGTCAAGAGAGTCTCAGTCCCTGTAACCTTTTGGCCAGGGGACC 300
Db      244 TTTCGAAGTACTACTGTCAAGAGAGTTCAGTACAGTCCCGTGAAGTGGCCAGGGGACC 303
Qy      301 AAGGTGAGATCAAAACGA 318
Db      304 AAGGTGAGATCAAAACGA 321

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RESULT 5
US-09-240-274-107
; Sequence 107, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240, 274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 107
US-09-240-274-107

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Query Match      87.9%; Score 279.6; DB 3; Length 321;
Best Local Similarity 92.5%; Pred. No. 6e-88;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

```

```

Qy      1 GAGCTCACTGATCTCCATCTCCCTGTCGATCTGAGGAGACAGATCAACATCACT 60
Db      4 GAGCTCACTGATCTCCATCTCCCTGTCGATCTGAGGAGACAGATCAACATCACT 63
Qy      61 TCGCGGCAAGTCAGAGATTAAACCTATTAAATGGTATCAGCATTAACAGGGAAA 120
Db      64 TCGCGGCAAGTCAGAGATTAAACCTATTAAATGGTATCAGCATTAACAGGGAAA 123
Qy      121 GCCCCTAAGCTCCGATCTATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTC 180
Db      124 GCCCCTAAGCTCCGATCTATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTC 183
Qy      181 AGTGGCAGTGTATGGGACAGACTTCACTCTCAACATCAGACAGTCTGACCTGAAGAT 240
Db      184 AGTGGCAGTGTATGGGACAGATTTCATCTCTCAACATCAGACAGTCTGACCTGAAGAT 243
Qy      241 TTTCGAAGTACTACTGTCAAGAGAGTCTCAGTCCCTGTAACCTTTTGGCCAGGGGACC 300
Db      244 TTTCGAAGTACTACTGTCAAGAGAGTTCAGTACAGTCCCGTGAAGTGGCCAGGGGACC 303
Qy      301 AAGGTGAGATCAAAACGA 318
Db      304 AAGGTGAGATCAAAACGA 321

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RESULT 6
US-09-240-274-113
; Sequence 113, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240, 274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 113
US-09-240-274-113

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```

Query Match      87.9%; Score 279.6; DB 3; Length 321;
Best Local Similarity 92.5%; Pred. No. 6e-88;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

```

```

Qy      1 GAGCTCACTGATCTCCATCTCCCTGTCGATCTGAGGAGACAGATCAACATCACT 60
Db      4 GAGCTCACTGATCTCCATCTCCCTGTCGATCTGAGGAGACAGATCAACATCACT 63
Qy      61 TCGCGGCAAGTCAGAGATTAAACCTATTAAATGGTATCAGCATTAACAGGGAAA 120
Db      64 TCGCGGCAAGTCAGAGATTAAACCTATTAAATGGTATCAGCATTAACAGGGAAA 123
Qy      121 GCCCCTAAGCTCCGATCTATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTC 180
Db      124 GCCCCTAAGCTCCGATCTATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTC 183
Qy      181 AGTGGCAGTGTATGGGACAGACTTCACTCTCAACATCAGACAGTCTGACCTGAAGAT 240
Db      184 AGTGGCAGTGTATGGGACAGATTTCATCTCTCAACATCAGACAGTCTGACCTGAAGAT 243
Qy      241 TTTCGAAGTACTACTGTCAAGAGAGTCTCAGTCCCTGTAACCTTTTGGCCAGGGGACC 300
Db      244 TTTCGAAGTACTACTGTCAAGAGAGTTCAGTACAGTCCCGTGAAGTGGCCAGGGGACC 303
Qy      301 AAGGTGAGATCAAAACGA 318
Db      304 AAGGTGAGATCAAAACGA 321

```

```

RESULT 7
US-09-240-274-221
; Sequence 221, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240, 274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221

```

LENGTH: 321  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH52  
US-09-240-274-221

Query Match 87.9%; Score 279.6; DB 3; Length 321;  
Best Local Similarity 92.5%; Pred. No. 6e-88;  
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTAGTCTCCATCTCCCTGTCGATCTGTGGAGACAGAGTCACATCATGT 60  
DB 4 GAGCTCACTAGTCTCCATCTCCCTGTCGATCTGTGGAGACAGAGTCACATCATGT 63  
QY 61 TGCCGGGCAAGTCAAGAAATTAACACCTATTAAATGGTATGATCAAGAAACGAGGAAA 120  
DB 64 TGCCGGGCAAGTCAAGAAATTAACACCTATTAAATGGTATGATCAAGAAACGAGGAAA 123  
QY 121 GCCCTTAAGCTCTGATCTATGTCGATCAAGTTGCAAGTGGGGTCCCATCAAGTTTC 180  
DB 124 GCCCTTAAGCTCTGATCTATGTCGATCAAGTTGCAAGTGGGGTCCCATCAAGTTTC 183  
QY 181 AGTGGCAGTGAATATGGAGACAGCTTCCTCAACATCAGAGTCTGACCTGGAAGAT 240  
DB 184 AGTGGCAGTGAATATGGAGACAGCTTCCTCAACATCAGAGTCTGGAAGAT 243  
QY 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGACC 300  
DB 244 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGACC 303  
QY 301 AAGGTGAGATCAAAACA 318  
DB 304 AAGGTGAGATCAAAACA 321

## RESULT 8

US-09-240-274-222  
Sequence 222, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 222  
LENGTH: 321  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH54  
US-09-240-274-222

Query Match 87.9%; Score 279.6; DB 3; Length 321;  
Best Local Similarity 92.5%; Pred. No. 6e-88;  
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTAGTCTCCATCTCCCTGTCGATCTGTGGAGACAGAGTCACATCATGT 60  
DB 4 GAGCTCACTAGTCTCCATCTCCCTGTCGATCTGTGGAGACAGAGTCACATCATGT 63  
QY 61 TGCCGGGCAAGTCAAGAAATTAACACCTATTAAATGGTATGATCAAGAAACGAGGAAA 120  
DB 64 TGCCGGGCAAGTCAAGAAATTAACACCTATTAAATGGTATGATCAAGAAACGAGGAAA 123

QY 121 GCCCTTAAGCTCTGATCTATGTCGATCAAGTTGCAAGTGGGGTCCCATCAAGTTTC 180  
DB 124 GCCCTTAAGCTCTGATCTATGTCGATCAAGTTGCAAGTGGGGTCCCATCAAGTTTC 183  
QY 181 AGTGGCAGTGAATATGGAGACAGCTTCCTCAACATCAGAGTCTGACCTGGAAGAT 240  
DB 184 AGTGGCAGTGAATATGGAGACAGCTTCCTCAACATCAGAGTCTGGAAGAT 243  
QY 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGACC 300  
DB 244 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGACC 303  
QY 301 AAGGTGAGATCAAAACA 318  
DB 304 AAGGTGAGATCAAAACA 321

## RESULT 9

US-09-240-274-201  
Sequence 201, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 201  
LENGTH: 321  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH16  
US-09-240-274-201

Query Match 86.9%; Score 276.4; DB 3; Length 321;  
Best Local Similarity 91.8%; Pred. No. 7.9e-87;  
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGCTCACTAGTCTCCATCTCCCTGTCGATCTGTGGAGACAGAGTCACATCATGT 60  
DB 4 GAGCTCACTAGTCTCCATCTCCCTGTCGATCTGTGGAGACAGAGTCACATCATGT 63  
QY 61 TGCCGGGCAAGTCAAGAAATTAACACCTATTAAATGGTATGATCAAGAAACGAGGAAA 120  
DB 64 TGCCGGGCAAGTCAAGAAATTAACACCTATTAAATGGTATGATCAAGAAACGAGGAAA 123  
QY 121 GCCCTTAAGCTCTGATCTATGTCGATCAAGTTGCAAGTGGGGTCCCATCAAGTTTC 180  
DB 124 GCCCTTAAGCTCTGATCTATGTCGATCAAGTTGCAAGTGGGGTCCCATCAAGTTTC 183  
QY 181 AGTGGCAGTGAATATGGAGACAGCTTCCTCAACATCAGAGTCTGACCTGGAAGAT 240  
DB 184 AGTGGCAGTGAATATGGAGACAGCTTCCTCAACATCAGAGTCTGGAAGAT 243  
QY 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGACC 300  
DB 244 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGACC 303  
QY 301 AAGGTGAGATCAAAACA 318  
DB 304 AAGGTGAGATCAAAACA 321

RESULT 10  
US-09-240-274-211

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; Sequence 211, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 211
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-240-274-211

Query Match      86.9%; Score 276.4; DB 3; Length 321;
Best Local Similarity 91.8%; Pred. No. 7.9e-87;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGCTCACTCACTGTCCTCCCTGTCGATCTGTGGAGACAGATCACTCACT 60
DB 4 GAGCTCACTCACTGTCCTCCCTGTCGATCTGTGGAGACAGATCACTCACT 63
QY 61 TCCCGGCAAGTCAAGATTAACACCTATTAAATGGATATGACAGAAACAGGAAA 120
DB 64 TCCCGGCAAGTCAAGATTAACACCTATTAAATGGATATGACAGAAACAGGAAA 123
QY 121 GCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGGAGAGGCTCCATCAAGTTTC 180
DB 124 TCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGGAGAGGCTCCATCAAGTTTC 183
QY 181 AGTGGCAGTGAATGGAGACAGATCTCACTCACTCACTCACTCACTCACTCACT 240
DB 184 AGTGGCAGTGAATGGAGACAGATCTCACTCACTCACTCACTCACTCACTCACT 243
QY 241 TTTCAGTGAATCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 244 TTTCAGTGAATCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 303
QY 301 AAGGTGAGATCAACGA 318
DB 304 AAGGTGAGATCAACGA 321

RESULT 11
US-09-240-274-101
; Sequence 101, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 101
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-101
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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-101

Query Match      86.9%; Score 276.2; DB 3; Length 324;
Best Local Similarity 93.5%; Pred. No. 9.3e-87;
Matches 300; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

QY 1 GAGCTCACTCACTGTCCTCCCTGTCGATCTGTGGAGACAGATCACTCACT 60
DB 4 GAGCTCACTCACTGTCCTCCCTGTCGATCTGTGGAGACAGATCACTCACT 63
QY 61 TCCCGGCAAGTCAAGATTAACACCTATTAAATGGATATGACAGAAACAGGAAA 120
DB 64 TCCCGGCAAGTCAAGATTAACACCTATTAAATGGATATGACAGAAACAGGAAA 123
QY 121 GCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGGAGAGGCTCCATCAAGTTTC 180
DB 124 GCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGGAGAGGCTCCATCAAGTTTC 183
QY 181 AGTGGCAGTGAATGGAGACAGATCTCACTCACTCACTCACTCACTCACTCACT 240
DB 184 AGTGGCAGTGAATGGAGACAGATCTCACTCACTCACTCACTCACTCACTCACT 243
QY 241 TTTCAGTGAATCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 244 TTTCAGTGAATCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 303
QY 298 ACCAAGTGAATCAACGA 318
DB 304 ACCAAGTGAATCAACGA 324

RESULT 12
US-09-240-274-112
; Sequence 112, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 112
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-112

Query Match      86.9%; Score 276.2; DB 3; Length 324;
Best Local Similarity 93.5%; Pred. No. 9.3e-87;
Matches 300; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

QY 1 GAGCTCACTCACTGTCCTCCCTGTCGATCTGTGGAGACAGATCACTCACT 60
DB 4 GAGCTCACTCACTGTCCTCCCTGTCGATCTGTGGAGACAGATCACTCACT 63
QY 61 TCCCGGCAAGTCAAGATTAACACCTATTAAATGGATATGACAGAAACAGGAAA 120
DB 64 TCCCGGCAAGTCAAGATTAACACCTATTAAATGGATATGACAGAAACAGGAAA 123
QY 121 GCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGGAGAGGCTCCATCAAGTTTC 180
DB 124 GCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGGAGAGGCTCCATCAAGTTTC 183
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QY      1 GAGCTCACTCACTCTCCATCTCCCTGTCTGCAATCTGTGGAGACAGAGTCACCATCAGT 60
      |||||||
Db      4 GAGCTCAACCCAGTCTCCATCTCCCTGTCTGCAATCTGTAGGAGACAGAGTCACCATCAGT 63
      |||||||
QY      61 TGGCGGGCAAGTCAGAGAAATTAAACCCATTTAAATTGTAATCAGCATTAACCCAGGAAA 120
      |||||||
Db      64 TGGCGGGCAAGTCAGAGCAATTAGGAGGTATTAAATTGTAATCAGCACAAACCCAGGAAA 123
      |||||||
QY      121 GCCCTTAAGCTCTGATCTATGCTGCAATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTT 180
      |||||||
Db      124 GCCCTTAAGCTCTGATCTTTGCTGCAATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTT 183
      |||||||
QY      181 AGTGGAGTGAATATGGAGACAGACTTCACTCAACCATCAGCAGTCTGCAAGCTGAAGAT 240
      |||||||
Db      184 ACTGGCAGTGGATCTGGGACAGATTTCACCTCAACCATCAGCAGTCTGCAACCTGAAGAT 243
      |||||||
QY      241 TTTGCAAGTCTACTCTGCAAGAGAGTCTCAGTGCTCTGTACACTTTGGCCAGGGGACC 300
      |||||||
Db      244 TTTGCAACTTACTCTGTCAACAGAGTTACAGTACCCCTCAAAACGTTGGCCAGGGGACC 303
      |||||||
QY      301 AAGGTGAGATCAACGA 318
      |||||||
Db      304 AAGGTGAAATCAACGA 321
      |||||||
```

Search completed: July 27, 2005, 12:41:21  
Job time : 88.6545 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:42:26 ; Search time 95.3455 Seconds  
(without alignments)  
5869.253 Million cell updates/sec

Title: US-10-027-725A-3

Perfect score: 342  
Sequence: 1 ctgcagctcgtgccaccagact.....ccctgtcaccgtctctctca 342

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 240568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PTUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	267.2	78.1	516	4 US-09-472-087-33	Sequence 33, Appl
2	263.6	77.1	357	1 US-08-360-125-3	Sequence 3, Appl
3	263.6	77.1	357	2 US-08-450-578-3	Sequence 3, Appl
4	263.6	77.1	357	2 US-09-014-880-3	Sequence 3, Appl
5	263.6	77.1	357	2 US-09-014-880-3	Sequence 3, Appl
6	263.6	77.1	357	3 US-08-450-363-3	Sequence 3, Appl
7	263.6	77.1	357	4 US-09-467-903-3	Sequence 3, Appl
8	257	75.1	631	4 US-08-545-809A-31	Sequence 31, Appl
9	255.8	74.8	450	4 US-09-583-337-13	Sequence 13, Appl
10	251.8	73.6	1567	3 US-09-048-672A-17	Sequence 17, Appl
11	246.2	72.0	351	4 US-09-720-493-1	Sequence 1, Appl
12	246.2	72.0	351	4 US-09-720-493-21	Sequence 21, Appl
13	245.8	71.9	1543	4 US-09-800-729-74	Sequence 74, Appl
14	244.8	71.6	504	4 US-09-471-276-100	Sequence 100, App
15	244.2	71.4	466	4 US-09-471-276-51	Sequence 51, Appl
16	241.8	70.7	366	1 US-08-360-125-9	Sequence 9, Appl
17	241.8	70.7	366	2 US-08-450-578-9	Sequence 9, Appl
18	241.8	70.7	366	2 US-09-017-628-9	Sequence 9, Appl
19	241.8	70.7	366	2 US-09-014-880-9	Sequence 9, Appl
20	241.8	70.7	366	3 US-08-450-363-9	Sequence 9, Appl
21	241.8	70.7	366	4 US-09-467-903-9	Sequence 9, Appl
22	237.8	69.5	1212	3 US-08-545-809A-61	Sequence 61, Appl
23	233	68.1	800	3 US-08-545-809A-39	Sequence 39, Appl
24	226.2	66.1	840	3 US-09-260-527-4	Sequence 4, Appl
25	224.8	65.7	403	3 US-09-042-353-357	Sequence 357, App
26	224.8	65.7	403	3 US-08-758-417A-205	Sequence 205, App
27	220.8	64.6	288	3 US-08-851-362D-7	Sequence 7, Appl

28	218.8	64.0	417	4 US-09-203-768A-1	Sequence 1, Appl
29	217.8	63.7	357	2 US-08-652-816A-20	Sequence 58, Appl
30	217.2	63.5	469	4 US-09-471-276-58	Sequence 20, Appl
31	216.8	63.4	524	3 US-09-042-353-419	Sequence 419, App
32	216.8	63.4	524	3 US-08-758-417A-219	Sequence 219, App
33	216.8	63.4	4926	3 US-09-042-353-418	Sequence 418, App
34	216.8	63.4	4926	3 US-08-758-417A-268	Sequence 268, App
35	216.2	63.2	291	3 US-08-851-362D-11	Sequence 11, Appl
36	215.8	63.1	622	3 US-08-545-809A-59	Sequence 59, Appl
37	215.4	63.0	624	3 US-08-545-809A-28	Sequence 28, Appl
38	214.2	62.6	404	3 US-09-042-353-355	Sequence 355, App
39	214.2	62.6	404	3 US-08-758-417A-203	Sequence 203, App
40	213.2	62.3	360	4 US-09-424-840B-19	Sequence 19, Appl
41	212.8	62.2	294	3 US-08-851-362D-3	Sequence 3, Appl
42	212.6	62.2	650	3 US-08-545-809A-4	Sequence 4, Appl
43	212.2	62.0	456	4 US-09-471-276-49	Sequence 49, Appl
44	211.4	61.8	392	4 US-09-471-276-52	Sequence 52, Appl
45	211.4	61.8	402	1 US-08-259-372A-5	Sequence 5, Appl

#### ALIGNMENTS

RESULT 1  
US-09-472-087-33  
Sequence 33, Application US/09472087

Patent No. 6682736

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: NEVEU, MARK J.

APPLICANT: MUELLER, EILEEN B.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: DAVIS, C. GEORGE

APPLICANT: CORVALAN, JOSE R.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PPI

CURRENT APPLICATION NUMBER: US/09/472,087

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/113,647

NUMBER OF SEQ ID NOS: 147

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 33

LENGTH: 516

TYPE: DNA

ORGANISM: Homo sapiens

US-09-472-087-33

Query Match  
Best Local Similarity 78.1%; Score 267.2; DB 4; Length 516;  
Matches 303; Conservative 0; Mismatches 33; Indels 6; Gaps 1;

QY	7	TCTGAGCCAGAGCTGTGTAACCTTCAAGACCTGTCTCTACCTGCTGCTGTCTGT	66
DB	1	TGCGGCCAGAGCTGTGTAACCTTCAAGACCTGTCTCTACCTGCTGCTGTCTGT	60
QY	67	GCTTCATCCGAGTGTGTATTAATCTGAGTTGATCCGACGCTCCAGGAGGCG	126
DB	61	GCTTCATCCGAGTGTGTATTAATCTGAGTTGATCCGACGCTCCAGGAGGCG	120
QY	127	CTGAGTGTGATCCGATCATTAATCAAGTGGCAACCTTCAAGACCGTCCCTCAAG	186
DB	121	CTGAGTGTGATCCGATCATTAATTAATGGAACCTTCAAGACCGTCCCTCAAG	180
QY	187	AGTGAAGTATCAATGATGATGAGACGCTTAAGAACCTTCTCTGAGGCTGAGCTCT	246
DB	181	AGTGAAGTATCAATGATGATGAGACGCTTAAGAACCTTCTCTGAGGCTGAGCTCT	240
QY	247	GTGACTGCGCGGACACGCGCTGTATTAATCTGTGAGAGTGAATGCGG-----TACACT	300
DB	241	GTGACTGCGCGGACACGCGCTGTATTAATCTGTGAGAGTGAATGCGGACTTACGCT	300

QY 301 TTGGACAACCTGGGCGAGGAAACCTGTGACCGCTCTCCCTCA 342  
DB 301 ATAGACGCTGGGGCCAGGAGCACGATCACGCTCTCTCTCA 342

## RESULT 2

US-08-360-125-3

Sequence 3, Application US/08360125  
Patent No. 5767246  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5767246ihiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL LINE: antibody G4H  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:

CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-3

Query Match 77.1%; Score 263.6; DB 1; Length 357;  
Best Local Similarity 87.7%; Pred. No. 5,4e-75;  
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGCTTGCCCGACGAGCTGTGAAGCCTTCAACAACCTGTGCTACCTGCATCTCTCT 63  
DB 16 GAGTCGGGGCCAGGACTGTGAAGCCTTCAACAACCTGTGCTACCTGCATCTCTCT 75  
QY 64 GGTGGCTTCCATCCGCACTGTGTATTACTGAGTTGATCCGCGCGCTCCAGGGAG 123  
DB 76 GGTGGCTTCCATCCGCACTGTGTATTACTGAGTTGATCCGCGCGAGGAG 135  
QY 124 GGCCTGAGTGATCCGCTACATCTATCAAGTGAGCAACCTAACAACCCGCTCC 183  
DB 136 GGCCTGAGTGATCCGCTACATCTATCAAGTGAGCAACCTAACAACCCGCTCC 195  
DB 184 AAGAGTCGAGTTACATGTACAGACACGCTTAAGAACCACTTCTCCGAGGTGAGC 243  
DB 196 AAGAGTCGAGTTACATGTACAGACACGCTTAAGAACCACTTCTCCGAGGTGAGC 255  
QY 244 TCTGTGATCCCGGACACGGCCGTATTATTAATGTCGAGGATCAAGTGTACACTT 303  
DB 256 TCTGTGATCCCGGACACGGCCGTATTATTAATGTCGAGGATCAAGTGTACACTT 315  
QY 304 ---GACAACCTGGGCGAGGAAACCTGTGACCGCTCTCTCA 342  
DB 316 GCTGACTACTGGGCGAGGAAACCTGTGACCGCTCTCTCA 357

## RESULT 3

US-08-450-578-3

Sequence 3, Application US/08450578  
Patent No. 5837845  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845ihiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHEetical:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL LINE: antibody GAH  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-3

Query Match 77.1%; Score 263.6; DB 2; Length 357;  
Best Local Similarity 87.7%; Pred. No. 5.4e-75;  
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGGACTGTGTAAGCCCTTCAAGACCCCTGTCCCTCACTGACTGTCTCT 63  
DB 16 GAGTCGGGCCCAAGACTGTGTAAGCCCTTCAAGACCCCTGTCCCTCACTGACTGTCTCT 75  
QY 64 GGTGGCTTCATCCGCACTGGTGGTTTATTAATCTGAGTTGATCCGCCACCGTCCAGGAAG 123  
DB 76 GGTGGCTTCATCCGCACTGGTGGTTTATTAATCTGAGTTGATCCGCCACCGTCCAGGAAG 135  
QY 124 GGCCTGAGTGGATCGGGTACATCTATCAACAGTGGCAACCTTCAACAAACCGTCCCTC 183  
DB 136 GGCCTGAGTGGATCGGGTACATCTATTAATCTGAGTTGATCCGCCACCGTCCCTC 195  
QY 184 AAGAGTCAGTTTACATGTCAGTAGACAGCTTAAGAACCTTCTCCCTGAGGCTGAGC 243  
DB 196 AAGAGTCAGTTTACATGTCAGTAGACAGCTTAAAGACCGTCTCCCTGAGGCTGAGC 255  
QY 244 TCTGTGACTGCGCGGACACGCGGTGTTATTAATCTGAGTTGATCCGCCACCGTCCCTC 303  
DB 256 TCTGTGACTGCGCGGACACGCGGTGTTATTAATCTGAGTTGATCCGCCACCGTCCCTC 315  
QY 304 ---GACAACTGGGGCGAGGGAACCCCTGTCACCGTCTCTCA 342  
DB 316 GCTGACTGAGGGGCGAGGGAACCGTCTCTCA 357

RESULT 4  
US-09-017-628-3  
Sequence 3, Application US/09017628  
Patent No. 5990287  
GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saijo  
APPLICANT: TAGAWA, Toshiaki  
APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITO, No. 5990287hiko  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
FILE REFERENCE: 177/527361KH  
CURRENT FILING DATE: 1998-02-02  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 357  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody GAH  
US-09-017-628-3

Query Match 77.1%; Score 263.6; DB 2; Length 357;  
Best Local Similarity 87.7%; Pred. No. 5.4e-75;  
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGGACTGTGTAAGCCCTTCAAGACCCCTGTCCCTCACTGACTGTCTCT 63  
DB 16 GAGTCGGGCCCAAGACTGTGTAAGCCCTTCAAGACCCCTGTCCCTCACTGACTGTCTCT 75  
QY 64 GGTGGCTTCATCCGCACTGGTGGTTTATTAATCTGAGTTGATCCGCCACCGTCCAGGAAG 123  
DB 76 GGTGGCTTCATCCGCACTGGTGGTTTATTAATCTGAGTTGATCCGCCACCGTCCAGGAAG 135  
QY 124 GGCCTGAGTGGATCGGGTACATCTATCAACAGTGGCAACCTTCAACAAACCGTCCCTC 183  
DB 136 GGCCTGAGTGGATCGGGTACATCTATTAATCTGAGTTGATCCGCCACCGTCCCTC 195  
QY 184 AAGAGTCAGTTTACATGTCAGTAGACAGCTTAAGAACCTTCTCCCTGAGGCTGAGC 243  
DB 196 AAGAGTCAGTTTACATGTCAGTAGACAGCTTAAAGACCGTCTCCCTGAGGCTGAGC 255  
QY 244 TCTGTGACTGCGCGGACACGCGGTGTTATTAATCTGAGTTGATCCGCCACCGTCCCTC 303

Db 256 TCTGTACTGCGCGGACACGCGGTGATTACTGTGAGGTCTTACCCGACTAGGGGG 315  
Qy 304 ---GACAACTGGGGCCAGGGAACCGTGTCAACCGTCTCTCA 342  
Db 316 GCTGACTACTGGGGCCAGGGAACATGTGTCAACCGTCTCTCA 357

## RESULT 5

US-09-014-880-3  
Sequence 3, Application US/09014880  
Patent No. 5990297  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA et al.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Menderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014,880  
FILING DATE: January 28, 1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,578  
FILING DATE: May 25, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
US-09-014-880-3

Query Match 77.1%; Score 263.6; DB 2; Length 357;  
Best local similarity 87.7%; Pred.No. 5.4e-75;  
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

Qy 4 GAGTCTGCGCCAGAGACTGTGAAGCTTCAAGACCTGTCTCACTGCACTGTCTCT 63  
Db 16 GAGTCGGGGCCAGAGACTGTGAAGCTTCAAGACCTGTCTCACTGCACTGTCTCT 75  
Qy 64 GGTGGCTTCATCCGAGGAGTGTATTACTGAGTTGAGTCCGACAGGTCAGGGAG 123  
Db 76 GGTGGCTTCATCCGAGGAGTGTATTACTGAGTCCGACAGGTCAGGGAG 135

Qy 124 GCGCTGAGTGTGATCGGCTACATCTATCAAGTGGCAACCTTAGAACACCCGCTCCTC 183  
Db 136 GCGCTGAGTGTGATCGGCTACATCTATCAAGTGGGAGCACTTAGAACACCCGCTCCTC 195  
Qy 184 AAGAGTGAAGTTACCATGATAGTACAGACGTTCAAGAACCACTTCTCCCTGAGGCTAGC 243  
Db 196 AAGAGTGAAGTTACCATGATAGTACAGACGTTCAAGAACCACTTCTCCCTGAGGCTAGC 255  
Qy 244 TCTGTACTGCGCGGACACGCGCGTATTACTGTGCGAGTTCAGATGGATACACTTTG 303  
Db 256 TCTGTACTGCGCGGACACGCGCGTATTACTGTGCGAGGTCTACCCGACTAGGGGG 315  
Qy 304 ---GACAACTGGGGCCAGGGAACCGTGTCAACCGTCTCTCA 342  
Db 316 GCTGACTACTGGGGCCAGGGAACATGTGTCAACCGTCTCTCA 357

## RESULT 6

US-08-450-363-3  
Sequence 3, Application US/08450363  
Patent No. 6436434  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 6436434Ihiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Menderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,363  
FILING DATE: May 25, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:

ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-363-3

Query Match 77.1%; Score 263.6; DB 3; Length 357;  
Best Local Similarity 87.7%; Pred. No. 5.4e-75;  
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGAGAGCTGTGAAGCCTTCACAGACCTGTCTCTCACTGTGCTCTCT 63  
DB 16 GAGTCGGGCGCCAGAGAGCTGTGAAGCCTTCACAGACCTGTCTCTCACTGTGCTCTCT 75  
QY 64 GGTGGCTCCATCCGAGAGGTGTATTAAGTGAAGTGGAGTGGAGTGGAGTGGAGTGGAG 123  
DB 76 GGTGGCTCCATCCGAGAGGTGTATTAAGTGAAGTGGAGTGGAGTGGAGTGGAGTGGAG 135  
QY 124 GGCCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 183  
DB 136 GGCCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 195  
QY 184 AAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 243  
DB 196 AAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 255  
QY 244 TCTGTGACTGCGCGGAGACCGCGGTATTAAGTGAAGTGGAGTGGAGTGGAGTGGAGTGGAG 303  
DB 256 TCTGTGACTGCGCGGAGACCGCGGTATTAAGTGAAGTGGAGTGGAGTGGAGTGGAGTGGAG 315  
QY 304 ---GACAACTGGGGCCAGGAAACCTGTGCAACCGTCTCTCA 342  
DB 316 GCTGACTACTGGGGCCAGGAAACCTGTGCAACCGTCTCTCA 357

RESULT 7  
US-09-467-903-3  
Sequence 3, Application US/09467903  
Patent No. 6787153  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
Toshiaki TAGAWA  
Yoko HIRAKAWA

No. 6787153hiko ITO  
Kazuhiko NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
Specifically Binding to Surface Antigen of Cancer  
Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Penack  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/467,903  
FILING DATE: 21-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,363  
FILING DATE: May 25, 1995  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER: JP158859/1991  
FILING DATE: June 28, 1991  
APPLICATION NUMBER: JP158860/1991  
FILING DATE: June 28, 1991  
APPLICATION NUMBER: JP158861/1991  
FILING DATE: June 28, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: <Unknown>  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: <Unknown>  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: Hybridoma producing human  
antibody GAH  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:

IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-467-903-3

Query Match 77.1%; Score 263.6; DB 4; Length 357;  
Best Local Similarity 87.7%; Pred. No. 5.4e-75;  
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTCTGACCCAGAGCTGTGTAAGCTTCAAGACCCCTGTCCTGACCTGACCTGCTCT 63  
DB 16 GAGTCGGGCCAGAGCTGTGTAAGCTTCAAGACCCCTGTCCTGACCTGACCTGCTCT 75  
QY 64 GGTGGCTTCATCCGAGTGTGTTATTACTGAGTTGGATCCGCCAGCGTCCAGGGAAG 123  
DB 76 GGTGGCTTCATCCAGAGTGTGTTCTTCACTGGAATGGATCCGCCAGACCCAGGGAAG 135  
QY 124 GGCCTGAGTGGATCGGGTACATCTATCAGATGGGCAACCTTCAACCAACCCGTCCTC 183  
DB 136 GGCCTGAGTGGATGGGTATCATCTATTACAGTGGGACACCTTCAACCAACCCGTCCTC 195  
QY 184 AAGAGTCAGATTACATGTCAAGTGAACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243  
DB 196 AAGAGTCAGATTACATGTCAAGTGAACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255  
QY 244 TCTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAGGTGATGAGTGGTACACTTTG 303  
DB 256 TCTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAGGTGATGAGTGGTACACTTTG 315  
QY 304 ---GACAACTGGGGCGAGGAAACCTGTGTCACCGTCTCTCA 342  
DB 316 GCTGACTACTGGGGCGAGGAAACATGTGTACCGTCTCTCA 357

RESULT 8  
US-08-545-809A-31  
Sequence 31, Application US/08545809A  
Patent No. 6098878  
GENERAL INFORMATION:  
APPLICANT: Honjo, Tasuku  
APPLICANT: Matsuda, Fumihiko  
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE  
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME  
NUMBER OF SEQUENCES: 145  
CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,809A  
FILING DATE: 27-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/00603

FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 06501/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 631 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: human lymphoblast  
CELL LINE: GM1

US-08-545-809A-31

Query Match 75.1%; Score 257; DB 3; Length 631;  
Best Local Similarity 94.7%; Pred. No. 9.4e-73;  
Matches 266; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 4 GAGTCTGACCCAGAGCTGTGTAAGCTTCAAGACCCCTGTCCTGACCTGACCTGCTCT 63  
DB 305 GAGTCGGGCCAGAGCTGTGTAAGCTTCAAGACCCCTGTCCTGACCTGACCTGCTCT 364  
QY 64 GGTGGCTTCATCCGAGTGTGTTATTACTGAGTTGGATCCGCCAGCGTCCAGGGAAG 123  
DB 365 GGTGGCTTCATCCAGAGTGTGTTCTTCACTGGAATGGATCCGCCAGACCCAGGGAAG 424  
QY 124 GGCCTGAGTGGATCGGGTACATCTATCAGTGGGCAACCTTCAACCAACCCGTCCTC 183  
DB 425 GGCCTGAGTGGATGGGTATCATCTATTACAGTGGGACACTTCAACCAACCCGTCCTC 484  
QY 184 AAGAGTCAGATTACATGTCAAGTGAACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243  
DB 485 AAGAGTCAGATTACATGTCAAGTGAACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 544  
QY 244 TCTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAG 284  
DB 545 TCTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAG 585

RESULT 9  
US-09-582-337-13  
Sequence 13, Application US/09582337  
Patent No. 6562618  
GENERAL INFORMATION:  
APPLICANT: Japan Tobacco, Inc.  
TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor  
TITLE OF INVENTION: and Medicinal Uses Thereof  
FILE REFERENCE: JI-009PCT  
CURRENT APPLICATION NUMBER: US/09/582,337  
CURRENT FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: JP P1997-367699  
PRIOR FILING DATE: 1997-12-25  
PRIOR APPLICATION NUMBER: JP P1998-356183  
PRIOR FILING DATE: 1998-12-15  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 450  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(450)  
NAME/KEY: sig\_peptide  
LOCATION: (1)..(58)



NAME/KEY: V region  
LOCATION: (59) .. (353)  
US-09-582-337-13

Query Match 74.8%; Score 255.8; DB 4; Length 450;  
Best Local Similarity 87.1%; Pred. No. 2e-72; Indels 19; Gaps 2;  
Matches 311; Conservative 0; Mismatches 27

4 GAGTCTGGCCGAGAGCTGTGAAGCCCTTCAAGACCTGTCCCTCACTGAGCTGTCT  
74 GAGTCTGGCCGAGAGCTGTGAAGCCCTTCAAGACCTGTCCCTCACTGAGCTGTCT  
64 GGTGCTTCATCCGAGTGTGTATTACTGAGTGTGATCCGACGCTTCAAGGAG 123  
133 GGTGCTTCATCCGAGTGTGTATTACTGAGTGTGATCCGACGCTTCAAGGAG 192  
124 GGTGCTTCATCCGAGTGTGTATTACTGAGTGTGATCCGACGCTTCAAGGAG 183  
193 GGTGCTTCATCCGAGTGTGTATTACTGAGTGTGATCCGACGCTTCAAGGAG 252  
184 AAGAGTGAAGTACATGATGATGATGATGATGATGATGATGATGATGATGATG 243  
253 AAGAGTGAAGTACATGATGATGATGATGATGATGATGATGATGATGATGATG 312  
244 TCTGTGACTGCGCGGAGACGCGCGTGTATTACTGTGTGAGGT----- 286  
313 TCTGTGACTGCGCGGAGACGCGCGTGTATTACTGTGTGAGGTATTAGTGTGT 372  
287 -CAGATGGGTACCTTTGAGCACTGGGGCCAGGAAACCTGTGATGATGATGATG 342  
373 GGTATTATGAGTACTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 429

RESULT 10  
US-09-049-672A-17  
Sequence 17, Application US/09049672A  
Patent No. 6135941

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Young, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baughn, Mariah R.  
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,672A  
FILING DATE: HEREWITH  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Carrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1567 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PANTUM01  
CLONE: 1513264  
US-09-049-672A-17

Query Match 73.6%; Score 251.8; DB 3; Length 1567;  
Best Local Similarity 84.6%; Pred. No. 6.7e-71;  
Matches 302; Conservative 0; Mismatches 37; Indels 18; Gaps 1;

4 GAGTCTGGCCGAGAGCTGTGAAGCCCTTCAAGACCTGTCCCTCACTGAGCTGTCT 63  
150 GAGTCTGGCCGAGAGCTGTGAAGCCCTTCAAGACCTGTCCCTCACTGAGCTGTCT 209  
64 GGTGCTTCATCCGAGTGTGTATTACTGAGTGTGATCCGACGCTTCAAGGAG 123  
210 GGTGCTTCATCCGAGTGTGTATTACTGAGTGTGATCCGACGCTTCAAGGAG 269  
124 GGTGCTTCATCCGAGTGTGTATTACTGAGTGTGATCCGACGCTTCAAGGAG 183  
270 GGTGCTTCATCCGAGTGTGTATTACTGAGTGTGATCCGACGCTTCAAGGAG 329  
184 AAGAGTGAAGTACATGATGATGATGATGATGATGATGATGATGATGATGATG 243  
330 AAGAGTGAAGTACATGATGATGATGATGATGATGATGATGATGATGATGATG 389  
244 TCTGTGACTGCGCGGAGACGCGCGTGTATTACTGTGTGAGGT----- 292  
390 TCTGTGACTGCGCGGAGACGCGCGTGTATTACTGTGTGAGGTATTAGTGTGT 449  
293 -----GGTACACTTTGAGCACTGGGGCCAGGAAACCTGTGATGATGATGATG 342  
450 GGTACACTTTGAGCACTGGGGCCAGGAAACCTGTGATGATGATGATGATGATG 506

RESULT 11  
US-09-720-493-1  
Sequence 1, Application US/09720493  
Patent No. 6827925

GENERAL INFORMATION:

APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Williams, Andrew J  
APPLICANT: Tempest, Philip R  
APPLICANT: Holter, Thor L  
APPLICANT: Main, Sarah H  
APPLICANT: Jackson, Helen  
APPLICANT: Daromola, Olatokun  
TITLE OF INVENTION: Improvements relating to antibodies  
FILE REFERENCE: AHB/CP575333  
CURRENT APPLICATION NUMBER: US/09/720,493  
CURRENT FILING DATE: 2002-10-23  
PRIOR APPLICATION NUMBER: GB 9814383.7  
PRIOR FILING DATE: 1998-07-02  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 351  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1) .. (351)  
US-09-720-493-1

Query Match 72.0%; Score 246.2; DB 4; Length 351;  
Best Local Similarity 85.0%; Pred. No. 2.2e-69;

Matches 288; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGGACTGTGTGAACCTTACAGACCTGTCTCTCACTGACTGTCTCT 63  
Db 16 GAGTCCGCCCCAGGACTGTGTGAACCTTACAGACCTGTCTCTCACTGACTGTCTCT 75  
QY 64 GGTGGCTCCATCCGCGAGTGGTGTATTACTGAGATTGGATCCGCGAGCGTCCAGGGAG 123  
Db 76 GGTACTCTCAACACA--GTGTTACTACTGGGAGTGGATTTGGAGCCCCCAGGGAG 132

QY 124 GGCCTGAGTGAATCGGGTACATCTATCAACAGTGGCAACCTTCAACACCCGCTCC 183  
Db 133 GGCCTGAGTGAATCGGGTACATCTATCAACAGTGGCAACCTTCAACACCCGCTCC 192

QY 184 AAGAGTGAATTACATGTCTAGTGAACAGCTGTAAAGCACTTCTCTGAGGCTGAGC 243  
Db 193 AAGAGTGAATGACCATATTCAGTGAACAGCTGTAAAGCACTTCTCTGAGGCTGAGC 252

QY 244 TCTGTGACTGCGCGGAGACGCGCTGTATTACTGTGAGAGTCAAGATGCTACATTG 303  
Db 253 TCTGTGACCGCGGAGACGCGCTGTATTACTGTGAGAGTGAAGAGTGTGAGATT 312

QY 304 GACAACCTGGGCGCAGGGAACCTGTGTCAACGCTCTCTCA 342  
Db 313 GACTATTGGGCGCAGGGAACCTGTGTCAACGCTCTCTCA 351

RESULT 12  
US-09-720-493-21/c  
; Sequence 21, Application US/09720493  
; Patent No. 6827925  
; GENERAL INFORMATION:  
; APPLICANT: Cambridge Antibody Technology Limited  
; APPLICANT: Williams, Andrew J  
; APPLICANT: Tempest, Philip R  
; APPLICANT: Hollet, Thor L  
; APPLICANT: Main, Sarah H  
; APPLICANT: Jackson, Helen  
; APPLICANT: Daromola, Olatokun  
; TITLE OF INVENTION: Improvements relating to antibodies  
; FILE REFERENCE: AHB/CP577533  
; CURRENT APPLICATION NUMBER: US/09/720,493  
; PRIORITY FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: GB 9814383.7  
; PRIORITY FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 351  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-720-493-21

Query Match 72.0%; Score 246.2; DB 4; Length 351;  
Best Local Similarity 85.0%; Pred. No. 2.2e-69;

Matches 288; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGGACTGTGTGAACCTTACAGACCTGTCTCTCACTGACTGTCTCT 63  
Db 336 GAGTCCGCCCCAGGACTGTGTGAACCTTACAGACCTGTCTCTCACTGACTGTCTCT 277

QY 64 GGTGGCTCCATCCGCGAGTGGTGTATTACTGAGATTGGATCCGCGAGCGTCCAGGGAG 123  
Db 276 GGTACTCTCAACACA--GTGTTACTACTGGGAGTGGATTTGGAGCCCCCAGGGAG 220

QY 124 GGCCTGAGTGAATCGGGTACATCTATCAACAGTGGCAACCTTCAACACCCGCTCC 183  
Db 219 GGCCTGAGTGAATCGGGTACATCTATCAACAGTGGCAACCTTCAACACCCGCTCC 160

QY 184 AAGAGTGAATTACATGTCTAGTGAACAGCTGTAAAGCACTTCTCTGAGGCTGAGC 243  
Db 159 AAGAGTGAATGACCATATTCAGTGAACAGCTGTAAAGCACTTCTCTGAGGCTGAGC 100

QY 244 TCTGTGACTGCGCGGAGACAGCGCGTGTATTACTGTGCGGAGTCAATGGGTACATTG 303  
Db 99 TCTGTGACCGCGGAGACAGCGCGTGTATTACTGTGCGGAGAGGAGTGTGAGATT 40

QY 304 GACAACCTGGGCGCAGGGAACCTGTGTCAACGCTCTCTCA 342  
Db 39 GACTATTGGGCGCAGGGAACCTGTGTCAACGCTCTCTCA 1

RESULT 13  
US-09-800-729-74  
; Sequence 74, Application US/09800729  
; Patent No. 6605592  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: P2044P1  
; CURRENT APPLICATION NUMBER: US/09/800,729  
; PRIORITY FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIORITY FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 74  
; LENGTH: 1543  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-800-729-74

Query Match 71.9%; Score 245.8; DB 4; Length 1543;  
Best Local Similarity 83.1%; Pred. No. 5.7e-69;  
Matches 280; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 4 GAGTCTGCCCCAGGACTGTGTGAACCTTACAGACCTGTCTCTCACTGACTGTCTCT 63  
Db 90 GAGTCCGCCCCAGGACTGTGTGAACCTTACAGACCTGTCTCTCACTGACTGTCTCT 149

QY 64 GGTGGCTCCATCCGCGAGTGGTGTATTACTGAGATTGGATCCGCGAGCGTCCAGGGAG 123  
Db 150 GGTGGCTCCATCCGCGAGTGGTGTATTACTGAGATTGGATCCGCGAGCGTCCAGGGAG 209

QY 124 GGCCTGAGTGAATCGGGTACATCTATCAACAGTGGCAACCTTCAACACCCGCTCC 183  
Db 210 GGCCTGAGTGAATCGGGTACATCTATCAACAGTGGCAACCTTCAACACCCGCTCC 269

QY 184 AAGAGTGAATTACATGTCTAGTGAACAGCTGTAAAGCACTTCTCTGAGGCTGAGC 243  
Db 270 AAGAGTGAATGACCATATTCAGTGAACAGCTGTAAAGCACTTCTCTGAGGCTGAGC 329

QY 244 TCTGTGACTGCGCGGAGACAGCGCGTGTATTACTGTGCGGAGTCAATGGGTACATTG 303  
Db 330 TCTGTGACTGCGCGGAGACAGCGCGTGTATTACTGTGCGGAGTCAATGGGTACATTG 389

QY 304 GACAACCTGGGCGCAGGGAACCTGTGTCAACGCTCTCTCA 340  
Db 390 GACCGGTACCAAGCTGGAATACCGAGGCTTGAATCACT 426

RESULT 14  
US-09-471-276-100  
; Sequence 100, Application US/09471276  
; Patent No. 6822072  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duetler A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.025CP1  
; Patent No. 6822072  
; CURRENT APPLICATION NUMBER: US/09/471,276  
; PRIORITY FILING DATE: 1999-12-21

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; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 100
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 39..503
; NAME/KEY: sig_peptide
; LOCATION: 39..95
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 9.3000019073486
; OTHER INFORMATION: seq FULLVAGPRWLS/QV
US-09-471-276-100
```

```
Query Match 71.6%; Score 244.8; DB 4; Length 504;
Best Local Similarity 83.4%; Pred. No. 7.2e-69;
Matches 287; Conservative 3; Mismatches 51; Indels 3; Gaps 1;
```

```
QY 1 CTGAGCTGGCCAGAGCTGGTGAAGCTTCACAGACCCCTGCTCAGCTGACTGTC 60
DB 108 SDRKAGTCGGGCCCAAGACTGTGAAGCTTCACAGACCCCTGCTCAGCTGTA 167
QY 61 TCTGTGGCTCCATCCGAGTGTGTATTACTGAGATTGGATCCGCGACGTCAGGG 120
DB 168 TCTGGGCTCCGTCAGAGCTGTGGTACTGATTTGAGACTGGATCCGCGACTCC 227
QY 121 AAGGCTGAGTGTGATCGGATCATCTATCAACAGTGGCAACCTTCAACACCCG 180
DB 228 AAGGCTGAGTGTGATCGGATCATCTATCAACAGTGGCAACCTTCAACACCCG 287
QY 181 CTCAAGAGTCAAGTTCATGTCAGTACAGACGCTTAAGAACCACTTCCCTGAGG 240
DB 288 CTCAAGAGTCAAGTTCATGTCAGTACAGACGCTTAAGAACCACTTCCCTGAGG 347
QY 241 AGCTGTGACTGCGCGAGACAGCGCGGTATTACTGTGCGAGGTGAGTACACT 300
DB 348 AGCTGTGACTGCGCGAGACAGCGCGGTATTACTGTGCGAGGTGAGTACACT 407
QY 301 ---TTGACAACTGGGGCCAGGAAACCTGTGTCAACCGTCTCTCTC 341
DB 408 CTATTGACCCCTGGGGCCAGGAAACCTGTGTCAACCGTCTCTCTC 451
```

```
RESULT 15
US-09-471-276-51
; Sequence 51, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Dugliet A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CPI
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 51
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; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 38..466
; NAME/KEY: sig_peptide
; LOCATION: 38..94
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 10.899996185303
; OTHER INFORMATION: seq FULLVAAPRWLS/QV
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 423
; OTHER INFORMATION: n=a, g, c or t
; OTHER INFORMATION: Oligonucleotide
US-09-471-276-51
```

```
Query Match 71.4%; Score 244.2; DB 4; Length 466;
Best Local Similarity 82.4%; Pred. No. 1.1e-68;
Matches 285; Conservative 7; Mismatches 47; Indels 7; Gaps 1;
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```
QY 4 GAGTCTGGCCAGAGCTGGTGAAGCTTCACAGACCCCTGCTCAGCTGACTGTC 63
DB 110 GAGTCTGGCCAGAGCTGGTGAAGCTTCACAGACCCCTGCTCAGCTGTC 169
QY 64 GGTGGCTCCATCCGAGTGTGTTTACTGAGATTGGATCCGCGACGTCAGGGAG 123
DB 170 GGTGGCTCCATCCGAGTGTGTTTACTGAGATTGGATCCGCGACGTCAGGGAG 229
QY 124 GGCCTGAGTGTGATCGGATCATCTATCAAGTGGCAACCTTCAACACCCGTC 183
DB 230 GGCCTGAGTGTGATCGGATCATCTATCAAGTGGCAACCTTCAACACCCGTC 289
QY 184 AAGAGTCAAGTTCATGTCAGTACAGACGCTTAAGAACCACTTCTCTGAGG 243
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QY 297 CACTTGGACAACTGGGGCCAGGAAACCTGTGTCAACCGTCTCTCTCA 342
DB 410 TGGTTCAASHMCTTGGGGCMAGGGRACCGGTACCGTCTCTCTCA 455
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Search completed: July 27, 2005, 12:41:21
Job time : 96.3455 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:09:06 ; Search time 1819.51 Seconds  
(without alignments)  
8468.649 Million cell updates/sec

Title: US-10-027-725A-4  
318  
Perfect score: 1 gagctcactcagctccatc.....ccaagtcgagatccaacga 318  
Sequence:

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318	100.0	318	9	HS458379 Homo sapi
2	290.8	91.4	322	9	HUMIGHCD L03142 Homo sapien
3	290.8	91.4	326	9	HUMIGHGY L03160 Homo sapien
4	289.2	90.9	796	9	AB064138 Homo sapi
5	287.6	90.4	321	6	AR161027 Sequence
6	286.6	90.1	324	9	AB063929 Homo sapi
7	286.6	90.1	828	9	AB064098 Homo sapi
8	286	89.9	321	9	HS1GK16F X73855 H. sapiens m
9	286	89.9	328	9	HUMIGHHC L03164 Homo sapien
10	284.4	89.4	324	9	AB095286 Homo sapi
11	284	89.3	369	12	AF453186 AF453186 Synthetic
12	282.8	88.9	324	9	AB063932 Homo sapi
13	282	88.7	321	9	AY240163 Homo sapi
14	281.8	88.6	324	9	AB095281 Homo sapi
15	281.2	88.4	321	6	AR160973 Sequence
16	281.2	88.4	321	6	AR160980 Sequence
17	281.2	88.4	321	6	AR161046 Sequence
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19	281.2	88.4	711	12	HS1GK131 X93750 Synthetic c

20	280.4	88.2	321	6	E12913 Human CDNA
21	280.2	88.1	316	9	HUMIGHHS L03178 Homo sapien
22	280.2	88.1	387	12	AF453148 AF453148 Synthetic
23	279.6	87.9	321	6	AR160978 Sequence
24	279.6	87.9	321	6	AR160984 Sequence
25	279.6	87.9	321	6	AR161049 Sequence
26	279.6	87.9	321	6	AR161050 Sequence
27	279.6	87.9	348	9	HS1GK1050 Sequence
28	278.6	87.6	324	9	HS1GK1050 Sequence
29	278.6	87.6	324	9	HS1GK1050 Sequence
30	278.6	87.6	735	6	CO849413 Sequence
31	278.6	87.6	735	6	CO849425 Sequence
32	278.6	87.6	735	6	CO849427 Sequence
33	278.6	87.6	736	6	CO758827 Sequence
34	278.6	87.6	736	6	CO849415 Sequence
35	278.6	87.6	750	6	CO849417 Sequence
36	278.6	87.6	750	6	CO849421 Sequence
37	278.6	87.6	761	9	AB064051 Homo sapi
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#### ALIGNMENTS

RESULT 1  
HSA458379  
LOCUS HSA458379 318 bp mRNA linear PRI 30-APR-2002  
DEFINITION Homo sapiens partial mRNA for immunoglobulin kappa light chain  
ACCESSION AJ458379  
VERSION AJ458379.1 GI:20387057  
KEYWORDS IGV gene; immunoglobulin kappa; light chain; variable region.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Flicker, S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y.,  
Valent, P., Kraft, D. and Valenta, R.  
TITLE Conversion of grass allergen-specific human IGB into a protective  
JOURNAL Igb1 antibody  
REFERENCE 2 (bases 1 to 318)  
AUTHORS Flicker, S.  
TITLE Direct Submission  
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,  
General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090  
Vienna, AUSTRIA  
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## ORIGIN

99

27

दु

or

D'b

QY

5

AB0641

## DEFINI

ACCESS  
VBPSTO

**SOURCE**

## REFERENCES

**YOUR  
PREFERS**

TITL

**COMMEN**

## FEATURE

Location/Qualifiers

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## ORIGIN

25

1

2

23

Db .

QY

5

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Dib

AR1610  
10000DEFINITION  
ACCESS

## KEYWORDS

ORGA

AUTH

**Topic**

8  
9

source 1. .321

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Best Local Similarity	94.0%;	Pred. No. 2.7e-83;		
Matches 299; Conservative	0;	Mismatches 19;	Indels 0;	Gaps 0;

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RESULT 6				
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LOCUS	AB063929			
DEFINITION	AB063929	324 bp	mRNA	PRI 02-JUL-2002
	Homo sapiens IGH mRNA for immunoglobulin kappa light chain VJ7 region, partial cds, clone:k102.			

ACCESSION	AB063929
VERSION	AB063929.1
	GI:21669064

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominae; Homo.

REFERENCE	AUTHORS	TITLE
1	Akhoriz, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukei, Y., Honda, T., Katsumi, H., Okeda, J., Miura, K. and Kurosawa, Y.	Construction and characterization of antibody libraries: isolation

## of therapeutic human antibodies and application to functional genomics

JOURNAL REFERENCE	Unpublished 2 (bases 1 to 324)
1. "The	

AUTHORS	TITLE	Direct Submission	Submitted (of the 2001)	Web-based Reviews	Published
Kurosawa, Y.					

Submitted (25-JUN-2001) IOSHIKAZU ARIOSAWA, Institute of Comprehensive Medical Science, Fujita Health University; Kunitake-cho, Toyouke 470-1192, Japan

COMMENT  
kurosawa@fujiita-hu.ac.jp, Tel: 81-562-93-9387)  
Natsunaka-Chu, Toyane 7-0-1122, Yamanashi  
Please visit our web site

URL: <http://www.fujita-hu.ac.jp/immunity/>.  
Location: Osaka, Japan

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LOCUS AB064098

DEFINITION	DESCRIPTION
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ACCESSION	AB064098
VERSION	AB064098.1
GI	21669402

NEIMOKRDS	.	Homo sapiens (human)
SOURCE		
ORIGINATOR		

ORGANISM  
 Nucleo basilaris  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Dermatales; Carnivora; Hominoidea; Homo

REFERENCE

1. Yamamoto, T., Iba, Y., Morino, K., Shinohara, M., Hirano, Y., Kato, A., and Matsuda, T. *Environ. Health Perspect.* 101: 103-107 (1993).

Suzuki, K., Torii, H., Ukal, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.

TITLE	ABSTRACT	KEYWORDS	INDEXING	REFERENCES
Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional				

**JOURNAL**  
**genomics**  
**unpublished**

REFERENCE	2 (bases 1 to 828)
AUTHORS	Kurosawa, Y.

**TITLE** Direct Submission  
**JOURNAL** Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for

Comprehensive Medical Science, Fujita Health University,  
Kutsukake-cho, Toyooka 470-1192, Japan

COMMENT  
(E-mail: [kurosawa@tj.ita-hu.ac.jp](mailto:kurosawa@tj.ita-hu.ac.jp), Tel: 81-562-93-9387)  
Please visit our web site

URL: <http://www.fujita-hu.ac.jp/immunity/>  
Location/Qualifiers

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QY 2 AGCTCACTCACTTCATCTCCCTGCTGTCATCTGTGGAGACAGAGTCACCATCAGTT 61  
DB 74 AGATGACCCAGCTCTCCATCTCCCTGCTGTCATCTGTAGAGACAGAGTCACCATCAGTT 133  
QY 62 GCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGATTCAGCATTAACCGAGGAAG 121  
DB 134 GCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGATTCAGCATTAACCGAGGAAG 193  
QY 122 CCCCTAAGCTCTGATCTATGCTGTCATCAGTTTGCAAGTGGGGTCCCATCAAGTTCA 181  
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DB 254 GTGGCAGTGATATGAGAGACAGCTTCACTTCACCATCAGAGTGTGACGCTGAAGATT 313  
QY 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTCTGTAACCTTTTGGCCAGGGGACCA 301  
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QY 302 AGGTGAGATCAACGA 318  
DB 374 AGGTGAGATCAACGA 390

RESULT 8  
HSIGVK16F 321 bp mRNA linear PRI 30-MAR-1995  
LOCUS DEFINITION H.sapiens mRNA for Ig kappa light chain variable region (V-J), subgroup I.  
X73855  
ACCESSION X73855.1 GI:516316  
VERSION K03855.1  
KEYWORDS autoantibody; Ig J-segment; Ig kappa light chain; Ig subgroup I; Ig variable region; immunoglobulin.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Hexham,J.M., Furmaniak,J., Pegg,C., Burton,D.R. and Smith,B.R.  
TITLE Cloning of a human autoimmune response: preparation and sequencing of a human anti-thyroglobulin autoantibody using a combinatorial approach  
JOURNAL Autoimmunity 12 (2), 135-141 (1992)  
MEDLINE 92314301  
PUBMED 1617110  
REFERENCE 2 (bases 1 to 321)  
AUTHORS Hexham,J.M., Partridge,L.J., Furmaniak,J., Petersen,V.B.,

## TITLE

Colls,J.C., Pegg,C., Rees Smith,B. and Burton,D.R.  
Cloning and characterisation of TPO autoantibodies using  
combinatorial phage display libraries

## JOURNAL

Autoimmunity 17 (3), 167-179 (1994)

## MEDLINE

95035699

## PUBMED

7524700

## REFERENCE

3

## AUTHORS

Hexham,J.M., Partridge,L.J., Furmaniak,J., Petersen,V.B.,

## TITLE

Colls,J.C., Pegg,C.A.S., Rees-Smith,B. and Burton,D.R.  
Probing the human anti-thyroid peroxidase repertoire of a  
Hashimoto's thyroiditis patient using combinatorial phage display  
libraries

## JOURNAL

Eur. J. Immunol.

## REFERENCE

4 (bases 1 to 321)

## AUTHORS

Hexham,J.

## TITLE

Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept. of  
Mol. Biology and Biotechnology, P. O. Box 594, Firth Court, Western  
Bank, Sheffield S10 2UH, UK

## JOURNAL

Location/Qualifiers

## FEATURES

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QY 301 AAGGTGAGATCAACGA 318  
DB 301 AAGGTGAGATCAACGA 318

RESULT 9  
HNMIGHHC 328 bp mRNA linear PRI 03-MAY-2000  
LOCUS DEFINITION Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region (IGHV) mRNA, partial cds.  
ACCESSION L03164  
VERSION L03164.1 GI:185399  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Collet,T.A., Roben,P., O'Kennedy,R., Barbac,C.F. III, Burton,D.R. and Lerner,R.A.  
TITLE A binary plasmid system for shuffling combinatorial antibody libraries  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)  
MEDLINE 93066172  
PUBMED 1438192  
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QY 241 TTGGCAAGTTACTACTCTCAAGAGAGTCTGAGCTGCTCTGACACTTTTGGCCAGGGGACC 300  
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QY 301 AAGGTGAGATCAACACA 318  
DB 301 AAGGTGAGATCAACACA 318  
RESULT 10  
AB095286 324 bp mRNA linear PRI 25-JUL-2003  
LOCUS Homo sapiens VL mRNA for immunoglobulin kappa light chain, partial  
DEFINITION cds, V region, clone:L-LA10.

ACCESSION AB095286  
VERSION AB095286.1 GI:33235623  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Tachibana,H., Matanabe,K., Cheng,X.-J., Tsukamoto,H., Kaneda,Y., Takeuchi,T., Ihara,S. and Petri,Jr.W.A. Jr.  
TITLE V $\lambda$ 3 Gene Usage in Neutralizing Human Antibodies Specific for the Entamoeba histolytica Gal/GalNAc Lectin Heavy Subunit  
JOURNAL Infect. Immun. 71 (8), 4313-4319 (2003)  
MEDLINE 12874307  
PUBMED 12874307  
REFERENCE 2 (bases 1 to 324)  
AUTHORS Tachibana,H.  
TITLE Direct Submission  
JOURNAL Submitted (02-NOV-2002) Hiroshi Tachibana, Tokai University School of Medicine, Department of Infectious Diseases, Bohseidai, Isehara, Kanagawa 259-1193, Japan (E-mail:htachiba@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121(ex.2603), Fax:81-463-95-5450)  
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Best Local Similarity 93.4%; Pred. No. 3.1e-82;  
Matches 297; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 1 GAGCTCACTGATCTCCATCTCCCTGTCTGCATCTGTGGAGACAGATCACCATCACT 60  
DB 7 GTGATGACTGATCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGATCACCATCACT 66  
QY 61 TGCCGGCAAGTCAGAGATTACACCTATTAAATTGATCTGACGCTAAACCGAGGAAA 120  
DB 67 TGCCGGCAAGTCAGAGATTACACCTATTAAATTGATCTGACGCTAAACCGAGGAAA 126  
QY 121 GCCCCTAAGCTCTGATCTATGTCGATCCAGTTTGGCAAGTGGGTCCTCATCAAGTTTC 180  
DB 127 GCCCCTAAGCTCTGATCTATGTCGATCCAGTTTGGCAAGTGGGTCCTCATCAAGTTTC 186  
QY 181 AGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACACATCAGACGCTGCAACCTGAAGAT 240  
DB 187 AGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACACATCAGACGCTGCAACCTGAAGAT 246  
QY 241 TTGGCAAGTTACTACTCTCAAGAGAGTCTGAGCTGCTCTGACACTTTTGGCCAGGGGACC 300  
DB 247 TTGGCAAGTTACTACTCTCAAGAGAGTCTGAGCTGCTCTGACACTTTTGGCCAGGGGACC 306  
QY 301 AAGGTGAGATCAACACA 318  
DB 307 AAGGTGAGATCAACACA 324

RESULT 11  
AF453186 369 bp mRNA linear SYN 11-MAR-2004  
LOCUS AF453186  
DEFINITION Synthetic construct clone R-129VL immunoglobulin light chain  
ACCESSION AF453186  
VERSION AF453186.1 GI:25988329  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE other sequences; artificial sequences.  
AUTHORS 1 (bases 1 to 369)  
Wettkamp,J.H., Kallewaard,N., Kuehara,K., Bures,E., Williams,J.V.,  
Lafleur,B., Greenberg,H.B. and Crowe,J.E. Jr.  
TITLE Infant and adult human B cell responses to rotavirus share common  
immunodominant variable gene repertoires  
J. Immunol. 171 (9), 4680-4688 (2003)  
JOURNAL 22930557  
MEDLINE 14568943  
REFERENCE 2 (bases 1 to 369)  
Wettkamp,J.-H. and Crowe,J.E. Jr.  
AUTHORS Direct Submission  
TITLE Submitted (28-NOV-2001) Pediatrics, Vanderbilt University Medical  
Center, 1161 21st Avenue South, D-7235 Medical Center North,  
Nashville, TN 37232-2581, USA  
JOURNAL Location/Qualifiers  
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Matches 296; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
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QY 62 GCCGGGCAAGTCAAGATTTAACTTTAAATTGGTATCAGATTAACCGAGGAAAG 121  
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QY 122 CCCCTAAGCTCTGATCTATGCTGATCAGTTTGGCAAGTGGGCTCCCATCAAGTTCA 181  
DB 152 CCCCTAAGCTCTGATCTATGCTGATCAGTTTGGCAAGTGGGCTCCCATCAAGTTCA 211  
QY 182 GTGGCAGTGTATTTGGAGACAGATTTCACTTCAACCATCAGAGTGTGAGCTTGAAGTT 241  
DB 212 GTGGCAGTGTATTTGGAGACAGATTTCACTTCAACCATCAGAGTGTGAGCTTGAAGTT 271  
QY 242 TTGCAAGTTACTATCTGTCAAGAGTCTCAGTGCCTGTGACATTTTGGCCAGGGAGCA 301  
DB 272 TTGCAAGTTACTATCTGTCAAGAGTGTGACAGTACAGTACCCGTCGACCTTTGGCCAGGGAGCA 331  
QY 302 AGGTGAGATCAACG 317  
DB 332 AAGTGATATCAACG 347  
RESULT 12  
AB063932 324 bp mRNA linear PRI 02-JUL-2002  
LOCUS AB063932  
DEFINITION Homo sapiens IGH mRNA for immunoglobulin kappa light chain VLJ  
region, partial cds, clone:KI05.  
ACCESSION AB063932  
VERSION AB063932.1 GI:21669070

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1  
Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hiroo,Y., Kakita,M.,  
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,T.,  
Mura,K. and Kurosawa,Y.  
TITLE Construction and characterization of antibody libraries: isolation  
of therapeutic human antibodies and application to functional  
genomics  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 324)  
AUTHORS Kurosawa,Y.  
TITLE Direct Submission  
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for  
Comprehensive Medical Science, Fujita Health University;  
Kutsukake-cho, Toyosake 470-1192, Japan  
AUTHORS (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)  
COMMENT Please visit our web site  
URL:http://www.fujita-hu.ac.jp/immunity/  
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SOURCE  
1..324  
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ORIGIN  
Query Match 88.9%; Score 282.8; DB 9; Length 324;  
Best Local Similarity 93.1%; Pred. No. 1e-81;  
Matches 296; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 1 GAGCTCACTCACTCCATCCCTCCCTGCTGATCTGTGGAGACAGATCCATCACT 60  
DB 7 GTGATGACCCAGTCTCCATCCCTCCCTGCTGATCTGTGGAGACAGATCCATCACT 66  
QY 61 TGCCGGGCAAGTCAAGATTTAACTTTAAATTGGTATCAGATTAACCGAGGAA 120  
DB 67 TGCCGGGCAAGTCAAGATTTAACTTTAAATTGGTATCAGATTAACCGAGGAA 126  
QY 121 GCCCTAAGCTCTGATCTATGCTGATCAGTTTGGCAAGTGGGCTCCCATCAAGTTTC 180  
DB 127 GCCCTAAGCTCTGATCTATGCTGATCAGTTTGGCAAGTGGGCTCCCATCAAGTTTC 186  
QY 181 AGTGGCAGTGTATTTGGAGACAGATTTCACTTCAACCATCAGAGTGTGAGCTTGAAGAT 240  
DB 187 AGTGGCAGTGTATTTGGAGACAGATTTCACTTCAACCATCAGAGTGTGAGCTTGAAGAT 246  
QY 241 TTGCAAGTTACTATCTGTCAAGAGTCTCAGTGCCTGTGACATTTTGGCCAGGGAGCC 300  
DB 247 TTGCAAGTTACTATCTGTCAAGAGTCTCAGTGCCTGTGACATTTTGGCCAGGGAGCC 306  
QY 301 AAGGTGAGATCAACGA 318  
DB 307 AAGGTGAGATCAACGA 324

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RESULT 13
LOCUS      AY240163                      321 bp    mRNA      linear      PRI 04-MAR-2004
DEFINITION Homo sapiens clone HAI anti-HAV capsid immunoglobulin G light chain
ACCESSION  AY240163
VERSION     AY240163.1
KEYWORDS    GI:29650328
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 321)
AUTHORS     Kim,S.-J., Jang,M.H., Stapleton,J.T., Yoon,S.O., Kim,K.S.,
            Jeon,H.-S., and Hong,H.-J.
TITLE       Neutralizing human monoclonal antibodies to hepatitis A virus
            recovered by phage display
JOURNAL     Virology 318 (2), 598-607 (2004)
PUBMED      14972527
REFERENCE   2 (bases 1 to 321)
AUTHORS     Kim,S.-J., Jang,M.H., Stapleton,J.T., Yoon,S.O., Jeon,E.-S. and
            Hong,H.-J.
TITLE       Direct Submission
JOURNAL     Submitted (20-FEB-2003) Antibody Engineering RU, Korea Research
            Institute of Bioscience and Biotechnology, Yuseung, Daejeon 305-333,
            Korea

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Query Match      88.7%; Score 282; DB 9; Length 321;
Best Local Similarity 93.6%; Pred. No. 1.9e-81;
Matches 294; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Oy      62 GCCGGGCAAGTCAGAGATTAAACCTATTAAATTTGGTATCAGCATAAACAGGGAAG 121
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Db      128 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTCA 187
Oy      182 GTGGCAGTGATATGGGACAGACTTCACTTCACCATCAGCAGTGTGAGGCTGAAGTT 241
Db      188 GTGGCAGTGATCTGGGACAGATTTCATCTTCACCATCAGCAGTGTGAACTGAAGTT 247
Oy      242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGAGCA 301
Db      248 TTGCAACTTATTATTGTCAACAGAGTTTCAGTACCCGTAACCTTTTGGCCAGGGAGCA 307
Oy      302 AGGTGGAGATCAAA 315
Db      308 AGCTGGAGATCAAA 321

RESULT 14
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LOCUS      AB095281                      324 bp    mRNA      linear      PRI 25-JUL-2003
DEFINITION Homo sapiens VL mRNA for immunoglobulin kappa light chain, partial
            cds, V region, clone: L-CP17.
ACCESSION  AB095281
VERSION     AB095281.1
KEYWORDS    GI:33235613
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Tachibana,H., Metanabe,K., Cheng,X.-J., Tsukamoto,H., Kaneda,Y.,
            Takeuchi,T., Ihara,S. and Petri Jr.,M.A. Jr.
TITLE       Vh3 Gene Usage in Neutralizing Human Antibodies Specific for the
            Entamoeba histolytica Gal/GalNAc Lectin Heavy Subunit
JOURNAL     Infect. Immun. 71 (8), 4313-4319 (2003)
PUBMED      12874307
REFERENCE   2 (bases 1 to 324)
AUTHORS     Tachibana,H.
TITLE       Direct Submission
JOURNAL     Submitted (02-NOV-2002) Hiroshi Tachibana, Tokai University School
            of Medicine, Department of Infectious Diseases, Bohseidai, Isehara,
            Kanagawa 259-1193, Japan (E-mail:htachiba@is.icc.u-tokai.ac.jp,
            Tel:81-463-93-1121 (ex.2603), Fax:81-463-95-5450)

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ORIGIN
Query Match      88.6%; Score 281.8; DB 9; Length 324;
Best Local Similarity 93.1%; Pred. No. 2.2e-81;
Matches 295; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Oy      2 AGCTCACTCAGTCTCCATCTCCCTGCTGCATCTGTGGAGACAGAGTCCATCAGTT 61
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Oy      62 GCCGGGCAAGTCAGAGATTAAACCTATTAAATTTGGTATCAGCATAAACAGGGAAG 121
Db      68 GCCGGGCAAGTCAGAGATTAAATTTAAATTTGGTATCAGCAAAACAGGGAAG 127
Oy      122 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTCA 181
Db      128 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTCA 187
Oy      182 GTGGCAGTGATATGGGACAGACTTCACTTCACCATCAGCAGTGTGAGGCTGAAGTT 241
Db      188 GTGGCAGTGATCTGGGACAGATTTCATCTTCACCATCAGCAGTGTGAACTGAAGTT 247
Oy      242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGAGCA 301
Db      248 TTGCAACTTATTATTGTCAACAGAGTTTCAGTACCCGTAACCTTTTGGCCAGGGAGCA 307
Oy      302 AGGTGGAGATCAAA 318
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: July 27, 2005, 04:15:56 ; Search time 1958.75 Seconds  
(without alignments)  
6179.670 Million cell updates/sec

Title: US-10-027-725a-4

Perfect score: 318  
Sequence: 1 gagctcactcagctccatc.....ccaagtcgagatcaacaga 318

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hcc: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_g881: \*  
9: gb\_g882: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	280.2	88.1	447	2	AM405752 UI-HF-BL0
2	278.6	87.6	422	2	AM407804 UI-HF-BL0
3	278.6	87.6	525	6	CD705928 EST22455
4	278.6	87.6	624	6	CD690145 EST6668 h
5	277	87.1	487	2	AM405301 UI-HF-BL0
6	275.4	86.6	493	2	AM405753 UI-HF-BL0
7	275.4	86.6	748	6	CB956867 AGENCOURT
8	275.4	86.6	799	6	CB984750 AGENCOURT
9	275.4	86.6	807	6	CB958380 AGENCOURT
10	274.6	86.4	921	6	BC341239 602463904
11	274	86.2	454	5	BC397739 BX397739
12	273.8	86.1	498	6	CD684450 EST970 hu
13	273.8	86.1	499	6	CD685478 EST1998 h
14	273.8	86.1	608	2	AM404714 UI-HF-BL0
15	273.8	86.1	724	6	CB959008 AGENCOURT
16	273.8	86.1	745	6	CB958128 AGENCOURT
17	273.8	86.1	797	6	CB987347 AGENCOURT
18	272.2	85.6	550	6	CD709957 EST6484
19	272.2	85.6	598	6	CD692150 EST8689 h
20	272.2	85.6	671	4	BM830877 K-EST0104
21	272.2	85.6	684	4	BM769909 K-EST0053
22	272.2	85.6	750	6	CB985395 AGENCOURT
23	272.2	85.6	819	6	CB985931 AGENCOURT
24	270.8	85.2	471	2	AM406294 UI-HF-BL0

25	270.6	85.1	460	2	AM405906 UI-HF-BL0
26	270.6	85.1	532	4	BM823145 K-EST0094
27	270.6	85.1	619	6	CD693603 EST10126
28	270.6	85.1	693	6	CD684441 EST961 hu
29	269	84.6	391	2	AM404992 UI-HF-BL0
30	269	84.6	483	6	CD699627 EST16023
31	269	84.6	708	6	CB956923 AGENCOURT
32	269	84.6	738	6	CB987788 AGENCOURT
33	269	84.6	742	6	CB984723 AGENCOURT
34	269	84.6	750	6	CB956930 AGENCOURT
35	269	84.6	793	6	CB987506 AGENCOURT
36	269	84.6	807	6	CB957785 AGENCOURT
37	269	84.6	855	6	CB995312 AGENCOURT
38	269	84.6	864	4	BC548281 602575248
39	269	84.6	1084	6	CB986592 AGENCOURT
40	267.6	84.2	471	6	CD706522 EST23049
41	267.6	84.2	868	5	BM397738 BX397738
42	267.4	84.1	431	2	AM406886 UI-HF-BL0
43	267.4	84.1	444	5	BM56113 DKF2P781C
44	267.4	84.1	743	6	CB957909 AGENCOURT
45	267.4	84.1	837	6	CB984807 AGENCOURT

## ALIGNMENTS

RESULT 1  
AM405752  
LOCUS  
DEFINITION  
UI-HF-BL0-abp-a-01-0-UI.r1 NIH MGC\_37 Homo sapiens cDNA clone  
IMAGE:3057288 5', mRNA sequence.

ACCESSION  
AM405752  
VERSION  
AM405752.1 GI:6924809  
KEYWORDS  
EST.

SOURCE  
Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 447)

REFERENCE  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
Unpublished (1999)

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/IMG at: [www-bio.lnl.gov/bdbp/image/image.html](http://www-bio.lnl.gov/bdbp/image/image.html)

Seq primer: M13 Forward.

Location/Qualifiers

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/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI; constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

## ORIGIN

Query Match 88.1%; Score 280.2; DB 2; Length 447;  
Best Local Similarity 92.7%; Pred. No. 2.2e-76;

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Qy	62	GCCGGGCA	GTCAAGAAATTAA	CACCTTATTTAAATGTTATTCAGATTAACCGAGGAAG	121					
Db	150	GCCGGGCA	GTCAAGAGCAATTAAGACCTTTTAAATTTGTTATTCAGAGAGACCGAGGAAG	209						
Qy	122	CCCCTAAG	CTCTGATCTATGCTGATCCAGTTTGCAAGTGGGGTCCCATCAAGTTCA	181						
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Db	270	GTGGCAG	TGATATGGGACAGACTTCACTCTCAACCATGAGAGTGTGAACTGAAGATT	329						
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RESULT 2	
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LOCUS	AM407904 422 bp mRNA linear EST 16-FEB-2000
DEFINITION	UI-HF-BL0-add-a-01-0-UI_r2 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061128 5', mRNA sequence.

ORGANISM	Homo sapiens
SOURCE	Homo sapiens (human)
KEYWORDS	EST.
VERSION	AW407904.1
ACCESSION	AW407904
GI	6926961

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (pages 1 to 422)

**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Cloned distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNT at: [www-bio.1nl.gov/brd/image/image.html](http://www-bio.1nl.gov/brd/image/image.html) seq primer: M13 forward.

FEATURES	Location/Qualifiers
source	1. .422

Location/Qualifiers  
1. .422

Query Match	87.6%	Score 278.6	DB 2	Length 422
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				Gaps 0;
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QY	62	GCCGGGCAAGTCAGAGATTAAACACTATTAAATTGGTATCAGCATPAAACAGGGAAAG	121	
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QY	122	CCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTCA	181	
Db	150	CCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTCA	209	
QY	182	GTGCGAGTGAATAGGACAGACTTCACTCTCACCATCAGCAGTCTGACGCTGAAGATT	241	
Db	210	GTGCGAGTGAATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGACGCTGAAGATT	269	
QY	242	TTGCAAGTTACTACTGTTCAGAGAGTCTCAGTGGCTGTACACTTTTGGCCAGGGAGCCA	301	
Db	270	TTGCAACTTACTACTGTTCACAGAGTACAGTACCCGCTGAGACGTTGGCCAGGGAGCCA	329	
QY	302	AGGTGAGATCAACGA 318		
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RESULT 3	CD705928	CD705928	525 bp	mRNA	linear	EST 25-JUN-2003
LOCUS	CD705928					
DEFINITION	EST223455	human nasopharynx Homo sapiens cDNA, mRNA sequence.				

ACCESSION	CD705928	GI:32236558
VERSION	CD705928.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE  
1 (bases 1 to 525)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthalia; Primates; Catarrhini; Homiidae; Homo.

TITLE	AUTHORS
Transcriptional Gene Expression Profile of Human Nasopharynx	Lu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.

JOURNAL Unpublished (2003)

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Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@zsuns.edu.cn.

**FEATURES**  
**source**

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Matches 293;	Conservative	0;	Mismatches 24;	Indels 0;
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Db 124 AGATGACCAGTCTCCATCCCTCCGTCTGCATCTGTAGAGAGACGAGTCACCATTACTTT 183

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 SOURCE Homo sapiens (human)  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 624)  
 AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.  
 TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Yixin Zeng  
 Cancer Center  
 Sun Yat-sen University  
 651 Dongfeng Road East, Guangzhou 510060, China  
 Tel: 86-1380-9770-743  
 Fax: 86-20-8775-4506  
 Email: yxzeng@gzsunm.edu.cn.  
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 RESULT 5  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 487)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Eco RI site shown at the beginning of the sequence.  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.lnl.gov/bdrip/image/image.html  
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ACCESSION	IMAGE:3057290 5'				
VERSION	AM405753				
KEYWORDS	AM405753.1	GI:6924810			
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	NIH-MGC http://mgs.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cga@b-remail.nih.gov				
	Eco RI site shown at the beginning of the sequence.				
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.				
	cDNA Library Preparation: M.B. Soares Lab				
	cDNA Sequencing by: M.B. Soares Lab				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/BLNI at:				
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	M. Staudt, Ph.D. Library preparation by Maria de Fatima				
	Bonaldo, Ph.D. and M. Bento Soares, Ph.D."				
ORIGIN					
Query Match	86.6%	Score 275.4	DB 2	Length 493	
Best Local Similarity	91.8%	Pred. No. 7.8e-77			
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Db	79	AGATACCCCAAGTCTCAGACATTCAGACCTTAAATTTGGATCAGCAAAACCGAGAAAG	138		
QY	62	GCCGGGCAAGTCAGAAATTAACACCTATTAAATTTGGATCAGCTAAACCGAGAAAG	121		
Db	139	GCCGGGCAAGTCAGAGCATTTAGACCTATTAAATTTGGATCAGCAAAACCGAGAAAG	198		
QY	122	CCCTTAAGTCTCTGATCTATGCTGATCCAGTCTTGGCAAAAGTGGGTCCATTAAGTTCA	181		
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QY	242	TTGCAAGTACTACTGTGCAGAAGAGCTCAGATGGCTTCGTACACTTTGGCCAGGGGACCA	301
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QY	302	AGGTGAGATCAACAACA	318
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DEFINITION	AGENCOURT_13778741 NIH_MGC_184 Homo sapiens CDNA clone		
ACCESSION	IMAGE:30351770 5', mRNA sequence.		
VERSION	CB956867		
KEYWORDS	EST.		
SOURCE	CB956867.1 GI:30212984		
ORGANISM	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 748)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation . Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: NDCML49 row: n column: 03 High quality sequence stop: 528. Location/Qualifiers		
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	Library is oligo-dT primed and directionally cloned. cDNA		
	was prepared from a glandular pool of tissues from thyroid,		
	parathyroid, adrenal, cortex and pineal gland. 5' and 3'		
	adaptors were used in cloning as follows: 5' adaptor		
	sequence: 5'-CACGGCATTAATGACC-3' and 3' adaptor		
	sequence: 5'-ATTCTAGAGCCCGAGGGCCGACATG-dt(30)BN-3' (where B = A,		
	C, or G and N = A, C, G, or T). Average insert size 1.38		
	kb (range 0.60-3.5 kb). 15/15 colonies contained inserts		
	by PCR. This library was enriched for full-length clones		
	and was constructed by Clontech Laboratories (Palo Alto,		
	CA). Note: this is a NIH_MGC Library."		
ORIGIN			
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Oy 302 AGGTGAGATCAACGA 318  
Db 402 AGCTGAGATCAACGA 418

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IMAGE:30326373 5', mRNA sequence.  
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ACCESSION CB984750.1 GI:30279274  
VERSION  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 799)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNML Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovics  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
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Library is oligo-dT primed and directionally cloned. cDNA  
was prepared from a glandular pool of tissues from thyroid,  
parathyroid, adrenal, cortex and pineal gland. 5' and 3'  
adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.38  
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

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Best Local Similarity 91.8%; Pred. No. 9.1e-77;  
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Oy 302 AGGTGAGATCAACGA 318  
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IMAGE:30353194 5', mRNA sequence.  
CB958380  
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VERSION  
KEYWORDS EST.  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 807)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNML Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovics  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.lnl.gov>  
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Library is oligo-dT primed and directionally cloned. cDNA  
was prepared from a glandular pool of tissues from thyroid,  
parathyroid, adrenal, cortex and pineal gland. 5' and 3'  
adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.38  
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 86.6%; Score 275.4; DB 6; Length 807;

Best Local Similarity 91.8%; Pred. No. 9.1e-77;  
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QY 2 AGCTACTCACTGCTCCATCTCCCTGTCGTGATCTGGAGACAGATCCATCAGTT 61  
DB 101 AGATGACCCAGTCTCCATCTCCCTGTCGTGATCTGGAGACAGATCCATCAGTT 160

QY 62 GCCGGGCAAGTCAGAGATTAACACCTATTTAAATGGTATCAGCATTAACAGGAAG 121  
DB 161 GCCGGGCAAGTCAGAGATTAACACCTATTTAAATGGTATCAGCATTAACAGGAAG 220

QY 122 CCCCTAAGCTCTGATCTATGTCATCTCAGTTGCAAGGGGTCCTCATCAAGTTCA 181  
DB 221 CCCCTAAGCTCTGATCTATGTCATCTCAGTTGCAAGGGGTCCTCATCAAGTTCA 280

QY 182 GTGGCAGTGATATGGAAGACAGACTTCACTCTCACATCAGAGTCGTGACGCTGAAGATT 241  
DB 281 GTGGCAGTGATTTGGGACAGACTTCACTCTCACATCAGAGTCGTGACGCTGAAGATT 340

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QY 302 AGTGAGATCAACGA 318  
DB 401 AGCTGAGATCAACGA 417

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ACCESSION BG341239  
VERSION BG341239.1 GI:13147677  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 921)  
NIH-MGC http://mgs.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: LNCMI289 row: h column: 01  
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Location/Qualifiers  
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FEATURES  
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/clone="IMAGE:4576560"  
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for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 86.4%; Score 274.6; DB 4; Length 921;  
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DB 88 AGATGACCCAGTCTCCATCTCCCTGTCGTGATCTGGAGACAGATCCATCAGTT 147

QY 62 GCCGGGCAAGTCAGAGATTAACACCTATTTAAATGGTATCAGCATTAACAGGAAG 121  
DB 148 GCCGGGCAAGTCAGAGATTAACACCTATTTAAATGGTATCAGCATTAACAGGAAG 206

QY 122 CCCCTAAGCTCTGATCTATGTCATCTCAGTTGCAAGGGGTCCTCATCAAGTTCA 181  
DB 207 CCCCTAAGCTCTGATCTATGTCATCTCAGTTGCAAGGGGTCCTCATCAAGTTCA 266

QY 182 GTGGCAGTGATATGGAAGACAGACTTCACTCTCACATCAGAGTCGTGACGCTGAAGATT 241  
DB 267 GTGGCAGTGATTTGGGACAGACTTCACTCTCACATCAGAGTCGTGACGCTGAAGATT 326

QY 242 TTGCACTTACTACTGTCAAGAGAGTCTCAGTGCCTGTAACATTTTGGCCAGGGACCA 301  
DB 327 TTGCACTTACTACTGTCAAGAGATTAACAGTACCCCTGTCACTTTTGGCCAGGGACCA 386

QY 302 AGTGAGATCAACGA 318  
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RESULT 11  
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ACCESSION BX397739  
VERSION BX397739.2 GI:46847409  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 854)  
Li, W.B., Gruber, C.J., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On May 13, 2003 this sequence version replaced gi:30617375.  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
1696.i

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?cs=CSOD1041DH03QP1&c=1696.r.

FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="CSOD1041Y06"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_id="PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match	86.2%	Score 274	DB 5	Length 854
Best Local Similarity	93.4%	Pred. No. 2.6e-76		
Matches	297	Conservative	0	Mismatches 20, Indels 1, Gaps 1
Qy	2	AGCTCAGTCAAGTCTCCATCTCCCTGTCGATCTGTGGAGACAGAGTCAACCATCACTT	61	
Db	21	AGATGACCCAGTCTTCATCTCTCCCTGTCGATCTGTGAGAGACAGAGTCAACCATCACTT	80	
Qy	62	GCCGGGCAAGTCAGAGATTAAACCTTATTTAAATTGGTATCAGATTAACGAGGAAG	121	
Db	81	GCCGGGCAAGTCAGAGCATTTAGCAGCTATTTAAATTGGTATCAGAGAAACGAGGAAG	140	
Qy	122	CCCCTAAGCTCTGATCTATGCTGATCAGATTTGCAAGTGGGGTCCCATCAAGCTTCA	181	
Db	141	CCCCTAAGCTCTGATCTATGCTGATCAGATTTGCAAGTGGGGTCCCATCAAGCTTCA	200	
Qy	182	GTGGCAGTGATATATGGGACAGACTTCACTTCAACCATCAGCAGTCTGAGCCTGAAGAT	241	
Db	201	GTGGCAGTGATATATGGGACAGATTTCACTTCAACCATCAGCAGTCTGAGCCTGAAGAT	260	
Qy	242	-TTGCAAGTACTACTGTGCAAGAGAGTCTCAGTGGCTGTACACTTTTGGCCAGGGAC	300	
Db	261	ATTGCAAGTACTACTGTGCAAGAGAGTCTCAGTGGCTGTACACTTTTGGCCAGGGAC	320	
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Db	321	AAAGTGAGATCAACGCA	338	
RESULT 12				
LOCUS	CD684450	498 bp	mRNA	linear EST 25-JUN-2005
DEFINITION	EST1970 human nasopharynx Homo sapiens cDNA, mRNA sequence.			
ACCESSION	CD684450			
VERSION	CD684450.1	GI:32199455		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
AUTHORS	Li, X.-Q., Zhou, Y., Zhang, L.-D., Xu, H., Chen, H.-K., Pan, Z.-G., and Zeng, Y.-X.			
TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Yixin Zeng Cancer Center Sun Yat-sen University 651 Dongfeng Road East, Guangzhou 510060, China Tel: 86-1380-9770-743 Fax: 86-20-8775-4506 Email: yxzeng@gzsunm.edu.cn			
FEATURES	Location/Qualifiers			
SOURCE	1..498			
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	/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"			
ORIGIN				
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Best Local Similarity	91.5%	Pred. No. 2.6e-76		
Matches	290	Conservative	0	Mismatches 27, Indels 0, Gaps 0
Qy	2	AGCTCAGTCAAGTCTCCATCTCCCTGTCGATCTGTGGAGACAGAGTCAACCATCACTT	61	
Db	134	AGATGACCCAGTCTTCATCTCTCCCTGTCGATCTGTGAGAGACAGAGTCAACCATCACTT	193	
Qy	62	GCCGGGCAAGTCAGAGATTAAACCTTATTTAAATTGGTATCAGATTAACGAGGAAG	121	

Db	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	194	CCCGGGCAAGTCAGGCGCATAGCAACCTATTAAATTGGTATCAGCAAAAACCGAGGAAG	253									
Qy	122	CCCTTAAGCTCTGATCTATGCTGTCATCCAGTTTGAAAGTGGGGTCCCATCAAGTTTCA	181									
Db	254	CCCTTAAGCTCTGATCTCTGCTGTCATCCAGTTTGAAAGTGGGGTCCCATCAAGTTTCA	313									
Qy	182	GTGGCAGTGGATATATGGGACAGACTTCTACTCTCAGCATCAGACAGTCTGACGCTTAAGATT	241									
Db	314	GTGGCAGTGGATCTGGGACAGATTCTACTCTCAGCATCAGACAGTCTGACGCTTAAGATT	373									
Qy	242	TTGCAAGTTACTCTGTCAGAGAGAGTCAGTGCCTGTATCACTTTTGCCAGGGGACCA	301									
Db	374	TTGCAACTTACTCTATGTTCACAGAGTTTCAGTACCTCTGTAAGCTTGGCCAGGACCA	433									
Qy	302	AGGTGAGATCAACGCA 318										
Db	434	AGGTGAAATCAACGCA 450										
RESULT 13												
CD685478		499 bp	mRNA	linear	EST 25-JUN-2003							
LOCUS	CD685478											
DEFINITION	EST1998	human nasopharynx Homo sapiens	CDNA, mRNA sequence.									
ACCESSION	CD685478.1	GI:32201469										
VERSION	EST.											
KEYWORDS												
SOURCE		Homo sapiens										
ORGANISM		Homo sapiens (human)										
REFERENCE		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.										
AUTHORS		1 (bases 1 to 499)										
		Liu,X.-Q., Zhou,Y., Zhang,J.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.										
TITLE		Transcriptional Gene Expression Profile of Human Nasopharynx										
JOURNAL		Unpublished (2003)										
COMMENT		Contact: Yixin Zeng										
		Cancer Center										
		Sun Yat-sen University										
		651 Dongfeng Road East, Guangzhou 510060, China										
		Tel: 86-1380-9770-743										
		Fax: 86-20-8775-4506										
		Email: yxzeng@gzsums.edu.cn.										
FEATURES		location/Qualifiers										
source		1..499										
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ORIGIN												
Query Match		86.1%;	Score 273.8;	DB 6;	Length 499;							
Best Local Similarity		91.5%;	Pred. No. 2.66-76;									
Matches		290;	Conservative 0;	Mismatches 27;	Indels 0;	Gaps 0;						
Qy	2	AGCTCACTCACTCTCCATCTCTCTCTCTGTCATCTGTGGGAGACAGATCACTCACTT	61									
Db	137	AGATGACCACTCTCCATCTCTCTCTCTGTCATCTGTGGGAGACAGATCACTCACTT	196									
Qy	62	GCGGGGCAAGTCAGAGATTAAACAATTAATTAATGGTATCAGCATTAACGAGGAAG	121									
Db	197	GCGGGGCAAGTCAGAGCATTAAGCACTTAATTAATGGTATCAGCAAGAACGAGGAAG	256									
Db	257	CCCTTAAGCTCTGATCTATGCTGTCATCCAGTTTGAAAGTGGGGTCCCATCAAGTTCA	316									
Qy	122	CCCTTAAGCTCTGATCTATGCTGTCATCCAGTTTGAAAGTGGGGTCCCATCAAGTTCA	181									
Db	314	CCCTTAAGCTCTGATCTATGCTGTCATCCAGTTTGAAAGTGGGGTCCCATCAAGTTCA	373									
Qy	182	GTGGCAGTGGATATATGGGAC										

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QY      242 TTGCAAGTACTACTGTCAAGAGCTCAGTCCCTGTCATCCTTTGGCCAGGAGCA 301
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      377 TTGCAACTTACTACTGTCAAGAGCTTACAGTACCCTCCTCTTGGCGGAGGACCA 436
QY      302 AGGTGAGATCAACGA 318
      |||
      437 CGGTGAGATCAACGA 453

RESULT 14
AM404714      608 bp. mRNA linear EST 16-FEB-2000
LOCUS        AM404714
DEFINITION   UT-HF-BLO-acd-c-11-0-UT.r1 NIH_MGC_37 Homo sapiens cDNA clone
ACCESSION    AM404714
VERSION      AM404714.1 GI:6923771
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    NIH-MGC http://mgc.nci.nih.gov/
AUTHORS      1 (bases 1 to 608)
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Eco RI site shown at the beginning of the sequence.
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              CDNA Library Preparation: M.B. Soares Lab
              DNA Sequencing by: M.B. Soares Lab
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              www-bio.lnl.gov/bbrp/image/image.html
              Seq primer: M13 Forward.
              Location/Qualifiers
                1. 608
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                  /mol_type="mRNA"
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                  /clone_line="MGC85"
                  /lab_host="DH10B (LT)"
                  /clone_lib="NIH_MGC_37"
                  /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                  Constructed from size fractionated cytoplasmic mRNA
                  (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                  M. Staudt, Ph.D. Library preparation by Maria de Fatima
                  Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match      86.1%; Score 273.8; DB 2; Length 608;
Best Local Similarity 91.5%; Pred. No. 2.7e-76;
Matches 290; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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      |||
      169 CCCCTAAGCTCTGATCTGATCTGATCCAGTTTGCAGAGTGGGGTCCCATCAAGTTCA 228
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      182 GTGCGAGTGATATGGGACAGATTCATCTCAGCATAGCAAGTGTGACGCTGAAGATT 241
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Db      229 GTGGCAGTGATCTGGGACAGATTTTCACTTCACCATCAGACGTCTGCAACTGAAGATT 288
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QY      302 AGGTGAGATCAACGA 318
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RESULT 15
CB959008      724 bp. mRNA linear EST 29-APR-2003
LOCUS        CB959008
DEFINITION   AGENCOURT 13664954 NIH_MGC_184 Homo sapiens cDNA clone
ACCESSION    CB959008
VERSION      CB959008.1 GI:30215124
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    NIH-MGC http://mgc.nci.nih.gov/
AUTHORS      1 (bases 1 to 724)
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
              CDNA Library Preparation: CLONTECH Laboratories, Inc.
              DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.lnl.gov
              Plate: NDCM15 row: P column: 02
              High quality sequence stop: 549.
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                  /mol_type="mRNA"
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                  /clone="IMAGE:30354121"
                  /lab_host="DH10B (TI phage-resistance)"
                  /clone_lib="NIH_MGC_184"
                  /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
                  SfiI (ggccgctggcc); Site_2: SfiI (ggccgctggcc);
                  Library is oligo-dT primed and directionally cloned. cDNA
                  was prepared from a glandular pool of tissues from thyroid,
                  parathyroid, adrenal, cortex and pineal gland. 5' and 3'
                  adaptors were used in cloning as follows: 5' adaptor
                  sequence: 5'-CACGGCATTAATGCGC-3' and 3' adaptor sequence:
                  5'-ATTCTAAGGCCGACGCGCCGACATG-dT(30)BN-3' (where B = A,
                  C, or G and N = A, C, G, or T). Average insert size 1.38
                  kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
                  by PCR. This library was enriched for full-length clones
                  and was constructed by Clontech Laboratories (Palo Alto,
                  CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match      86.1%; Score 273.8; DB 6; Length 724;
Best Local Similarity 91.5%; Pred. No. 2.9e-76;
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      97 AGATGACCCAGCTTCATCTCCCTGCTGTCATCTGTGGAGACAGATCCACATCAATT 156
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OY 122 CCCCTAAGCTCCTGATCTATGCTGATCCAGTTTGCAAGTGGGTTCCCATCAAGTTCA 181
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OY 182 GTGGCAGTGGATATGGGACAGACTTCACTCAACCATCAGCAGTCTGCGAGCTGAAGATT 241
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Db 277 GTGGCAGTGGATCTGGGACAGATTTCACCTCAACCATCAGCAGTCTGCGAGCTGAAGATT 336
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OY 242 TTGCAAGTTACTACTGTCAGAGAGTCTCAGTGCCTCGTACACTTTTGCCAGGGGACCA 301
    |||||
Db 337 TTGCAACTTACTACTGTCAGAGAGTCTCAGTGCCTCGTACACTTTTGCCAGGGGACCA 396
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OY 302 AGGTGGAGATCAACGA 318
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Db 397 AGGTGSAATCAACGA 413
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Job time : 1961.75 secs

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XX	29-DEC-2000; 2000SE-00004892.
XX	(PMAA ) PHARMACIA DIAGNOSTICS AB.
XX	Flicker S, Steinberger P, Kraft D, Valenta R;
XX	MP1; 2002-583604/62.
DR	P-PSDB; ABG30448.
XX	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT	variable region of group 2 allergen specific-human IgE Fabs, useful for
PT	diagnosing or passive immunotherapy of type I allergy, for environmental
PT	allergen detection.
XX	Disclosure; Page 34; 45pp; English.
XX	This invention relates to the DNA and protein sequences of group 2
CC	allergen-specific human IgE Fabs and methods for their use. The proteins
CC	of the invention may have antiallergic activities and may be used as a
CC	vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
CC	antibodies to Phl p 2 (a major timothy grass pollen allergen). The group
CC	2 allergen-specific fabs of the invention may be useful for environmental
CC	allergen detection and for standardisation of allergen extracts. The fabs
CC	- or a vaccine against a type I allergy is useful for passive
CC	immunotherapy of type I allergy, it is also useful for diagnosing a type
CC	I allergy. The allergen-specific fabs of the invention are useful for
CC	inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC	also useful for identification of group 2 allergen-containing pollen and
CC	may be used for blocking the binding of grass pollen allergic patients
CC	IgE antibodies to Phl p 2. The present sequence represents the DNA
CC	encoding the human IgG fab, clone 94 light chain protein of the invention
XX	Sequence 318 BP; 84 A; 81 C; 77 G; 76 T; 0 U; 0 Other.
XX	Query Match 100.0%; Score 318; DB 6; Length 318;
XX	Best Local Similarity 100.0%; Pred. No. 1e-90; Indels 0; Gaps 0
XX	Matches 318; Conservative 0; Mismatches 0
QY	1 GAGCTCACTCACTCTCCATCTCCCTGTCGATCTGTGGAGACAGATCAACATCAGT 60
DB	1 GAGCTCACTCACTCTCCATCTCCCTGTCGATCTGTGGAGACAGATCAACATCAGT 60
QY	61 TGCCTGGGCAAGTCAGAGAAATTAAACACTTATTTAAATGGATATCAAGATCAAGGAAA 120
DB	61 TGCCTGGGCAAGTCAGAGAAATTAAACACTTATTTAAATGGATATCAAGATCAAGGAAA 120
QY	121 GCCCTTAAGCTCTGATCTATAGCTGATCAGTTTSCAAAGTGGGGTCCCATCAAGGTTT 180
DB	121 GCCCTTAAGCTCTGATCTATAGCTGATCAGTTTSCAAAGTGGGGTCCCATCAAGGTTT 180
QY	181 AGTGCAGTGTATATGGAGACAGACTTCACTCAACCATCAGCAGTCTGACGCTGAAGAT 240
DB	181 AGTGCAGTGTATATGGAGACAGACTTCACTCAACCATCAGCAGTCTGACGCTGAAGAT 240
QY	241 TTTCGAAGTACTACTGTCTCAAGAGAGTCTCAGTGCTCTGACATTTTGGCCAGGGGACC 300
DB	241 TTTCGAAGTACTACTGTCTCAAGAGAGTCTCAGTGCTCTGACATTTTGGCCAGGGGACC 300
QY	301 AAGGTGAGATCAACGA 318
DB	301 AAGGTGAGATCAACGA 318
RESULT 2	
AAH68701	AAH68701 standard; DNA; 321 BP.
XX	AAH68701;
XX	14-SEP-2001 (first entry)
DE	Human anti-Rh(D) antibody clone SH13 nucleotide sequence.

XX	Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW	red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX	
OS	Homo sapiens.
PN	US6255455-B1.
XX	
PD	03-JUL-2001.
XX	
PF	29-JAN-1999; 99US-00240274.
XX	
PR	11-OCT-1996; 96US-0028550P.
DR	27-JUN-1997; 97US-0088404S.
XX	
PA	10-APR-1998; 98US-0081380P.
XX	(TYPE-) UNIV PENNSYLVANIA.
P1	Siegel DL;
XX	
PI	WPI; 2001-388931/41.
XX	
DR	P-PSDB; AAG93644.
XX	
PT	New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT	diagnostics requiring a human instead of an animal antibody and in
PT	therapeutic medicine.
XX	
PS	Example 3; Col 74; 162pp; English.
XX	
CC	The present invention describes an isolated Rh(D) binding protein,
CC	preferably a human antibody, (I) having an amino acid sequence comprising
CC	one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC	immunostimulant activity, and can be used as an immune system stimulant.
CC	(I) can be used in diagnostic and therapeutic medicine. The antibodies
CC	are used in diagnostics that require human antibodies instead of animal
CC	antibodies, such as determine the Rh phenotype of human red blood cells.
CC	AAG68615 to AAH6726 represent the nucleotide sequence which encode
CC	AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC	chain CDR3 amino acid sequences which are given in the exemplification of
CC	the present invention
XX	
SO	Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;
Query Match	90.4%; Score 287.6; DB 5; Length 321;
Best Local Similarity	94.0%; Pred. No. 4.8e-81;
Matches 299; Conservative	0; Mismatches 19; Indels 0; Gaps 0
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Oy	61 TGCCGGCAATCAGAGAATTAAACCATTTAATTGGTATCAGACATAAACAGGAAA 120 
Dd	64 TGCCGGCAATCAGAGATTAAGCATTTAATTGGTATCAGACATAAACAGGAAA 123 
Oy	121 GCCCTTAAGTCTCGATCTATGTCGATCCAGTTTGAAGTGGGGTCCCATCAAGTTC 180 
Dd	124 GCCCTTAAGTCTCGATCTATGTCGATCCAGTTTGAAGTGGGGTCCCATCAAGTTC 183 
Oy	181 AGTGGCAGTGGATATGGAGACAGACTTCACTCTCACCATCAGAGTCTGCAAGCTGAAGT 240 
Dd	184 AGTGGCAGTGGATATGGAGACAGATTTCACCTCACAACATCAGAGTCTGCAAGTGAAGT 243 
Oy	241 TTGCAATTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 300 
Dd	244 TTGCAATTTACTACTGTCAAGAGAGTCAAGTGAAGTACCCCTTACACTTTTGGCCAGGGGACC 303 
Oy	301 AAGGTGAGATCAAACGA 318 
Dd	304 AAGGTGAGATCAAACGA 321 

RESULT 3

ACD45365  
ID ACD45365 standard; DNA; 321 BP.  
XX  
AC ACD45365;  
XX  
DT 12-SEP-2003 (first entry)  
XX  
DE Anti-Rh(D) light chain SH13 DNA.  
XX  
KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;  
XX magnetically activated cell sorting.  
XX  
OS Homo sapiens.  
XX  
PN US2003040605-A1.  
XX  
PD 27-FEB-2003.  
XX  
PF 04-MAY-2001; 2001US-00848798.  
XX  
PR 11-OCT-1996; 96US-0028550P.  
PR 27-JUN-1997; 97US-0088404S.  
PR 10-APR-1998; 98US-0081380P.  
PR 29-JAN-1999; 99US-00240274.  
XX  
PA (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Siegel DL;  
XX  
DR WPI; 2003-512273/48.  
DR P-PSDB; ABO27451.  
XX  
PT New human Rh(D) -binding protein useful for various diagnostic and  
XX therapeutic applications, including typing of blood or blood products.  
XX  
PS Claim 12; Page 57; 187pp; English.  
XX  
CC The invention relates to an isolated Rh(D) binding protein. The protein  
XX can be used for magnetically activated cell sorting. The protein is  
XX useful in various diagnostic and therapeutic applications in humans,  
XX including typing of blood or blood products. The present sequence  
XX represents DNA encoding a human anti-Rh(D) chain  
XX  
SQ Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;  
Query Match 90.4%; Score 287.6; DB 9; Length 321;  
Best Local Similarity 94.0%; Pred. No. 4.8e-81;  
Matches 299; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GAGCTCACTCACTGCTCCATCCCTGCTGATCTGTGGAGACAGATCACTCACT 60  
DB 4 GAGCTCACTCACTGCTCCATCCCTGCTGATCTGTGGAGACAGATCACTCACT 63

QY 61 TCCCGGGAAGTCAAGAGATTAACTATTAAATGGATACAGATTAACAGAGAAA 120  
DB 64 TCCCGGGAAGTCAAGAGATTAACTATTAAATGGATACAGATTAACAGAGAAA 123

QY 121 GCCCTAAGCTCTGATCTATGCTGATCCAGTTTGCAAAGTGGGTCCCATCAAGTTTC 180  
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QY 181 AGTGGCACTGATATGGGACAGACTTCACTCTCAACATCAGAGATCTGAGCTGAAGAT 240  
DB 184 AGTGGCACTGATATGGGACAGACTTCACTCTCAACATCAGAGATCTGAGCTGAAGAT 243

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DB 244 TTGCAAGTACTACTGTCAAGAGAGTCTCAGTGGCTGTGACACTTTTGGCCAGGGGACC 303

QY 301 AAGTGAGATCAAAAGA 318  
DB 304 AAGTGAGATCAAAAGA 321

RESULT 4  
AAH68720  
ID AAH68720 standard; DNA; 321 BP.  
XX  
AC AAH68720;  
XX  
DT 14-SEP-2001 (first entry)  
XX  
DE Human anti-Rh(D) antibody clone SH49 nucleotide sequence.  
XX  
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
XX red blood cell; Rh phenotype; diagnosis; therapeutic; ds.  
XX  
OS Homo sapiens.  
XX  
PN US6255455-B1.  
XX  
PD 03-JUL-2001.  
XX  
PF 29-JAN-1999; 99US-00240274.  
XX  
PR 11-OCT-1996; 96US-0028550P.  
PR 27-JUN-1997; 97US-0088404S.  
PR 10-APR-1998; 98US-0081380P.  
XX  
PA (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Siegel DL;  
XX  
DR WPI; 2001-388931/41.  
DR P-PSDB; AAG93663.  
XX  
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
XX diagnostics requiring a human instead of an animal antibody and in  
XX therapeutic medicine.  
XX  
PS Example 3; Col 79; 162pp; English.  
XX  
CC The present invention describes an isolated Rh(D) binding protein,  
XX preferably a human antibody, (I) having an amino acid sequence comprising  
XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
XX immunostimulant activity, and can be used as an immune system stimulant.  
XX (I) can be used in diagnostic and therapeutic medicine. The antibodies  
XX are used in diagnostics that require human antibodies instead of animal  
XX antibodies, such as determine the Rh phenotype of human red blood cells.  
XX AAH68615 to AAH68726 represent the nucleotide sequence which encode  
XX AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
XX chain CDR3 amino acid sequences which are given in the exemplification of  
XX the present invention  
XX  
SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;  
Query Match 88.4%; Score 281.2; DB 5; Length 321;  
Best Local Similarity 92.8%; Pred. No. 5.2e-79;  
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGTCACTCACTGCTCCATCCCTGCTGATCTGTGGAGACAGATCACTCACT 60  
DB 4 GAGTCACTCACTGCTCCATCCCTGCTGATCTGTGGAGACAGATCACTCACT 63

QY 61 TCCCGGGAAGTCAAGAGATTAACTATTAAATGGATACAGATTAACAGAGAAA 120  
DB 64 TCCCGGGAAGTCAAGAGATTAACTATTAAATGGATACAGATTAACAGAGAAA 123

QY 121 GCCCTAAGCTCTGATCTATGCTGATCCAGTTTGCAAAGTGGGTCCCATCAAGTTTC 180  
DB 124 GCCCTAAGCTCTGATCTATGCTGATCCAGTTTGCAAAGTGGGTCCCATCAAGTTTC 183

QY 181 AGTGGCACTGATATGGGACAGACTTCACTCTCAACATCAGAGATCTGAGCTGAAGAT 240  
DB 184 AGTGGCACTGATATGGGACAGACTTCACTCTCAACATCAGAGATCTGAGCTGAAGAT 243

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Qy 241 TTTCAGATTACTACTGCAAGAGCTCTCAGTCTGTAACCTTTTGGCCAGGGGACC 300
Db 244 TTTCACACTTACTACTGTCACAGAGTTCAGTACCCCGTAGCGTTCGGCCAAAGGGACC 303
Qy 301 AAGGTGAGATCAAAACGA 318
Db 304 AAGGTGAGATCAAAACGA 321

RESULT 5
ID AAH68654 standard; DNA; 321 BP.
AC AAH68654;
DT 14-SEP-2001 (first entry)
XX Human anti-Rh(D) chain I09 nucleotide sequence.
DE Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX Homo sapiens.
XX US6255455-B1.
XX 03-JUL-2001.
XX 29-JAN-1999; 99US-00240274.
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX (TYPE-) UNIV PENNSYLVANIA.
XX Siegel DL;
XX WPI; 2001-388931/41.
XX P-PSDB; AAG93597.
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX Example 2; Col 56; 162pp; English.
XX The present invention describes an isolated Rh(D) binding protein,
XX preferably a human antibody, (I) having an amino acid sequence comprising
XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has
XX immunostimulant activity, and can be used as an immune system stimulant.
XX (I) can be used in diagnostic and therapeutic medicine. The antibodies
XX are used in diagnostics that require human antibodies instead of animal
XX antibodies, such as determine the Rh phenotype of human red blood cells.
XX AAH68615 to AAH68726 represent the nucleotide sequence which encode
XX AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
XX chain CDR3 amino acid sequences which are given in the exemplification of
XX the present invention
SQ Sequence 321 BP; 85 A; 87 C; 73 G; 76 T; 0 U; 0 Other;
Qy Query Match 88.4%; Score 281.2; DB 5; Length 321;
Db Best Local Similarity 92.8%; Pred. No. 5.2e-79;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 GAGCTCACTGACTGCTCCATCTCCCTGCTGTCATCTTGCGAGACAGATCACTCACT 60
Db 4 GAGCTCACCAGTCTCCATCTCCCTGCTGTCATCTTGAGAGACAGATCACTCACTCACT 63
Qy 61 TGCCGGGCAAGTCAAGATTAACACCTATTAAATGGTATCAGCATTAACAGGAGAA 120
Db 64 TGCCGGGCAAGTCAAGATTAACAGCTATTAAATGGTATCAGCATTAACAGGAGAA 123

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Qy 121 GCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGCTCCATCAAGTTTC 180
Db 124 GCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGCTCCATCAAGTTTC 183
Qy 181 AGTGGCAGTGGATATGAGACAGACTTCACTTCACATCGACATCTTGACCTGAAGAT 240
Db 184 AGTGGCAGTGGATCTGGACAGATTCCACTCTTCACATCGACATCTTGACCTGAAGAT 243
Qy 241 TTTCAGATTACTACTGTCACAGAGCTCTCAGTCTGTAACCTTTTGGCCAGGGGACC 300
Db 244 TTTCACACTTACTACTGTCACAGAGTTCAGTACCCCGTAGCGTTCGGCCAAAGGGACC 303
Qy 301 AAGGTGAGATCAAAACGA 318
Db 304 AAGGTGAGATCAAAACGA 321

RESULT 6
ID AAH68647 standard; DNA; 321 BP.
AC AAH68647;
DT 14-SEP-2001 (first entry)
XX Human anti-Rh(D) chain I02 nucleotide sequence.
DE Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX Homo sapiens.
XX US6255455-B1.
XX 03-JUL-2001.
XX 29-JAN-1999; 99US-00240274.
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX (TYPE-) UNIV PENNSYLVANIA.
XX Siegel DL;
XX WPI; 2001-388931/41.
XX P-PSDB; AAG93590.
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX Example 2; Col 54; 162pp; English.
XX The present invention describes an isolated Rh(D) binding protein,
XX preferably a human antibody, (I) having an amino acid sequence comprising
XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has
XX immunostimulant activity, and can be used as an immune system stimulant.
XX (I) can be used in diagnostic and therapeutic medicine. The antibodies
XX are used in diagnostics that require human antibodies instead of animal
XX antibodies, such as determine the Rh phenotype of human red blood cells.
XX AAH68615 to AAH68726 represent the nucleotide sequence which encode
XX AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
XX chain CDR3 amino acid sequences which are given in the exemplification of
XX the present invention
SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
Qy Query Match 88.4%; Score 281.2; DB 5; Length 321;
Db Best Local Similarity 92.8%; Pred. No. 5.2e-79;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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Query Match 88.4%; Score 281.2; DB 9; Length 321;  
 Best Local Similarity 92.8%; Pred. No. 5.2e-79;  
 Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGCTCACTAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGATGCATCATG 60  
 DB 4 GAGCTCACTAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGATGCATCATG 63  
 QY 61 TGGCGGCAAGTCAAGAAATTAAACCTATTAAATTGGTATCAGCATTAACCAAGGAAA 120  
 DB 64 TGGCGGCAAGTCAAGAAATTAAACCTATTAAATTGGTATCAGCATTAACCAAGGAAA 123  
 QY 121 GCCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTTC 180  
 DB 124 GCCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTTC 183  
 QY 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAGCATCAGAGATCTGAGCTGAAAGAT 240  
 DB 184 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAGCATCAGAGATCTGAGCTGAAAGAT 243  
 QY 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 300  
 DB 244 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 303  
 QY 301 AAGGTGAGATCAACGA 318  
 DB 304 AAGGTGAGATCAACGA 321

RESULT 9  
 ACD45384  
 ID ACD45384 standard; DNA; 321 BP.  
 XX ACD45384;  
 XX  
 DT 12-SEP-2003 (first entry)  
 XX  
 DE Anti-Rh(D) light chain SH49 DNA.  
 XX  
 KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;  
 KW magnetically activated cell sorting.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003040605-A1.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 04-MAY-2001; 2001US-00848798.  
 XX  
 PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 PR 29-JAN-1999; 99US-00240274.  
 XX  
 PA (TYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Siegel DL;  
 XX  
 DR WPI; 2003-512273/48.  
 DR P-PSDB; ABO27470.  
 XX  
 PT New human Rh(D)-binding protein useful for various diagnostic and  
 PT therapeutic applications, including typing of blood or blood products.  
 XX  
 PS Claim 12; Page 61; 187bp; English.  
 XX  
 CC The invention relates to an isolated Rh(D) binding protein. The protein  
 CC can be used for magnetically activated cell sorting. The protein is  
 CC useful in various diagnostic and therapeutic applications in humans,  
 CC including typing of blood or blood products. The present sequence  
 CC represents DNA encoding a human anti-Rh(D) chain  
 XX

SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;  
 Query Match 88.4%; Score 281.2; DB 9; Length 321;  
 Best Local Similarity 92.8%; Pred. No. 5.2e-79;  
 Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGCTCACTAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGATGCATCATG 60  
 DB 4 GAGCTCACTAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGATGCATCATG 63  
 QY 61 TGGCGGCAAGTCAAGAAATTAAACCTATTAAATTGGTATCAGCATTAACCAAGGAAA 120  
 DB 64 TGGCGGCAAGTCAAGAAATTAAACCTATTAAATTGGTATCAGCATTAACCAAGGAAA 123  
 QY 121 GCCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTTC 180  
 DB 124 GCCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTTC 183  
 QY 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAGCATCAGAGATCTGAGCTGAAAGAT 240  
 DB 184 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAGCATCAGAGATCTGAGCTGAAAGAT 243  
 QY 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 300  
 DB 244 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 303  
 QY 301 AAGGTGAGATCAACGA 318  
 DB 304 AAGGTGAGATCAACGA 321

RESULT 10  
 AAT6781  
 ID AAT6781 standard; cDNA; 321 BP.  
 XX AAT6781;  
 XX  
 DT 29-JAN-1998 (first entry)  
 XX  
 DE Anti-cancer specific antigen MAb light chain variable region cDNA.  
 XX  
 KW Light chain; variable region; cancer specific antigen; human;  
 KW monoclonal antibody; hMab; diagnosis; cancer; immunotherapy;  
 KW purification; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP09098786-A.  
 XX  
 PD 15-APR-1997.  
 XX  
 PF 06-OCT-1995; 95JP-00284400.  
 XX  
 PR 06-OCT-1995; 95JP-00284400.  
 XX  
 PA (MOMI ) MORINAGA & CO LTD.  
 PA (SHKO ) SHINGIJUTSU JIGYODAN.  
 XX  
 DR WPI; 1997-275445/25.  
 DR P-PSDB; AAM16649.  
 XX  
 PT cDNA encoding human monoclonal antibody - useful in medicine, or to  
 PT purify cancer specific antigen.  
 XX  
 PS Claim 2; Fig 2; 7bp; Japanese.  
 XX  
 CC The present sequence encodes the light chain variable region of an anti-  
 CC cancer specific antigen human monoclonal antibody (hMab). The hMab can be  
 CC used in medicine, e.g. clinical diagnosis of cancer or immunotherapy, or

CC to purify cancer specific antigen. The industrial scale production of  
CC large amounts of the hMab is made feasible by genetic engineering using  
CC the hMab CDNA

XX Sequence 321 BP; 86 A; 89 C; 72 G; 74 T; 0 U; 0 Other;

Query Match 88.2%; Score 280.4; DB 2; Length 321;

Best Local Similarity 93.3%; Pred. No. 9.3e-79;  
Matches 293; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```
QY 2 AGCTCACTCACTCTCCATCCCTCTGCTGATCTGGAGACAGAGTCACTCACTT 61
DB 8 AGATGACCCAGTCTCCATCCCTCCCTGCTGATCTGGAGACAGAGTCACTT 67
QY 62 GCCGGGCAAGTCAGAGATTAAACACTATTAAATGGTATCAGCATTAACAGGAAAG 121
DB 68 GCCGGGCAAGTCAGAGATTAAACACTATTAAATGGTATCAGCATTAACAGGAAAG 127
QY 122 CCCCTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 181
DB 128 CCCCTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 187
QY 182 GTGCGCATGATATGAGACAGACTTCACTCACTCACTCACTCACTCACTCACTCA 241
DB 188 GTGCGCATGATATGAGACAGACTTCACTCACTCACTCACTCACTCACTCACTCA 247
QY 242 TTGCAAGTTACTACTGTCAGAGAGTCTCAGTGCCTGTCACATTTTGGCCAGGGA 301
DB 248 TTGCAAGTTACTACTGTCAGAGAGTCTCAGTGCCTGTCACATTTTGGCCAGGGA 307
QY 302 AGGTGAGATCAAA 315
DB 308 AGCTGAGATCAAA 321
```

## RESULT 11

AAH68723 standard; DNA; 321 BP.

XX AAH68723;

XX 14-SEP-2001 (first entry)

XX Human anti-Rh(D) antibody clone SHS2 nucleotide sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

XX red blood cell; Rh phenotype; diagnosis; therapeutic; ds.

XX Homo sapiens.

XX US6255455-B1.

XX 03-JUL-2001.

XX 29-JAN-1999; 99US-00240274.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

XX (UYPE-) UNIV. PENNSYLVANIA.

XX Siegel DL;

XX WPI; 2001-388931/41.

XX P-PSDB; AAG93666.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
XX diagnostics requiring a human instead of an animal antibody and in  
XX therapeutic medicine.  
XX Example 3; Col 79; 162p; English.

CC The present invention describes an isolated Rh(D) binding protein.

CC preferably a human antibody, (1) having an amino acid sequence comprising

CC one of the sequences (S) given in AAG93558 to AAG93669. (1) has

CC immunostimulant activity, and can be used as an immune system stimulant.

CC (1) can be used in diagnostic and therapeutic medicine. The antibodies

CC are used in diagnostics that require human antibodies instead of animal

CC antibodies, such as determine the Rh phenotype of human red blood cells.

CC AAG93558 to AAG93669 represent the nucleotide sequence which encode

CC chain CDR3 amino acid sequences which are given in the exemplification of

CC the present invention

XX Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;

Query Match 87.9%; Score 279.6; DB 5; Length 321;

Best Local Similarity 92.5%; Pred. No. 1.7e-78;  
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

```
QY 1 GAGCTCACTCACTCTCCATCCCTCTGCTGATCTGGAGACAGAGTCACTCACT 60
DB 4 GAGCTCACTCACTCTCCATCCCTCTGCTGATCTGGAGACAGAGTCACTCACT 63
QY 61 TCCCGGCAAGTCAGAGATTAAACACTATTAAATGGTATCAGCATTAACAGGAA 120
DB 64 TCCCGGCAAGTCAGAGATTAAACACTATTAAATGGTATCAGCATTAACAGGAA 123
QY 121 GCCCTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 180
DB 124 GCCCTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 183
QY 181 AGTGGAGTGGATATGAGACAGACTTCACTCACTCACTCACTCACTCACTCA 240
DB 184 AGTGGAGTGGATATGAGACAGACTTCACTCACTCACTCACTCACTCACTCA 243
QY 241 TTGCAAGTTACTACTGTCAGAGAGTCTCAGTGCCTGTCACATTTTGGCCAG 300
DB 244 TTGCAAGTTACTACTGTCAGAGAGTCTCAGTGCCTGTCACATTTTGGCCAG 303
QY 301 AAGGTGAGATCAAA 318
DB 304 AAGGTGAGATCAAA 321
```

## RESULT 12

AAH68658 standard; DNA; 321 BP.

XX AAH68658;

XX 14-SEP-2001 (first entry)

XX Human anti-Rh(D) chain I13 nucleotide sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

XX red blood cell; Rh phenotype; diagnosis; therapeutic; ds.

XX Homo sapiens.

XX US6255455-B1.

XX 03-JUL-2001.

XX 29-JAN-1999; 99US-00240274.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

XX (UYPE-) UNIV. PENNSYLVANIA.

XX Siegel DL;

XX WPI; 2001-388931/41.

DR P-PSDB; AAG93601.  
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine.  
XX  
XX  
PS Example 2; Col 57; 162pp; English.  
XX  
CC The present invention describes an isolated Rh(D) binding protein,  
CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AAG93558 to AAG93659. (I) has  
CC immunostimulant activity, and can be used as an immune system stimulant.  
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAG93558 to AAG93659 represent the nucleotide sequence which encode  
CC chain CDR3 amino acid sequences which are given in the exemplification of  
CC the present invention  
XX  
SQ Sequence 321 BP; 82 A; 88 C; 77 G; 74 T; 0 U; 0 Other;  
Query Match 87.9%; Score 279.6; DB 5; Length 321;  
Best Local Similarity 92.5%; Pred. No. 1.7e-78;  
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 1 GAGCTCACTAGTCCATCTCTCCCTGTCTGTCATCTGTGGAGACAGATCACCATCACT 60  
DB 4 GAGCTCACCAGTCTCCATCTCTCCCTGTCTGTCATCTGTGGAGACAGATCACCATCACT 63  
QY 61 TGCCGGGCAAGTCAAGATTAACACCTATTAAATGGTATCGACATAAACCAGGGGAAA 120  
DB 64 TGCCGGGCAAGTCAAGATTAACACCTATTAAATGGTATCGACATAAACCAGGGGAAA 123  
QY 121 GCCCCTAAGCTCTGATCTATGTCATCCAGTTTGGAAAGTGGGTCCTCAAGGTTTC 180  
DB 124 GCCCCTAAGCTCTGATCTATGTCATCCAGTTTGGAAAGTGGGTCCTCAAGGTTTC 183  
QY 181 AGTGGCAGTGGATATGGACAGACTTCACTCTCAACCATCAGCAGTCTGACCTGAAGAT 240  
DB 184 AGTGGCAGTGGATATGGACAGACTTCACTCTCAACCATCAGCAGTCTGACCTGAAGAT 243  
QY 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTGAGTCCCTGTACATTTTGGCAGGGGACC 300  
DB 244 TTTCGAAGTTACTACTGTCAAGAGAGTCTGAGTCCCTGTACATTTTGGCAGGGGACC 303  
QY 301 AAGGTGAGATCAACGA 318  
DB 304 AAGGTGAGATCAACGA 321  
RESULT 13  
AAH68724  
ID AAH68724 standard; DNA; 321 BP.  
XX  
AC AAH68724;  
DT 14-SEP-2001 (first entry)  
XX  
DE Human anti-Rh(D) antibody clone SH54 nucleotide sequence.  
XX  
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.  
XX  
OS Homo sapiens.  
XX  
PN US6255455-B1.  
PD 03-JUL-2001.  
PF 29-JAN-1999; 99US-00240274.  
XX  
PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.  
PR 10-APR-1998; 98US-0081380P.  
XX  
XX (VYPE-) UNIV PENNSYLVANIA.  
XX  
XX Siegel DL;  
XX  
XX WPI, 2001-388931/41.  
DR P-PSDB; AAG93667.  
XX  
XX  
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine.  
XX  
XX  
PS Example 3; Col 80; 162pp; English.  
XX  
CC The present invention describes an isolated Rh(D) binding protein,  
CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AAG93558 to AAG93659. (I) has  
CC immunostimulant activity, and can be used as an immune system stimulant.  
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAG93558 to AAG93659 represent the nucleotide sequence which encode  
CC chain CDR3 amino acid sequences which are given in the exemplification of  
CC the present invention  
XX  
SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;  
Query Match 87.9%; Score 279.6; DB 5; Length 321;  
Best Local Similarity 92.5%; Pred. No. 1.7e-78;  
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 1 GAGCTCACTAGTCCATCTCTCCCTGTCTGTCATCTGTGGAGACAGATCACCATCACT 60  
DB 4 GAGCTCACCAGTCTCCATCTCTCCCTGTCTGTCATCTGTGGAGACAGATCACCATCACT 63  
QY 61 TGCCGGGCAAGTCAAGATTAACACCTATTAAATGGTATCGACATAAACCAGGGGAAA 120  
DB 64 TGCCGGGCAAGTCAAGATTAACACCTATTAAATGGTATCGACATAAACCAGGGGAAA 123  
QY 121 GCCCCTAAGCTCTGATCTATGTCATCCAGTTTGGAAAGTGGGTCCTCAAGGTTTC 180  
DB 124 GCCCCTAAGCTCTGATCTATGTCATCCAGTTTGGAAAGTGGGTCCTCAAGGTTTC 183  
QY 181 AGTGGCAGTGGATATGGACAGACTTCACTCTCAACCATCAGCAGTCTGACCTGAAGAT 240  
DB 184 AGTGGCAGTGGATATGGACAGACTTCACTCTCAACCATCAGCAGTCTGACCTGAAGAT 243  
QY 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTGAGTCCCTGTACATTTTGGCAGGGGACC 300  
DB 244 TTTCGAAGTTACTACTGTCAAGAGAGTCTGAGTCCCTGTACATTTTGGCAGGGGACC 303  
QY 301 AAGGTGAGATCAACGA 318  
DB 304 AAGGTGAGATCAACGA 321  
RESULT 14  
AAH68652  
ID AAH68652 standard; DNA; 321 BP.  
XX  
AC AAH68652;  
DT 14-SEP-2001 (first entry)  
XX  
DE Human anti-Rh(D) chain I07 nucleotide sequence.  
XX  
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.  
XX  
OS Homo sapiens.



XX US6255455-B1.  
XX 03-JUL-2001.  
XX 29-JAN-1999; 99US-00240274.  
XX 11-OCT-1996; 96US-0028550P.  
XX 27-JUN-1997; 97US-00884045.  
XX 10-APR-1998; 98US-0081380P.  
XX (TYPE-) UNIV PENNSYLVANIA.  
XX Siegel DL;  
XX WPI; 2001-388931/41.  
XX P-PSDB; AAG93595.  
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
XX PT diagnostics requiring a human instead of an animal antibody and in  
XX PT therapeutic medicine.  
XX Example 2; Col 55; 162pp; English.  
XX The present invention describes an isolated Rh(D) binding protein,  
XX CC preferably a human antibody, (I) having an amino acid sequence comprising  
XX CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
XX CC immunostimulant activity, and can be used as an immune system stimulant.  
XX CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
XX CC are used in diagnostics that require human antibodies instead of animal  
XX CC antibodies, such as determine the Rh phenotype of human red blood cells.  
XX CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
XX CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
XX CC chain CDR3 amino acid sequences which are given in the exemplification of  
XX CC the present invention  
XX Sequence 321 BP; 85 A; 87 C; 76 G; 73 T; 0 U; 0 Other;  
SQ  
Query Match 87.9%; Score 279.6; DB 5; Length 321;  
Best Local Similarity 92.5%; Pred. No. 1.7e-78;  
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 1 GAGCTCACTAGTCCATCCCTCCTGTCGATCTGTGGGAGACAGATCACCATCAGT 60  
DB 4 GAGCTCACTAGTCCATCCCTCCTGTCGATCTGTGGGAGACAGATCACCATCAGT 63  
QY 61 TGCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGTATCAGCATPAAACAGGGAAA 120  
DB 64 TGCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGTATCAGCATPAAACAGGGAAA 123  
QY 121 GCCCTTAAGTCTTGATCTATGCTGCATCCAGTTTGCAGAGTGGGTCCTCATCAAGTTTC 180  
DB 124 GCCCTTAAGTCTTGATCTATGCTGCATCCAGTTTGCAGAGTGGGTCCTCATCAAGTTTC 183  
QY 181 AGTGCAGTGAATATGGGAGAGATTCATCTCAACATCAGAGATCTGAGGCTGAAGAT 240  
DB 184 AGTGCAGTGAATATGGGAGAGATTCATCTCAACATCAGAGATCTGAGGCTGAAGAT 243  
QY 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTGATCACTTTGGCCAGGGGACC 300  
DB 244 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTGATCACTTTGGCCAGGGGACC 303  
QY 301 AAGGTGAGATCAAAACGA 318  
DB 304 AAGGTGAGATCAAAACGA 321

RESULT 15

ACD45388  
ID ACD45388 standard; DNA; 321 BP.  
XX  
AC ACD45388;  
XX

DT 12-SEP-2003 (first entry)  
XX Anti-Rh(D) light chain SH54 DNA.  
XX Human; de; Gene; RH(D) binding protein; blood typing; blood product;  
XX KW magnetically activated cell sorting.  
XX OS Homo sapiens.  
XX US2003040605-A1.  
XX 27-FEB-2003.  
XX 04-MAY-2001; 2001US-00848798.  
XX 11-OCT-1996; 96US-0028550P.  
XX 27-JUN-1997; 97US-00884045.  
XX 10-APR-1998; 98US-0081380P.  
XX 29-JAN-1999; 99US-00240274.  
XX (TYPE-) UNIV PENNSYLVANIA.  
XX Siegel DL;  
XX WPI; 2003-512273/48.  
XX P-PSDB; ABO27474.  
XX New human Rh(D)-binding protein useful for various diagnostic and  
XX PT therapeutic applications, including typing of blood or blood products.  
XX Claim 12; Page 61; 187pp; English.  
XX The invention relates to an isolated Rh(D) binding protein. The protein  
XX CC can be used for magnetically activated cell sorting. The protein is  
XX CC useful in various diagnostic and therapeutic applications in humans,  
XX CC including typing of blood or blood products. The present sequence  
XX CC represents DNA encoding a human anti-Rh(D) chain  
XX Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;  
SQ  
Query Match 87.9%; Score 279.6; DB 9; Length 321;  
Best Local Similarity 92.5%; Pred. No. 1.7e-78;  
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 1 GAGCTCACTAGTCCATCCCTCCTGTCGATCTGTGGGAGACAGATCACCATCAGT 60  
DB 4 GAGCTCACTAGTCCATCCCTCCTGTCGATCTGTGGGAGACAGATCACCATCAGT 63  
QY 61 TGCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGTATCAGCATPAAACAGGGAAA 120  
DB 64 TGCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGTATCAGCATPAAACAGGGAAA 123  
QY 121 GCCCTTAAGTCTTGATCTATGCTGCATCCAGTTTGCAGAGTGGGTCCTCATCAAGTTTC 180  
DB 124 GCCCTTAAGTCTTGATCTATGCTGCATCCAGTTTGCAGAGTGGGTCCTCATCAAGTTTC 183  
QY 181 AGTGCAGTGAATATGGGAGAGATTCATCTCAACATCAGAGATCTGAGGCTGAAGAT 240  
DB 184 AGTGCAGTGAATATGGGAGAGATTCATCTCAACATCAGAGATCTGAGGCTGAAGAT 243  
QY 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTGATCACTTTGGCCAGGGGACC 300  
DB 244 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTGATCACTTTGGCCAGGGGACC 303  
QY 301 AAGGTGAGATCAAAACGA 318  
DB 304 AAGGTGAGATCAAAACGA 321

Search completed: July 27, 2005, 05:59:48  
Job time : 302.048 secs

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Db 61 TGGCGGCAAGTCAGAGATTAAACCTATTAAATTGATATCAGCATAAACGAGGAAA 120  
Qy 121 GCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTTC 180  
Db 121 GCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTTC 180  
Qy 181 AGTGGCAGTGGATATGGAGACGACTTCACTCCATCCATCAGACTTTCGACCTGGAAGAT 240  
Db 181 AGTGGCAGTGGATATGGAGACGACTTCACTCCATCCATCAGACTTTCGACCTGGAAGAT 240  
Qy 241 TTTCGAAGTTACTACTGTCAGAGAGTCTCAGTGCCTGTCACACTTTTGGCCAGGGGACC 300  
Db 241 TTTCGAAGTTACTACTGTCAGAGAGTCTCAGTGCCTGTCACACTTTTGGCCAGGGGACC 300  
Qy 301 AAGGTGAGATCAAAACA 318  
Db 301 AAGGTGAGATCAAAACA 318

## RESULT 2

US-09-848-798-199  
; Sequence 199, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 199  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13  
US-09-848-798-199

Query Match 90.4%; Score 287.6; DB 10; Length 321;  
Best Local Similarity 94.0%; Pred. No. 2.6e-85;  
Matches 299; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 GAGGTCACTAGTCTCCATCTCCCTGCTGCTGATCTGTGGAGACAGAGTCAACATCAGT 60  
Db 4 GAGGTCACTAGTCTCCATCTCCCTGCTGCTGATCTGTGGAGACAGAGTCAACATCAGT 63  
Qy 61 TGGCGGCAAGTCAGAGATTAAACCTATTAAATTGATATCAGCATAAACGAGGAAA 120  
Db 64 TGGCGGCAAGTCAGAGATTAAACCTATTAAATTGATATCAGCATAAACGAGGAAA 123  
Qy 121 GCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTTC 180  
Db 124 GCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTTC 183  
Qy 181 AGTGGCAGTGGATATGGAGACGACTTCACTCCATCCATCAGACTTTCGACCTGGAAGAT 240  
Db 184 AGTGGCAGTGGATATGGAGACGACTTCACTCCATCCATCAGACTTTCGACCTGGAAGAT 243  
Qy 241 TTTCGAAGTTACTACTGTCAGAGAGTCTCAGTGCCTGTCACACTTTTGGCCAGGGGACC 300  
Db 244 TTTCGAAGTTACTACTGTCAGAGAGTCTCAGTGCCTGTCACACTTTTGGCCAGGGGACC 303  
Qy 301 AAGGTGAGATCAAAACA 318  
Db 304 AAGGTGAGATCAAAACA 321

## RESULT 3

US-09-848-798-102  
; Sequence 102, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 102  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain 102  
US-09-848-798-102

Query Match 88.4%; Score 281.2; DB 10; Length 321;  
Best Local Similarity 92.8%; Pred. No. 3.6e-83;  
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 GAGGTCACTAGTCTCCATCTCCCTGCTGCTGATCTGTGGAGACAGAGTCAACATCAGT 60  
Db 4 GAGGTCACTAGTCTCCATCTCCCTGCTGCTGATCTGTGGAGACAGAGTCAACATCAGT 63  
Qy 61 TGGCGGCAAGTCAGAGATTAAACCTATTAAATTGATATCAGCATAAACGAGGAAA 120  
Db 64 TGGCGGCAAGTCAGAGATTAAACCTATTAAATTGATATCAGCATAAACGAGGAAA 123  
Qy 121 GCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTTC 180  
Db 124 GCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTTC 183  
Qy 181 AGTGGCAGTGGATATGGAGACGACTTCACTCCATCCATCAGACTTTCGACCTGGAAGAT 240  
Db 184 AGTGGCAGTGGATATGGAGACGACTTCACTCCATCCATCAGACTTTCGACCTGGAAGAT 243  
Qy 241 TTTCGAAGTTACTACTGTCAGAGAGTCTCAGTGCCTGTCACACTTTTGGCCAGGGGACC 300  
Db 244 TTTCGAAGTTACTACTGTCAGAGAGTCTCAGTGCCTGTCACACTTTTGGCCAGGGGACC 303  
Qy 301 AAGGTGAGATCAAAACA 318  
Db 304 AAGGTGAGATCAAAACA 321

## RESULT 4

US-09-848-798-109  
; Sequence 109, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 109  
; LENGTH: 321

```

; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; OTHER INFORMATION: anti-Rh(D) chain I09
US-03-848-798-109

```

Query Match	88.4%	Score 281.2;	DB 10;	Length 321;
Best Local Similarity	92.8%	Pred. No. 3.6e-83;		
Matches 295; Conservative	0;	Mismatches 23;	Indels 0;	Gaps 0;

Qy	1	GAGCTCACTAGTCTCCATCCTCCCTGATCTGGATCTGTGGGAGACAGAGTCACTCAGT	60	
Db	4	GAGCTCACCCAGTCTCCATCTCCCTGCTGGATCTGTGGAGACAGAGTCACTCAGT	63	
Qy		61	TGCCGGGCAAGTCAGAGATTAAACCACTATTAAAATGGTATACGATTAACCAAGGAAA	120
Db		64	TGCCGGGCAAGTCAGAGATTAAAGCACTATTTAAATGGATATCAGAGAAACCAAGGAAA	123
Qy		121	GCCCCTAAGCTCTGATCTATGCTGCATCAAGTTTCCAAAGTGGGGTCCCATCAAGGTTT	180
Db		124	GCCCCTAAGCTCTGATCTATGCTGCATCAAGTTTCCAAAGTGGGGTCCCATCAAGGTTT	183
Qy		181	AGTGCAGTGGATTATGGGACAGACTTCACTTCACCAATCAGCAGTCTGCACCTGAAGAT	240
Db		184	AGTGCAGTGGATTATGGGACAGATTCCACTTCACCATCAGCAGTCTGCACCTGAAGAT	243
Qy		241	TTTGCAGTACTACTGTCTCAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACC	300
Db		244	TTTGCAGTACTATTAATCTGTCAACAGCTTAATAGTTAACCCGTAACACTTTTGGCCAGGGGACC	303
Qy		301	AAAGTGGAGATCAAAAGA 318	
Db		304	AAAGTGGAGATCAAAAGA 321	

```

; RESULT 5
; US-09-848-798-218
; Sequence 218, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:

```

	Query Match	Similarity	Score	DB 10	Length	32
Best Local	Similarity	92.8%	Pred.	No. 3.6e-83		
Matches	295	Conservative	0	Mismatches	23	Indels
						Gaps
						0

  

QY	1	GAGCTCAGTCAGTCCATCCCTCGTGTGCATCTGTGGAGACAGAGTCAACATCACT	60
DB	4	GAGCTCAGCCAGTCTCCATCTCTCCTGTGCATCTGTGGAGACAGAGTCAACCTCACT	63
QY	61	TGCGGGGCAAGTCAGAGAAATTAAACCTATTTAAATTTGGTATCAGCATTAACCAAGGAAA	120
DB	64	TGCGGGGCAAGTCAGAGCATTTAGACAGCTATTTAAATTTGTATTCAGAGAAAACCAAGGAAA	123
QY	121	GCCCTAAGTCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTTC	180

Db 124 GCCCTTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 183

Qy 181 AGTGGCAGTGTGATATGGGACAGACTTTCATCTTCACCATCAGCAGTCTGCAGCCTGAAGT 240

Db 184 AGTGGCAGTGTGATCTGGGACAGATTTCATCTTCACCATCAGCAGTCTGCACCTGAAGAT 243

Qy 241 TTTCGAAGTATCTACTGTCAAGAGAGTCTCACTGCTCGTACATCTTTGGCCAGGGGACC 300

Db 244 TTTCGAATCTTACTGTCTCAACAGAGTTAACAGTACCCTGGACGTTGGCCAAAGGACC 303

Qy 301 AAGGTGAGATCAAAAGA 318

Db 304 AAGGTGAAATCAAAAGA 321

```

, RESULT 6
, US-09-848-798-107
, Sequence 107, Application US/09848798
, Publication No. US20030040605A1
, GENERAL INFORMATION:
, APPLICANT: Siegel, Donald L.
, TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
, TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
, FILE REFERENCE: 09596-42U2
, CURRENT APPLICATION NUMBER: US/09/848, 798
, CURRENT FILING DATE: 2001-05-04
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
, PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
, PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
, NUMBER OF SEQ ID NOS: 224
, SOFTWARE: PatentIn Ver. 2.0
, SEQ ID NO 107
, LENGTH: 321
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, OTHER INFORMATION: anti-Rh(D) chain 107
, US-09-848-798-107

```

Query Match	87.9%	Score 279.6	DB 10	Length 321
Best Local Similarity	92.5%	Pred. No. 1.28-82		
Matches	294	Conservative	0	Mismatches 24
			Indels	0
			Gaps	0

  

QY	1	GAGCTCACTCAGTCTCCATCCTCCTCTGTCTGCATCTGTGGGAGACAGAGTCAACATCACT	60
DB	4	GAGCTCACCCAGTGTCCATCTCTCCCTGTGTCATCTGTAGGAGACAGAGTCAACATCACT	63
QY	61	TGCCGGGCAATCAGAGATTAACAACCTATTAAATTGGTATCAGCATAAACAGGGAAA	120
DB	64	TGCCGGGCAATCAGAGATTAAGCAGCATTTAAATTGGTATCAGCAGAAACAGGGAAA	123
QY	121	GCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCATCAAGTTTC	180
DB	124	GCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCATCAAGGTTTC	183
QY	181	AGTGGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGACGTGTGACGCTGAAGAT	240
DB	184	AGTGGCAGTGGATCTGGGACAGATTTCACTCTCAACATCAGACGTGTGCAACCTGAAGAT	243
QY	241	TTTGGCAATTACTATCTGTCAAGAAGAGTCTCAGTGTCTGTACACTTTTGGCAGGGGACC	300
DB	244	TTTGGCAATTACTATCTGTCAAGAAGAGTACCTCTGCAACTTTTGGGCGAGGGGACC	303
QY	301	AAGGTGAGATCAAAACGA 318	
DB	304	AAGGTGAGATCAAAACGA 321	

  

RESULT 7
US-09-848-798-113
; Sequence 113, Application US/09848798

Publicatio No. US20030040605A1  
 GENERAL INFORMATION:  
 APPLICANT: Siegel, Donald L.  
 TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
 TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
 FILE REFERENCE: 09596-4202  
 CURRENT APPLICATION NUMBER: US/09/848,798  
 PRIOR APPLICATION DATE: 2001-05-04  
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
 PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
 NUMBER OF SEQ ID NOS: 224  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 113  
 LENGTH: 321  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: anti-Rh(D) chain I13  
 US-09-848-798-113

Query Match	87.9%;	Score 279.6;	DB 10;	Length 321;
Best Local Similarity	92.5%;	Pred. No. 1.2e-82;		
Matches 294;	Conservative 0;	Mismatches 24;	Indels 0;	Gaps 0;

OY	1	GAGGCTCACTCAAGTCTCCACATCCCTCCGTCGTGATCTGTGGGAGACAGAGGACCAATCAAGT	60
Db	4	GAGCTCAACCCAGACTCTCCATCTCTCCCTGTGCTCTGTGTAGAGACAGAGTACCAATCACT	63
OY	61	TGCCGGGCAAGTCAAGAAATTAAACACTTATTTTAAATTGGTATCAGCATAAACCAGGGAAA	120
Db	64	TGCCGGGCAAGTCAGAGCAATTAGCAGATTTTAAATTGGATCAGCAGAAACCAGGGAAA	123
OY	121	GCCCCTAAGCTCTGTATCATGTGTCATCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTC	180
Db	124	GCCCCTAAGCTCTGATCTATGCTGTGATCCAGTTTGCAAAGTGGGATCCCATCAAGGTTTC	183
OY	181	AGTGCAGATGATATATGGGACAGACTTCACCTTCACCATCAGCAGTCTGCAGCCTGAAGAT	240
Db	184	AGTGCAGATGATATCTGGGACAGATTTCACTCTCCACCATCAGCAGTCTGCACCACTGAAGAT	243
OY	241	TTTGCAGATTACTACTGTCAAGAGATCTCAGTGCTCCGACACTTTTGGCCAGGGGACC	300
Db	244	TTTGGAACTTACTACTGTCAACAGATTACGGTACCCCTCACAGTTTGGCCGGGGACC	303
OY	301	AAGGTGAGATCAAAACA	318
Db	304	AAGCTGAGATCAAAACA	321

```

1 RESULT 8
2 US-09-848-798-221
3 ; Sequence 221, Application US/09848798
4 ; Publication No. US2003004605A1
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Siegel, Donald L.
7 ; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
8 ; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
9 ; FILE REFERENCE: 09596-4202
10 ; CURRENT APPLICATION NUMBER: US/09/848, 798
11 ; PRIOR FILING DATE: 2001-05-04
12 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
13 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
14 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
15 ; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
16 ; NUMBER OF SEQ ID NOS: 224
17 ; SOFTWARE: PatentIn Ver. 2.0
18 ; SEQ ID NO 221
19 ; LENGTH: 321
20 ; TYPE: DNA
21 ; ORGANISM: Homo sapiens
22 ; FEATURE:

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OTHER INFORMATION: anti-Rh(D) antibody clone SH52  
US-09-848-798-221

Query Match	87.9%	Score 279.6;	DB 10;	Length 321;
Best Local Similarity	92.5%	Pred. No. 1.2e-82;		
Matches 294; Conservative	0;	Mismatches 24;	Indels 0;	Gaps 0;

OY	1	GAGCTCACTCACTGCTCCATCTCTCTCTGATCTGTGGGAGACAGAGTCACATCACT	60
Db	4	GAGCTCACCCAGTCTCCATCTCTCCATGCTCGATCTGTAGGAGACAGATCTCACATCACT	63
OY	61	TGCCGGGCAAGTCAGAGAAATTAACCACTATTAAATTTGGATCAGCATTAACGAGGAAA	120
Db	64	TGCCGGGCAAGTCAGAGCAATTTGGCACTTAATTTAAATTTGGATCAGCAAAACGAGGAAA	123
OY	121	GCCCCTAAGTCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTTC	180
Db	124	GCCCCTAAGTCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTTC	183
OY	181	AGTGCAGATGATATATGGGACAGACTTCACTTCACATCATGACAGTCTGCAGCTTGAAGAT	240
Db	184	AGTGCAGATGATATGAGGACAGATTTCACTCTCACATCAGCAGTCTGCACCTGAAAGAT	243
OY	241	TTTGGCAATTACTACTGTCAAGAGAGTCTCAAGTCTCTGTAACACTTTTGGCCAGGGGACC	300
Db	244	TTTGGCAATTACTACTGTCAACAGAGTTACAAGTACCCTCGTGACGTTTGGCCAAAGGAGAC	303
OY	301	AAAGTGCAGATCAAAACGA	318
Db	304	AAAGTGCAGATCAAAACGA	321

RESULT 9  
US-09-848-798-222

; Sequence 222, Application US/09848798  
; Publication No. US20030040605A1

;  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.

1. TITLE OF INVENTION: Rn(D) -BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

```

; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,796

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; CURRENT FILING DATE: 2001-05-04  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLIC

; PRIOR FILING DATE: 1999-01-29  
 ; PRIOR APPLICATION NUMBER: 60/028,550  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:

PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 324

SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 333; SEQ ID NO 222  
; LENGTH: 321  
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; TYPE: DNA
; ORGANISM: Homo sapiens

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;; FEATURE: anti-Rh(D) antibody clone SH54
;; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
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US-09-848-798-222

Query Match	87.9%; Score 279.6; DB 10; length 321;
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Best Local Similarity 92.5%; Pred. No. 1.2e-82;  
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTCACTCTCCATCCTCCCTGTTCGATCTGTGTGGAGACAGAGTCAACATCACT 60

Db 4 GAGCTCACCACAGTCTCCATCCTCCATGTCGTGCATCTGTGTGGAGACAGAGTCAACATCACT 63

QY 61 TGCCTGGGCAAGTCAGAGAAATTAAACCACTTTAAATTGGTATCAGATAAAACAGGGAAA 120

Db 64 TGCCTGGGCAAGTCAGAGCAATTGGCACTTAATTTAAATGGTATCAGAGAAACAGGGAAA 123

QY 121 GCCCTTAAGCTCCGATCTATAGCTGTCATCCACTTTGCAGAAAGGGGGTCCCATCAAGGTTT 180

Db 124 GCCCTTAAGCTCTATATGATGTCGTCATCCAGTTTGCAGAAAGGGGGTCCCATCAAGGTTT 183



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Db      68 GCGGGGCAAGTCAGAGCATTTAGCAGCTATTAAATTGGTATCAGCAGAAACCAAGGAAAG 127
Qy      122 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTCA 181
Db      128 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTCA 187
Qy      182 GTGGCAGTGTATATGGGACAGACTTTCACCTCCACCATAGACAGTCTGAGGCTGAAGATT 241
Db      188 GTGGCAGTGTATATGGGACAGACTTTCACCTCCACCATAGAGTCTGCAACCTGAAGATT 247
Qy      242 TTGCAAGTTACTACTGTCTCAAGAGAGTCTCAGTGCCTGTAACATTTTGGCCAGGGGACCA 301
Db      248 TTGCAACTTACTACTGTCTCAAGAGTTACAGTACCCGCTCACTTTGGCCGAGGACCA 307
Qy      302 AGGTGAGATCAAAACG 317
Db      308 AGGTGAGATCAAAACG 323
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RESULT 13
US-10-203-754A-64
; Sequence 64, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSURA, Matsuharu
; APPLICANT: SHIBUI, Taisuro
; APPLICANT: YOTSUKOTO, Yoshinisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent version 3.1
; SEQ ID NO 64
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-754A-64
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Query Match      87.3%; Score 277.6; DB 16; Length 900;
Best Local Similarity 92.4%; Pred. No. 8.2e-82;
Matches 292; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
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Qy      2 AGCTCACTCAGTCTTCATCTCCTGCTGTGCACTGTGGGAGACAGAGTCAACATCAGTT 61
Db      503 AGATGACCCAGTCTTCATCTCCTGCTGTGCACTGTGGGAGACAGAGTCAACATCAGTT 562
Qy      62 GCGGGGCAAGTCAGAGCATTTAAACCTTAAATGATACAGATTAACCAAGGAAAG 121
Db      563 GCGGGGCAAGTCAGAGCATTTAAACCTTAAATGATACAGAGAAACCAAGGAAAG 622
Qy      122 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTCA 181
Db      623 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTCA 682
Qy      182 GTGGCAGTGTATATGGGACAGACTTTCACCTCCACCATAGAGTCTGAGGCTGAAGATT 241
Db      683 GTGGCAGTGTATATGGGACAGACTTTCACCTCCACCATAGAGTCTGCAACCTGAAGATT 742
Qy      242 TTGCAAGTTACTACTGTCTCAAGAGTCTCAGTGCCTGTAACATTTTGGCCAGGGGACCA 301
Db      743 TTGCAACTTACTACTGTCTCAAGAGTTACAGTACCCGCTCACTTTGGCCGAGGACCA 802
Qy      302 AGGTGAGATCAAAACG 317
Db      803 AGGTGAGATCAAAACG 818
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RESULT 14
US-10-783-311-15
; Sequence 15, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light Chain nucleic acid sequence
US-10-783-311-15
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Query Match      87.1%; Score 277; DB 21; Length 405;
Best Local Similarity 92.1%; Pred. No. 9.8e-82;
Matches 292; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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Qy      2 AGCTCACTCAGTCTTCATCTCCTGCTGTGCACTGTGGGAGACAGAGTCAACATCAGTT 61
Db      68 AGATGACCCAGTCTTCATCTCCTGCTGTGCACTGTGGGAGACAGAGTCAACATCAGTT 127
Qy      62 GCGGGGCAAGTCAGAGCATTTAAACCTTAAATGATACAGATTAACCAAGGAAAG 121
Db      128 GCGGGGCAAGTCAGAGCATTTAAACCTTAAATGATACAGAGAAACCAAGGAAAG 187
Qy      122 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTCA 181
Db      188 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTCA 247
Qy      182 GTGGCAGTGTATATGGGACAGACTTTCACCTCCACCATAGAGTCTGAGGCTGAAGATT 241
Db      248 GTGGCAGTGTATATGGGACAGACTTTCACCTCCACCATAGAGTCTGCAACCTGAAGATT 307
Qy      242 TTGCAAGTTACTACTGTCTCAAGAGTCTCAGTGCCTGTAACATTTTGGCCAGGGGACCA 301
Db      308 TTGCAACTTACTACTGTCTCAAGAGTTACAGTACCCGCTCACTTTGGCCGAGGACCA 367
Qy      302 AGGTGAGATCAAAACG 318
Db      368 AGGTGAGATCAAAACG 384
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RESULT 15
US-10-783-311-16
; Sequence 16, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORM  
S-10-783-311-16

Query Match	87.1%;	Score 277;	DB 21;	Length 405;
Best Local Similarity	92.1%;	Pred. No. 9.8e-82;		
Matches 292;	Conservative	0;	Mismatches 25;	Indels

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Db	68	AGATACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGAGACAGATCACCATCATT	127
Qy	62	GCCGGGCAAGTCAGAGAAATTAACCCATATTTAATTGATACGATTAACAGGAAAG	121
Db	128	GCCGGGCAAGTCAGAGCAATTAAGAGCATTTTAATTGTATACGAGAAACAGGGAAAG	187
Qy	122	CCCCTAAGTCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTCA	181
Db	188	CCCCTAAGTCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTCA	247
Qy	182	GTTGCAGATGAGATATGGGACAGACTTACTCTCACCATCAGCAGTCTGCAGCTTGAAAGTT	241
Db	248	GTTGCAGATGAGATCTGGGACAGATTCTACTCTCACCATCAGCAGTCTGCACCTGGAAGATT	307
Qy	242	TTGCAAGTTACTACTGTCAAGAGAGTCTAGTCCCTCGTACACTTTTGGCCAGGAGCA	301
Db	308	TTGCAACTTACTACTGTCTCAACAGAGATTACAGTACCAAGTGGAGCGTTTCGGCCAAAGGACCA	367
Qy	302	AGGTGAGATCAAAACGA	318
Db	368	AGGTGAAATCAAAACGA	384

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Job time : 477.839 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:09:06 ; Search time 1956.83 Seconds

(without alignments)  
8468.649 Million cell updates/sec

Title: US-10-027-725a-3

Perfect score: 342  
Sequence: 1 ctcgagctcgtccacgagact.....ccctgctcacgcctcctca 342

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

GenBmb1:\*  
1: gb ba:\*  
2: gb beg:\*  
3: gb in:\*  
4: gb om:\*  
5: gb ov:\*  
6: gb pat:\*  
7: gb ph:\*  
8: gb pl:\*  
9: gb pr:\*  
10: gb ro:\*  
11: gb sts:\*  
12: gb sy:\*  
13: gb un:\*  
14: gb vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	338.8	99.1	342	9	HS458384 Homo sapi
2	332.8	94.4	342	9	HS458383 Homo sapi
3	308.4	90.2	342	9	HS458382 Homo sapi
4	300.6	87.9	355	9	AY640487 Homo sapi
5	299	87.4	355	9	AY640580 Homo sapi
6	297.4	87.0	355	9	AY640579 Homo sapi
7	292.6	85.6	355	9	AY640509 Homo sapi
8	291	85.1	355	9	AY640564 Homo sapi
9	284.6	83.2	414	9	AF062112 Homo sapi
10	284.4	83.2	351	9	HS4244930 Homo sapi
11	283.6	82.9	360	6	AX061463 Sequence
12	283.4	82.9	411	9	HS722X1
13	283	82.7	354	9	HS4245064 Homo sapi
14	283	82.7	360	9	HS4245064 Homo sapi
15	283	82.7	360	9	HS4245064 Homo sapi
16	282.8	82.7	358	9	AF021954 Homo sapi
17	281.8	82.4	403	12	AF452917 Synthetic
18	281.4	82.3	351	9	HS4245020 Homo sapi
19	280.2	81.9	341	9	AY607380 Homo sapi

20	280.2	81.9	414	9	HS458384 Homo sapi	275365 H. sapiens m
21	280.2	81.9	414	9	HS458384 Homo sapi	275378 H. sapiens m
22	280	81.8	363	9	HS458383 Homo sapi	U80131 Human immun
23	279.8	81.8	355	9	AY640507 Homo sapi	AY640507 Homo sapi
24	279.8	81.8	432	9	HS4491911 Homo sapi	AJ491911 Homo sapi
25	278.4	81.4	357	9	HS4244949 Homo sapi	AJ244849 Homo sapi
26	278.2	81.3	432	9	HS4491912 Homo sapi	AJ244849 Homo sapi
27	277.2	81.1	354	9	HS4244955 Homo sapi	AJ244849 Homo sapi
28	276.6	80.9	354	9	HS4579125 Homo sapi	AJ279523 Homo sapi
29	276.4	80.8	357	9	HS4279523 Homo sapi	U80166 Human immun
30	276.2	80.8	362	9	HS4279523 Homo sapi	AF452912 Synthetic
31	275.8	80.6	412	12	AF452912 Synthetic	275383 H. sapiens m
32	275.6	80.6	417	9	HS452909 Synthetic	AF452909 Synthetic
33	275.4	80.5	400	12	AF453047 Synthetic	AF453047 Synthetic
34	275	80.4	406	12	AF453047 Synthetic	AJ279541 Homo sapi
35	274.8	80.4	357	9	HS4279541 Homo sapi	U80166 Human immun
36	274.8	80.4	357	9	HS4279541 Homo sapi	U80166 Human immun
37	274.2	80.2	351	9	AY607364 Homo sapi	AY607364 Homo sapi
38	273.8	80.1	369	6	AX061433 Sequence	U80128 Human immun
39	273.6	80.0	363	9	HS4244953 Homo sapi	AF452947 Synthetic
40	273.6	80.0	409	12	AF452947 Synthetic	AJ233698 Homo sapi
41	272	79.5	366	9	HS4233698 Homo sapi	AF452947 Synthetic
42	271.8	79.5	339	9	AY607360 Homo sapi	AY607360 Homo sapi
43	271.8	79.5	351	9	HS4244953 Homo sapi	AJ244849 Homo sapi
44	271.8	79.5	351	9	HS4244958 Homo sapi	AJ244849 Homo sapi
45	271.8	79.5	360	9	HS4579300 Homo sapi	AY579300 Homo sapi

## ALIGNMENTS

RESULT 1	HS458384	342 bp	mRNA	linear	PRI 30-APR-2002
LOCUS	HS458384				
DEFINITION	Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 100.				
ACCESSION	AJ458384.1	GI:20387067			
VERSION	AJ458384.1	GI:20387067			
KEYWORDS	IGHV gene; immunoglobulin heavy chain; variable region.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1				
AUTHORS	Flicker S., Steinberger P., Norderhaug L., Sperr W.R., Majlesi Y.,				
TITLE	Valent P., Kratz D. and Valentia R. Conversion of grass allergen-specific human IGE into a protective				
JOURNAL	unpublished				
AUTHORS	2 (bases 1 to 342)				
TITLE	Flicker S.				
JOURNAL	Direct Submission				
TITLE	Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,				
JOURNAL	General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090				
	Vienna, AUSTRIA				
FEATURES	location/Qualifiers				
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CDS	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="100"				
	/rearranged				
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	<1..>342				
	/gene="IGHV"				
	/codon_start=1				
	/product="immunoglobulin heavy chain"				
	/protein_id="CAD30446.1"				
	/db_xref="GI:20387068"				
	/translation="LESGPGLVKPSQTLSTCTVSGGIRSGGYWMSIRPPGKLE				
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Best Local Similarity 99.4%; Pred. No. 3.9e-86;
Matches 340; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTCAGTCTGGCCAGGACTGTGTAAGCTTCACAGACCTGTCCCTCAGCTGACTGTC 60
Db      1 CTCAGTCTGGCCAGGACTGTGTAAGCTTCACAGACCTGTCCCTCAGCTGACTGTC 60
QY      61 TCTGTGGCTTCATCCGAGTGTGTATTACTGAGATTGGATCCGCAAGCTCCAGGG 120
Db      61 TCTGTGGCTTCATCCGAGTGTGTATTACTGAGATTGGATCCGCAAGCTCCAGGG 120
QY      121 AAGGGCTGGAGTGATCGGGTACATCTATCAGTGGCAACACTTCAACACCCGTCC 180
Db      121 AAGGGCTGGAGTGATCGGGTACATCTATCAGTGGCAACACTTCAACACCCGTCC 180
QY      181 CTCAGAGTGGAGTTACATGTCACTAGACACGCTCTAAGAACACTTCTCCCTGAGGCTG 240
Db      181 CTCAGAGTGGAGTTACATGTCACTAGACACGCTCTAAGAACACTTCTCCCTGAGGCTG 240
QY      241 AGCTCTGTACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGTGAGATGGGTACACT 300
Db      241 AGCTCTGTACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGTGAGATGGGTACACT 300
QY      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342

RESULT 2
HSA458383      342 bp mRNA linear PRI 30-APR-2002
LOCUS          Homo sapiens partial mRNA for immunoglobulin heavy chain variable
DEFINITION     region (IGHV gene), clone 60.
ACCESSION     AJ458383
VERSION       AJ458383.1 GI:20387065
KEYWORDS      IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1
AUTHORS      Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y.,
               Valent,P., Kraft,D. and Valenta,R.
TITLE        Conversion of grass allergen-specific human IGE into a protective
JOURNAL      IgG1 antibody
REFERENCE     2 (bases 1 to 342)
AUTHORS      Flicker,S.
TITLE        Unpublished
JOURNAL      Direct Submission
REFERENCE     Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
JOURNAL      General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090
JOURNAL      Vienna, AUSTRIA
FEATURES       Location/Qualifiers
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               /clone="60"
               /rearranged
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               /codon_start=1
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               /protein_id="CAD30445.1"
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CDS
gene
CDS

V_region      /translation="LSSGRLVPSQTLSTCTVSGGSIRSGYMSWHPQPEKLE
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Query Match      94.4%; Score 322.8; DB 9; Length 342;
Best Local Similarity 96.5%; Pred. No. 1.5e-81;
Matches 330; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      1 CTCAGTCTGGCCAGGACTGTGTAAGCTTCACAGACCTGTCCCTCAGCTGACTGTC 60
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QY      61 TCTGTGGCTTCATCCGAGTGTGTATTACTGAGATTGGATCCGCAAGCTCCAGGG 120
Db      61 TCTGTGGCTTCATCCGAGTGTGTATTACTGAGATTGGATCCGCAAGCTCCAGGG 120
QY      121 AAGGGCTGGAGTGATCGGGTACATCTATCAGTGGCAACACTTCAACACCCGTCC 180
Db      121 AAGGGCTGGAGTGATCGGGTACATCTATCAGTGGCAACACTTCAACACCCGTCC 180
QY      181 CTCAGAGTGGAGTTACATGTCACTAGACACGCTCTAAGAACACTTCTCCCTGAGGCTG 240
Db      181 CTCAGAGTGGAGTTACATGTCACTAGACACGCTCTAAGAACACTTCTCCCTGAGGCTG 240
QY      241 AGCTCTGTACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGTGAGATGGGTACACT 300
Db      241 AGCTCTGTACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGTGAGATGGGTACACT 300
QY      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342

RESULT 3
HSA458382      342 bp mRNA linear PRI 30-APR-2002
LOCUS          Homo sapiens partial mRNA for immunoglobulin heavy chain variable
DEFINITION     region (IGHV gene), clone 94.
ACCESSION     AJ458382
VERSION       AJ458382.1 GI:20387063
KEYWORDS      IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1
AUTHORS      Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y.,
               Valent,P., Kraft,D. and Valenta,R.
TITLE        Conversion of grass allergen-specific human IGE into a protective
JOURNAL      IgG1 antibody
REFERENCE     2 (bases 1 to 342)
AUTHORS      Flicker,S.
TITLE        Unpublished
JOURNAL      Direct Submission
REFERENCE     Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
JOURNAL      General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090
JOURNAL      Vienna, AUSTRIA
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CDS
gene
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 Best Local Similarity 93.9%; Pred. No. 2e-77;  
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QY 1 CTGAGCTGGCCAGAGACTGGTGAAGCTTACAGAGCCCTGTCCTCAGCTGACGTC 60  
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 Db 121 AAGGCTGAGTGAATCGGCTACATCTATACAGTGGCAACACCTACCAACCCGTC 180  
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 QY 241 AGCTCTGAGTGGCGGAGACAGCGCGTGTATTACTGTGAGAGTTCAGATGGGTACT 300  
 Db 241 AACTCTGTACTGCGGAGACAGCGCGTGTATTACTGTGAGAGTTCAGATGGGTACT 300  
 QY 301 TTGGACAACCTGGGCGCAGGGAACCTGTGTCACCGTCTCTCTCA 342  
 Db 301 TTGGACAACCTGGGCGCAGGGAACCTGTGTCACCGTCTCTCTCA 342

RESULT 4  
 AY640487 355 bp mRNA linear PRI 03-JUL-2004  
 LOCUS Homo sapiens clone AP immunoglobulin E variable region mRNA,  
 DEFINITION partial cds.  
 ACCESSION AY640487 GI:49354726  
 VERSION AY640487.1  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 355)  
 AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
 TITLE Biased use of VHS Ige+ B cells in the nasal mucosa of allergic  
 rhinitis patients  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 355)  
 AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
 Thomas Street, London SE1 1UL, UK  
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 Best Local Similarity 92.9%; Pred. No. 3.5e-75;  
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 Db 16 GAGTCTGGCCAGAGACTGGTGAAGCTTACAGAGCCCTGTCCTCAGCTGTCCT 75  
 QY 64 GGTGGCTTCATCCGAGTGTGTATTACTGAGTTGATCCGCGACGTCAGAGAG 123  
 Db 76 GGTGGCTTCATCCGAGTGTGTATTACTGAGTTGATCCGCGACGTCAGAGAG 135  
 QY 124 GGCTGAGTGAATCGGCTACATCTATACAGTGGCAACACCTACCAACCCGTCCTC 183  
 Db 136 GGCTGAGTGAATCGGCTACATCTATACAGTGGCAACACCTACCAACCCGTCCTC 195  
 QY 184 AAGAGTGAATTCATCTACATGACACGCTTAAGAACCACTTCTCCCTGAGCTGAGC 243  
 Db 196 AAGAGTGAATTCATCTACATGACACGCTTAAGAACCACTTCTCCCTGAGCTGAGC 255  
 QY 244 TCTGTACTGCGGAGACAGCGCGTGTATTACTGTGAGAGTTCAGATGGGTACTT 303  
 Db 256 TCTGTACTGCGGAGACAGCGCGTGTATTACTGTGAGAGTTCAGATGGGTACTT 315  
 QY 304 GACAACCTGGGCGCAGGGAACCTGTGTCACCGTCTCTCTCA 342  
 Db 316 GACTACTGGGCGCAGGGAACCTGTGTCACCGTCTCTCTCA 354

RESULT 5  
 AY640580 355 bp mRNA linear PRI 03-JUL-2004  
 LOCUS Homo sapiens clone RU immunoglobulin E variable region mRNA,  
 DEFINITION partial cds.  
 ACCESSION AY640580  
 VERSION AY640580.1 GI:49354901  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 355)  
 AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
 TITLE Biased use of VHS Ige+ B cells in the nasal mucosa of allergic  
 rhinitis patients  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 355)  
 AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
 Thomas Street, London SE1 1UL, UK  
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ORIGIN XFDYWGQGLTVTVSS"

Query Match 87.4%; Score 299; DB 9; Length 355;  
Best Local Similarity 92.6%; Pred. No. 1e-74;  
Matches 314; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 4 GAGTCTGCCCCAGAGACTGTGTAAGCCCTTCACAGACCCCTGTCCCTCAGCTGCTCTCT 63  
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Db 76 GGTGCTCCATCCGACAGTGTGTATTAATCTGAGTTGATCGGCGACGCGTCCAGGGAG 135  
QY 124 GGCTGAGTGAATCGGGTACATCTATCAAGTGGCAACCTTCAACAAACCGTCCCTC 183  
Db 136 GGCTGAGTGAATCGGGTACATCTATCAAGTGGCAACCTTCAACAAACCGTCCCTC 195  
QY 184 AAGAGTGAATTCACATGTCAGTGAACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243  
Db 196 AAGAGTGAATTCACATGTCAGTGAACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255  
QY 244 TCTGTGACTCCCGGACACGCGCGTGTATTAATCTGTCGAGGTGAGATGAGTACACTTTG 303  
Db 256 TCTGTGACTCCCGGACACGCGCGTGTATTAATCTGTCGAGGTGAGATGAGTACACTTTG 315  
QY 304 GACAACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342  
Db 316 GACTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 354

RESULT 6  
AY640579 355 bp mRNA linear PRI 03-JUL-2004  
LOCUS Homo sapiens clone RT immunoglobulin E variable region mRNA,  
DEFINITION partial cds.

ACCESSION AY640579  
VERSION AY640579.1 GI:49354899  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE 1 (bases 1 to 355)  
JOURNAL Blased use of VHS Igb+ B cells in the nasal mucosa of allergic  
TITLE rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
JOURNAL Thomas Street, London SE1 1UL, UK

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ORIGIN  
Query Match 87.0%; Score 297.4; DB 9; Length 355;

Best Local Similarity 92.3%; Pred. No. 2.9e-74;  
Matches 313; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 4 GAGTCTGCCCCAGAGACTGTGTAAGCCCTTCACAGACCCCTGTCCCTCAGCTGCTCTCT 63  
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QY 64 GGTGCTCCATCCGACAGTGTGTATTAATCTGAGTTGATCGGCGACGCGTCCAGGGAG 123  
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QY 124 GGCTGAGTGAATCGGGTACATCTATCAAGTGGCAACCTTCAACAAACCGTCCCTC 183  
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Db 196 AAGAGTGAATTCACATGTCAGTGAACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255  
QY 244 TCTGTGACTCCCGGACACGCGCGTGTATTAATCTGTCGAGGTGAGATGAGTACACTTTG 303  
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QY 304 GACAACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342  
Db 316 GACTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 354

RESULT 7  
AY640509 355 bp mRNA linear PRI 03-JUL-2004  
LOCUS Homo sapiens clone BM immunoglobulin E variable region mRNA,  
DEFINITION partial cds.

ACCESSION AY640509  
VERSION AY640509.1 GI:49354765  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE 1 (bases 1 to 355)  
JOURNAL Blased use of VHS Igb+ B cells in the nasal mucosa of allergic  
TITLE rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
JOURNAL Thomas Street, London SE1 1UL, UK

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Matches 310; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Db 16 GAGTCGGAGCCAGGACGTCGTGAAGCCCTTCTCAGACCCCTGCTCACCCTGACCTGACCTGCTCT 75  
Qy 64 GGTGGCTCCATCCGACAGTGGTGTATTACTGAGTTGGATGCGCCAGCGTCCAGGGAG 123  
Db 76 GGTGGCTCCATCAGACAGTGGTGTATTACTGAGTTGGATGCGCCAGGAG 135  
Qy 124 GGCCTGAGTGGATCGGGTACATCTATCAGATGAGCAACCTTCAACACCCGCTCC 183  
Db 136 GGCCTGAGTGGATGAGTGGATCATCTATTACATGAGGAGCAACCTTCAACACCCGCTCC 195  
Qy 184 AAGAGTGAAGTACCATGTCAGTGAACAAGCTTAAACAACCTTCTCTGAGGCTGAGC 243  
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Qy 304 GACACTGGGGCCAGGAAACCTGTGACCGTCTCTCA 342  
Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGTCTCTCA 354

RESULT 8  
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LOCUS Homo sapiens clone RE immunoglobulin E variable region mRNA,  
partial cds.  
ACCESSION AY640564  
VERSION AY640564.1 GI:49354872  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VH5 IGE+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK

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WTDYWGQGLTVSSS"

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Best Local Similarity 91.2%; Pred. No. 2e-72;  
Matches 309; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 4 GAGTCTGCCCCAGAGACGTCGTGAAGCCTTCAAGACCTTCACTGACCTGCTCTCT 63  
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Qy 64 GGTGGCTCCATCCGACAGTGGTGTATTACTGAGTTGGATGCGCCAGGGAG 123

Db 76 GGTGGCTCCATCAGACAGTGGTGTATTACTGAGTGGATGCGCCAGTACCCAGGAG 135  
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Db 136 GGCCTGAGTGGATGAGTGGATCATCTATTACATGAGGAGCAACCTTCAACACCCGCTCC 195  
Qy 184 AAGAGTGAAGTACCATGTCAGTGAACAAGCTTAAACAACCTTCTCTGAGGCTGAGC 243  
Db 196 AAGAGTGGGTTACCATGTCAGTGAACAAGCTTAAACAACCTTCTCTGAGGCTGAGC 255  
Qy 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGAGAGTCAAGTGGTACACTTTG 303  
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Qy 304 GACACTGGGGCCAGGAAACCTGTGACCGTCTCTCA 342  
Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGTCTCTCA 354

RESULT 9  
AF062112 414 bp mRNA linear PRI 08-MAY-2001  
LOCUS Homo sapiens clone 21u-26 immunoglobulin heavy chain variable  
region (IGH) mRNA, partial cds.  
ACCESSION AF062112  
VERSION AF062112.1 GI:3170686  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Wang,X. and Stollat,B.D.  
TITLE Immunoglobulin VH gene expression in human aging  
JOURNAL Clin. Immunol. 93 (2), 132-142 (1999)  
MEDLINE 99459182  
PUBMED 10527689  
REFERENCE 2 (bases 1 to 414)  
AUTHORS Wang,X. and Stollat,B.D.  
TITLE Direct Submission  
JOURNAL Submitted (22-APR-1998) Biochemistry Department, Tufts University  
School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA

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QY 64 GGTGGCTCCATCCGCACTGGTGTATTACTGAGATTGAGATCCGCGCCGACGAGAG 123
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QY 124 GGCTGTGAGTGTGATCGGGTACATCTATCACAGTGGCAACCTTCAACAAACCCGTCCCTC 183
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QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGGTCAAGATGGGTACACTTTG 303
Db 313 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGGTGAGTACCAAGCTGCTTT 372
QY 304 GACAACTGGGGCCAGGAAACCTGTGACCGCTCTCTCA 342
Db 373 GACTACTGGGGCCAGGAAACCTGTGACCGCTCTCTCA 411

RESULT 10
HSA244930 351 bp mRNA linear PRI 01-JUN-2000
LOCUS Homo sapiens mRNA for immunoglobulin mu heavy chain variable
DEFINITION region, partial, clone 1-A34.
ACCESSION AJ244930
VERSION AJ244930.1 GI:4995319
KEYWORDS IGM; IGM heavy chain; immunoglobulin mu heavy chain; variable
region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A.,
Chiorazzi, N. and Ferrarini, M.
TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)
MEDLINE 20281644
PUBMED 10820234
REFERENCE 2 (bases 1 to 351)
AUTHORS Dono, M.
TITLE Direct Submission
SUBMITTER Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
ITALY
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Best Local Similarity 91.5%; Pred. No. 1.5e-70;
Matches 313; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
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QY 301 TTGGCAACTGGGGCCAGGAAACCTGTGACCGCTCTCTCA 342
Db 310 TTGGCAACTGGGGCCAGGAAACCTGTGACCGCTCTCTCA 351

RESULT 11
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DEFINITION Sequence 32 from Patent WO0100678.
ACCESSION AX061463
VERSION AX061463.1 GI:12406598
KEYWORDS Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
SOURCE Human immunodeficiency virus 1
Virus; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
REFERENCE 1
AUTHORS Watkins, B.A. and Reitz, M.S.
TITLE Human monoclonal antibodies to hiv-1 envelope glycoprotein gp120
JOURNAL Patent: WO 0100678-A 32 04-JAN-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
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ORIGIN
Query Match 83.2%; Score 284.4; DB 6; Length 360;
Best Local Similarity 91.5%; Pred. No. 1.5e-70;
Matches 313; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
4 GAGTCTGCCCCAGAGACTGTGTGAACCTTTACAGACCCCTGTCCCTCACCTGACATGTCTCT 63
Db 19 GAGTCGGGGCCAGAGACTGTGTGAACCTTTACAGACCCCTGTCCCTCACCTGACATGTCTCT 78
QY 64 GGTGGCTCCATCCGCACTGGTGTATTACTGAGATTGAGATCCGCGCCGACGAGAG 123
Db 79 GGTGGCTCCATCCGCACTGGTGTATTACTGAGATTGAGATCCGCGCCGACGAGAG 138
QY 124 GGCTGTGAGTGTGATCGGGTACATCTATCACAGTGGCAACCTTCAACAAACCCGTCCCTC 183
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Db      139  GGCTGGAGTGGATYGGGTACATCTATTACAGTGGAGACCTACTACMACCCGTCCTC 198
Qy      184  AAGAGTGAATTAACATGTCAGTGAACAACCTTAAGAACCACTTCCTCGAGGCTGAGC 243
Db      199  AAGAGTGAATTAACATGTCAGTGAACAACCTTAAGAACCACTTCCTCGAGGCTGAGC 258
Qy      244  TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGA--GTCAGATGGGTACACT 300
Db      259  TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAAGGGGTAGTGTGACTGG 318
Qy      301  TTGACAACTGGGGCCAGGGAACTGTGACCGTCTCTCTCA 342
Db      319  TTCAGCCCTGGGGCCAGGGAACTGTGACCGTCTCTCTCA 360

RESULT 12
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LOCUS   H.sapiens mRNA for Ig heavy chain variable region (VH4D) (clone
DEFINITION T22.1).
ACCESSION Z75385.1 GI:2062048
VERSION    Z75385
KEYWORDS   immunoglobulin; immunoglobulin heavy chain; immunoglobulin
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 411)
AUTHORS    Tonnelie,C., D'Excrole,C., Depaertere,V., Metras,D., Boublil,L. and
            Fougereau,M.
TITLE      Human thymic B cells largely overexpress the VH4 Ig gene family. A
            possible role in the control of tolerance in situ?
JOURNAL    Int. Immunol. 9 (3), 407-414 (1997)
MEDLINE    97244170
PUBMED     9088979
REFERENCE   2 (bases 1 to 411)
AUTHORS    Tonnelie,C.
TITLE      Direct Submission
JOURNAL    Submitted (26-JUN-1996) Cecile Tonnelie, Centre d'Immunologie
            Marseille Luminy, Marseille, 13288, France
FEATURES
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Best Local Similarity 89.9%; Pred. No. 2.6e-70;
Matches 304; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Qy      244  TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAAGGGGTAGTGTGACTGG 303
Db      313  TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAAGGGGTAGTGTGACTGG 372
Qy      304  GACAACTGGGGCCAGGGAACTGTGACCGTCTCTCTC 341
Db      373  TCCAGCTGGGGCCAGGGAACTGTGACCGTCTCTCTC 410

RESULT 13
HSA245064 354 bp mRNA linear PRI 02-JUN-1999
LOCUS   HSA245064
DEFINITION Homo sapiens mRNA for immunoglobulin gamma heavy chain variable
            region, partial, clone 2-D123.
ACCESSION AJ245064.1 GI:4995589
VERSION    AJ245064.1
KEYWORDS   IgG; IgG heavy chain; immunoglobulin gamma heavy chain; variable
            region.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS    Dono,M., Zupo,S., Chiorazzi,N. and Ferrarini,M.
TITLE      Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
            marginal zone equivalents
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 354)
AUTHORS    Dono,M.
TITLE      Direct Submission
JOURNAL    Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
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            ITALY
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Query Match 82.7%; Score 283; DB 9; Length 354;
Best Local Similarity 89.7%; Pred. No. 3.9e-70;
Matches 304; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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D      16  GAGTCGGGGCCCAAGACTGCTGGAACCTTCAAGAACCTGTCTCTCACTGACCTGTCTCT
QY      64  GGTGGCTCCATCCGACAGTGGTGTATTACTGAGATTGGATCCGACAGCGTCCAGGGAG
D      76  GGTGGCTCCATCCGACAGTGGTGTATTACTGAGATTGGATCCGACAGCGTCCAGGGAG
QY      124  GGCCTGAGTGGATCGGGTACATCTATCAAGTGGCAACACTTAACAACCCGCTCC
D      136  GGCCTGAGTGGATCGGGTACATCTATCAAGTGGCAACACTTAACAACCCGCTCC
QY      184  AAGAGTGAATTACCATGTCACTAGACAGCTCTAAGAACCTTCTCTGAGGCTGAGC
D      196  AAGAGTGAATTACCATGTCACTAGACAGCTCTAAGAACCTTCTCTGAGGCTGAGC
QY      244  TCTGTGACTGCGCGGACAGCGCGCTGTATTACTGTGAGAGTCAAGTGGTACACTTTG
D      256  TCTGTGACTGCGCGGACAGCGCGCTGTATTATTGTGCGAGGGGAGATTAGTTACTT
QY      304  GACAACCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA 342
D      316  GACTACTGGGGCCAGGAGCCCTGTGTCAACCGTCTCTCA 354

RESULT 14
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LOCUS      Human immunoglobulin heavy chain variable region (V4-31) gene,
DEFINITION  partial cds.
ACCESSION  U80129
VERSION     U80129.1  GI:1791100
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1  (bases 1 to 360)
AUTHORS     Glas,A.M., Nottenburg,C. and Milner,E.C.
TITLE       Analysis of rearranged immunoglobulin heavy chain variable region
            genes obtained from a bone marrow transplant (BMT) recipient
JOURNAL     Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE     97182739
PUBMED      9030878
REFERENCE   2  (bases 1 to 360)
AUTHORS     Glas,A.M., Nottenburg,C. and Milner,E.C.B.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
            1000 Seneca Street, Seattle, WA 98101, USA
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Best Local Similarity 91.0%; Pred. No. 3, 9e-70;
Matches 314; Conservative 0; Mismatches 25; Indels 6; Gaps 1;

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D      16  GAGTCGGGGCCCAAGACTGCTGGAACCTTCAAGAACCTGTCTCTCACTGACCTGTCTCT
QY      64  GGTGGCTCCATCCGACAGTGGTGTATTACTGAGATTGGATCCGACAGCGTCCAGGGAG
D      76  GGTGGCTCCATCCGACAGTGGTGTATTACTGAGATTGGATCCGACAGCGTCCAGGGAG
QY      124  GGCCTGAGTGGATCGGGTACATCTATCAAGTGGCAACACTTAACAACCCGCTCC
D      136  GGCCTGAGTGGATCGGGTACATCTATCAAGTGGCAACACTTAACAACCCGCTCC
QY      184  AAGAGTGAATTACCATGTCACTAGACAGCTCTAAGAACCTTCTCTGAGGCTGAGC
D      196  AAGAGTGAATTACCATGTCACTAGACAGCTCTAAGAACCTTCTCTGAGGCTGAGC
QY      244  TCTGTGACTGCGCGGACAGCGCGCTGTATTACTGTGCGAG-----GTCAATGGGTAC
D      256  TCTGTGACTGCGCGGACAGCGCGCTGTATTACTGTGCGAGGGGTCAAGTGGTGTAC
QY      298  ACTTGGACAACCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA 342
D      316  TATTTGACTACTGCGGCGAGGGAACCTGTGTCAACCGTCTCTCA 360

RESULT 15
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LOCUS      Human immunoglobulin heavy chain variable region (V4-31) gene,
DEFINITION  partial cds.
ACCESSION  U80130
VERSION     U80130.1  GI:1791102
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (bases 1 to 360)
AUTHORS     Glas,A.M., Nottenburg,C. and Milner,E.C.
TITLE       Analysis of rearranged immunoglobulin heavy chain variable region
            genes obtained from a bone marrow transplant (BMT) recipient
JOURNAL     Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE     97182739
PUBMED      9030878
REFERENCE   2  (bases 1 to 360)
AUTHORS     Glas,A.M., Nottenburg,C. and Milner,E.C.B.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
            1000 Seneca Street, Seattle, WA 98101, USA
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## ORIGIN

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Best Local Similarity 91.0%; Pred. No. 3.9e-70;  
Matches 314; Conservative 0; Mismatches 25; Indels 6; Gaps 1;
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QY      64 GGTGGCTCCATCCGCACTGTGTGTATTACTGTGATGGATCCGCCAGCGTCCAGGGAG 123  
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QY      124 GGCCTGAGTGTGATGGGTATCTATCACTGAGCAACACCTACACACACCCGTCCTC 183  
Db      136 GGCCTGAGTGTGATGGGTATCTATCACTGAGCAACACCTACACACCCGTCCTC 195  
QY      184 AAGAGTCAGTTACATGTCAGTAGACACGCTAAGAACCACTCTCCCTGAGGCTGAGC 243  
Db      196 AAGAGTCAGTTACATGTCAGTAGACACGCTAAGAACCACTCTCTGAAGCTGAGC 255  
QY      244 TCTGTGACTGCCGCGGACACGCGCGTATTACTGTGCGAG-----GTCAATGGGTAC 297  
Db      256 TCTGTGACTGCCGCGGACACGCGCGTATTACTGTGCGAGAGGGGTGAGTGGCTGTAC 315  
QY      298 ACTTTGACAACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 342  
Db      316 TATTTTGACTAGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 360
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:15:56 ; Search time 2106.58 Seconds  
(without alignments)  
6179.670 Million cell updates/sec

Title: US-10-027-725a-3

Perfect score: 342

Sequence: 1 ctgcagctgcgcccagcact.....ccctgcacgcctcctca 342

Scoring table: IDENTITY\_NUC

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gsal1:\*

9: gb\_gsal2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	273.4	79.9	832	1	AU122174 AU122174
2	264	77.2	607	4	BM783015 K-EST0060
3	261.4	76.4	677	4	BG686767 602650737
4	258.8	75.7	509	2	AM406349 UI-HF-BK0
5	257.8	75.4	490	6	CD689564 EST6087 h
6	256.6	75.0	369	2	AM404242 UI-HF-BK0
7	254	74.3	643	1	AU134293 AU134293
8	252.6	73.9	1108	5	BM920469 AGENCOURT
9	249.8	73.0	914	4	BG757054 602710478
10	248	72.5	904	5	BQ710488 AGENCOURT
11	246.4	72.0	447	2	AM402200 UI-HF-BK0
12	246.2	72.0	725	4	BG431274 602499844
13	246.2	72.0	959	5	BUS99307 AGENCOURT
14	246	71.9	813	5	BQ710364 AGENCOURT
15	245.8	71.9	582	2	AM401348 UI-HF-BK0
16	244.8	71.6	363	3	AM403420 UI-HF-BK0
17	244.6	71.5	903	5	BQ706579 AGENCOURT
18	244.2	71.4	814	4	BG685325 602637756
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20	244	71.3	421	2	AM407630 UI-HF-BK0
21	243.8	71.3	856	5	BQ421299 AGENCOURT
22	241.6	70.6	508	7	CR747031 CR747031
23	241.6	70.6	542	2	AM951834 EST163904
24	241.6	70.6	1019	5	BQ072420 AGENCOURT

25	241.6	70.6	1195	5	BQ707644 AGENCOURT
26	241.4	70.6	474	2	AM408410 UI-HF-BK0
27	241.4	70.6	924	5	BQ708516 AGENCOURT
28	240.6	70.4	368	2	AM403989 UI-HF-BK0
29	240.2	70.2	921	5	BQ710000 AGENCOURT
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31	239.8	70.1	915	5	BQ706358 AGENCOURT
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38	238.4	69.7	915	5	BQ711871 AGENCOURT
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#### ALIGNMENTS

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DEFINITION	AU122174	MAMMAL	Homo sapiens	cdna	clone	MAMMAL001802 5', mRNA
ACCESSION	AU122174					
VERSION	AU122174.1	GI:10937409				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 832)					
AUTHORS	Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isega, T.					
TITLE	HRI human CDNA project					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Takao Isega Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human CDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; CDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.					
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QY 304 GACAACTGGGGGCGAGGAACCGTGTCAACCGTCTCCTCA 342  
DB 410 GACTTCTGGGGCGAGGAACCGTGTCAACCGTCTCCTCA 448

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DEFINITION 5', mRNA sequence.  
ACCESSION BM783015  
VERSION BM783015.1 GI:19131247  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE Kim N.S., Hahn Y., Oh J.H., Lee J.Y., Ahn H.Y., Chu M.Y., Kim M.R.,  
Oh K.J., Cheong J.E., Sohn H.Y., Kim J.M., Park H.S., Kim S. and  
Kim Y.S.  
21C Frontier Korean EST Project 2001  
COMMENT Unpublished (2002)  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boseun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
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intact mRNA was ligated with DNA-RNA linker including EcoRI  
I site by treatment of T4 RNA ligase and the first strand  
cDNA was synthesized from oligo dt-selected mRNA by  
priming with dt-tailed vector. The dt-tailed vector was  
adjusted to have about 60nt. The cDNA vector was  
circularized with E. coli DNA ligase after digestion of  
EcoRI which site is also included in vector. An RNA strand  
converted to a DNA strand by Okayama-Berg method. The  
obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10F by electroporation method.  
The cDNA libraries constructed by this method are

ORIGIN full-length enriched cDNA library."

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Best Local Similarity 87.4%; Pred. No. 1,4e-66;  
Matches 304; Conservative 0; Mismatches 35; Indels 9; Gaps 1;

QY 4 GAGTCTGGCCGAGAGTGTGAAGCCCTTCAACAGCCCTGTCCCTACCTGCATGTCTCT 63  
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DB 232 GGCCTGAGTGGATCCGGTATCATCTATGACAGTGGCAACACTTACAAACCGTCCCTC 291  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
1 (bases 1 to 677)  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabs-rc@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
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High quality sequence stop: 675.  
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for average insert size 1.8kb. Library constructed by Ling

ORIGIN

Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

Query Match 76.4%; Score 261.4; DB 4; Length 677;  
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QY 124 GGCTGAGTGTGATCGGGTACATCTATCAAGTGGCAACACTTACAAACCCGCTCCCTC 183  
DB 218 GGCTGAGTGTGATCGGGTACATCTATCAAGTGGCAACACTTACAAACCCGCTCCCTC 277  
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DB 338 TCTGTGACTCGCGGGACACGGCCGTGATTAATCACTGTGCAAGATCGGAGAGAGAGAGGC 397  
QY 298 ACTTGGACAACACTGGGGCCAGGAACCTGTGCAACCTGCTCTCTCA 342  
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RESULT 4 509 bp mRNA linear EST 16-FEB-2000  
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REFERENCE 1 (bases 1 to 509)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-rc@mail.nih.gov](mailto:cgapbs-rc@mail.nih.gov)  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares Lab  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: [www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)  
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/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 75.7%; Score 258.8; DB 2; Length 509;  
Best Local Similarity 86.8%; Pred. No. 4.7e-65;  
Matches 297; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGAGACTGTGTAAAGCTTTCACAGACCTCTGCTCCTGACCTGTCTCT 63  
DB 54 GAGTCGGGCCAGAGACTGTGTAAAGCTTTCAGAGACCTGTGCTCCTGACCTGTCTCT 113  
QY 64 GGTGCTCCATCCGACAGTGTGTATTAATCACTGAGTTGGATCCGACAGCTCCAGGGAG 123  
DB 114 GGTGCTCCATCCGACAGTGTGTATTAATCACTGAGTTGGATCCGACAGCTCCAGGGAG 173  
QY 124 GGCTGAGTGTGATCGGGTACATCTATCAAGTGGCAACACTTACAAACCCGCTCCCTC 183  
DB 174 GGCTGAGTGTGATCGGGTACATCTATTAATCAAGTGGCAACACTTACAAACCCGCTCCCTC 233  
QY 184 AAGAGTCGAGTTACATCTGCTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243  
DB 234 AAGAGTCGAGTTACATCTGCTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 293  
QY 244 TCTGTGACTCGCGGGACACGGCCGTGATTAATCACTGTGCA-----GTCAAGTGGGTAC 300  
DB 294 TCTGTGACTCGCGGGACACGGCCGTGATTAATCACTGTGCAAGATCGGAGAGAGAGAGGC 353  
QY 301 TTGACAACACTGGGGCCAGGAACCTGTGCAACCTGCTCTCTCA 342  
DB 354 TTGACCCCTGGGGCCAGGAACCTGTGCAACCTGCTCTCTCA 395

RESULT 5 490 bp mRNA linear EST 25-JUN-2003  
CD689564  
LOCUS EST6087 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
DEFINITION CD689564  
ACCESSION CD689564  
VERSION CD689564.1 GI:32209443  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 490)  
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.  
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: [yxzeng@gzsums.edu.cn](mailto:yxzeng@gzsums.edu.cn)  
FEATURES  
SOURCE Location/Qualifiers  
1..490  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/issue\_type="normal nasopharynx"  
/clone\_lib="human nasopharynx"  
/note="ESTs generated from a normal nasopharynx cDNA  
library from southern Chinese"

ORIGIN

Query Match 75.4%; Score 257.8; DB 6; Length 490;  
Best Local Similarity 86.8%; Pred. No. 9.1e-65;  
Matches 296; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

QY 5 AGCTGCCCCAGAGACTGTGTAAGCCTTCAACAGACCTTGTCCCTCACTGCATGTCTCTG 64  
DB 111 AGTCGGGCCCCAGAGACTGTGTAAGCCTTCAACAGACCTTGTCCCTCACTGCATGTCTCTG 170  
QY 65 GTGGCTCATCCGAGTGTGTATTACTGAGTGTGATCCGCGAGGTCAGAGG 124  
DB 171 GTGACTCATTACAGAGTGTGTATTACTGAGTGTGATCCGCGAGGTCAGAGG 230  
QY 125 GCCTGAGTGTGATGGGTATCATCTATCAAGTGGCAACACTACAGAACCCGTCCTCA 184  
DB 231 GCCTGAGTGTGATGGGTATCATCTATCAAGTGGAGTGGCGATACACCCGTCCTCA 290  
QY 185 AGAGTCAGTTACCATGTCTAGTACACACGTTAAGAACCACTTCTCCCTGAGCTGAGCT 244  
DB 291 AGAGTCAGTTACCATGTCTAGTACACACGTTAAGAACCACTTCTCCCTGAGTGAAGT 350  
QY 245 CTGTGACTGCGCGGAGACAGCGCGTGTATTACTGTGAGAGTCAAGT---GGGTACACTT 301  
DB 351 CTGTGAGCGCGCGGAGACAGCGCGTGTATTACTGTGAGAGTGGTCCGAGCATTTAA 410  
QY 302 TGAGCAACTGGGGCCAGGGAACCTGTGTACCGTCTCTCA 342  
DB 411 TTGACTACTGGGGCCAGGGAATCCTGTGTACCGTCTCTCA 451

RESULT 6 369 bp mRNA linear EST 16-FEB-2000  
AM404242  
LOCUS UI-HF-BLO-abq-f-09-0-UI.r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
DEFINITION IMAGE:3057545 5', mRNA sequence.  
AM404242  
VERSION AM404242.1 GI:6923299  
KEYWORDS EST.

ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 369)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strauberg, Ph.D.  
Email: egadbs-remail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
cDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Cloned through the I.M.A.G.E. Consortium/LNL at:  
www-bio.1nl.gov/bdrrp/image/image.html  
Seq primer: M13 Forward.

FEATURES  
source location/Qualifiers  
1..369

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3057545"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LTI)"  
/clone\_id="NIH\_MGC\_37"  
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;  
Constructed from size fractionated cytoplasmic RNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonafide, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN  
Query Match 75.0%; Score 256.6; DB 2; Length 369;  
Best Local Similarity 87.8%; Pred. No. 1.9e-64;

Matches 280; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
QY 4 GAGCTTGCCAGAGACTGTGTAAGCCTTCAACAGACCTTGTCCCTCACTGCATGTCTCT 63  
DB 34 GAGTCGGGCCCCAGAGACTGTGTAAGCCTTCAACAGACCTTGTCCCTCACTGCATGTCTCT 93  
QY 64 GTGGCTCATCCGAGTGTGTATTACTGAGTGTGATCCGCGAGGTCAGAGG 123  
DB 94 GTGGCTCATCCGAGTGTGTATTACTGAGTGTGATCCGCGAGGTCAGAGG 153  
QY 124 GCCTGAGTGTGATGGGTATCATCTATCAAGTGGCAACACTACAGAACCCGTCCTCA 183  
DB 154 GCCTGAGTGTGATGGGTATCATCTATCAAGTGGAGTGGCGATACACCCGTCCTCA 213  
QY 184 AGAGTCAGTTACCATGTCTAGTACACACGTTAAGAACCACTTCTCCCTGAGCTGAGC 243  
DB 214 AGAGTCAGTTACCATGTCTAGTACACACGTTAAGAACCACTTCTCCCTGAGTGAAGT 273  
QY 244 TCTGTGACTGCGCGGAGACAGCGCGTGTATTACTGTGAGAGTCAAGTGGGTACACTTTG 303  
DB 274 TCTGTGACTGCGCGGAGACAGCGCGTGTATTACTGTGAGAGTCTTTGGGTATTACTTT 333  
QY 304 GACAACTGGGGCCAGGGAACCTGTGTACCGTCTCTCA 342  
DB 334 GATAGTACTGGGTACAGGAA 352

RESULT 7 643 bp mRNA linear EST 01-AUG-2002  
AUI34293  
LOCUS AUI34293 Homo sapiens cDNA clone OVARC1001672 5', mRNA  
DEFINITION AUI34293 OVARC1  
sequence.  
AUI34293  
VERSION AUI34293.1 GI:10994832  
KEYWORDS EST.

ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 643)  
AUTHORS Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,  
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Negai,T., Sugano,S. and  
Iisaga,T.  
HRI human cDNA project  
Unpublished (2000)  
Contact: Takao Iisaga  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: genomics@hri.co.jp  
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix  
Research Institute; cDNA library construction; Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.

FEATURES  
source location/Qualifiers  
1..643

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="OVARC1001672"  
/tissue\_type="ovary, tumor tissue"  
/clone\_id="OVARC1"  
/note="Vector: pME18SFJ3"

ORIGIN  
Query Match 74.3%; Score 254; DB 1; Length 643;  
Best Local Similarity 85.1%; Pred. No. 1.3e-63;  
Matches 303; Conservative 0; Mismatches 35; Indels 18; Gaps 1;  
QY 5 AGCTGCCCCAGAGACTGTGTAAGCCTTCAACAGACCTTGTCCCTCACTGCATGTCTCTG 64



Db 110 AGTGGGGCCAGAGCTGTGTGAAGCCTTCACAGACCCTGTCCCTCACTGTCTCTG 169  
 Qy 65 GTGGCTCATCCGAGTGTGTGTTATTACATGAGTTGGATCGGCAGCGTCAGGGAAG 124  
 Db 170 GTGGCTCATAGAGAGTGTGTATTTACTTGTGACCTGTGATCCGCAACACCCAGGGAAG 229  
 Qy 125 GCTTGAAGTGTAGTGGGTATCATCTATCAAGTGGCAACACTACAAACCCGTCCTCA 184  
 Db 230 GCTTGAAGTGTAGTGGGTATCATCTATCAAGTGGCAACACTACAAACCCGTCCTCA 289  
 Qy 185 AGAGTCGAGTTACCATGTCTAGTAGACAGCTTTAAGAACCACTTCTCCTGAGGCT 244  
 Db 290 AGAGTCGAGTTACCATGTCTAGTAGACAGCTTTAAGAACCACTTCTCCTGAGGCT 349  
 Qy 245 CTGTGACCTGGCGGACACGGCCGTGTATTACTGTGCGAGGTCAAGATGGTAACT--- 300  
 Db 350 CTGTGACCTGGCGGACACGGCCGTGTATTACTGTGCGAGTTTGAAGACCTTAAATAGT 409  
 Qy 301 -----TTGACAACTGGGGCCAGGAAACCTGTGTCACGCTCTCTCA 342  
 Db 410 GGACTTACAGTAAGTTTGAACCACTGGGCGCAGGGAACCTGTGTCACGCTCTCTCA 465

RESULT 8  
 BM920469 1108 bp mRNA linear EST 12-MAR-2002  
 LOCUS AGENCOURT\_6709612 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5750444  
 DEFINITION 5', mRNA sequence.

ACCESSION BM920469  
 VERSION BM920469.1 GI:19370848  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1108)  
 NIH-MGC http://mgs.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L16M12781 row: 9 column: 21  
 High quality sequence stop: 626.

# FEATURES

SOURCE 1..1108  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5750444"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_122"  
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;  
 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source  
 anonymous pool of 24 week female lung, 16 week female  
 spleen, and 20-22 week male spleen. Library is oligo-dT  
 primed and directionally cloned (EcoRV site is destroyed  
 upon cloning). Average insert size 1.4 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 026. Note:  
 this is a NIH\_MGC Library."

# ORIGIN

Query Match. 73.9%; Score 252.6; DB 5; Length 1108;  
 Best Local Similarity 85.5%; Pred. No. 3.7e-63;  
 Matches 295; Conservative 0; Mismatches 44; Indels 6; Gaps 1;

Qy 4 GAGTGTGCCCCAGAGACTGTGTAAACCTTCAAGACCCTGTCTTCACTGTGACTGTCT 63  
 Db 110 GAGTGTGCCCCAGAGACTGTGTAAACCTTCAAGACCCTGTCTTCACTGTGACTGTCT 169  
 Qy 64 GTTGGCTTCATCCGACGTGTGTATTATTCTGAGTTGATCGGCACGCTCGAGGAAG 123  
 Db 170 GTTGGCTTCGTCACAGCACTGTGTATTACTGAGTGTGATCCGACCGCCAGGGAAG 229  
 Qy 124 GACCTGAGTGTGATCGGTGTATCTATCAAGTGGCAACCTTCAACACCGCTCCCTC 183  
 Db 230 GACCTGAGTGTGATCGGTGTATCTATCAAGTGGCAACCTTCAACACCGCTCCCTC 289  
 Qy 184 AAGAGTCGAGTTACCATGTCTAGTAGACAGCTTTAAGAACCACTTCTCCTGAGGCTAGC 243  
 Db 290 AAGAGTCGAGTTACCATGTCTAGTAGACAGCTTTAAGAACCACTTCTCCTGAGGCTAGC 349  
 Qy 244 TCTGTGACTGGCGGACACGGCCGTGTATTACTGTGCGAGGTCAAGTGGG-----TAC 297  
 Db 350 TCTGTGACCGCTGGCGACACGGCCGTGTATTACTGTGCGAGCGGGGGGGGGGACTAC 409  
 Qy 298 ACTTGGACAACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342  
 Db 410 TACATGACGCTGTGGCGCAAGGACCAAGGTCACCGTCTCTCA 454

RESULT 9  
 BG757054 914 bp mRNA linear EST 15-MAY-2001  
 LOCUS 602710478F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4850851 5',  
 DEFINITION mRNA sequence.

ACCESSION BG757054  
 VERSION BG757054.1 GI:14067707  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 914)  
 NIH-MGC http://mgs.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L16M1692 row: 1 column: 20  
 High quality sequence stop: 854.

# FEATURES

SOURCE 1..914  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4850851"  
 /tissue\_type="Primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_48"  
 /note="Organ: B-cells; Vector: pOTB7, Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

# ORIGIN

Query Match 73.0%; Score 249.8; DB 4; Length 914;  
Best Local Similarity 86.7%; Pred. No. 2,4e-62;  
Matches 301; Conservative 0; Mismatches 37; Indels 9; Gaps 2;

QY 4 GAGTCTGAGCCAGGACTGTTGAAAGCCTTCACAGACCCCTGTCCTCCTGCTGCTCTCT 63  
DB 93 GAGTCTGAGCCAGGACTGTTGAAAGCCTTCACAGACCCCTGTCCTCCTGCTGCTCTCT 152  
QY 64 GGTGGCTCCATCCGACAGTGTGTATTATCTGAGTTGGATCCGCCAGCGTCCAGGGAG 123  
DB 153 GGTGGCTCCATCCGACAGTGTGTATTATCTGAGTTGGATCCGCCAGCGTCCAGGGAG 211  
QY 124 GGCCTGAGTGGATCGGCTATCTATTCACAGTGGCAACCTTCACAAACCCGTCCTC 183  
DB 212 GGCCTGAGTGGATCGGCTATCTATTCACAGTGGCAACCTTCACAAACCCGTCCTC 271  
QY 184 AAGAGTGAAGTTACCATGTAGTACAGCTCTAAGAACCTTCCTCCCTGAGGCTGAGC 243  
DB 272 AAGAGTGAAGTTACCATGTAGTACAGCTCTAAGAACCTTCCTCCCTGAGGCTGAGC 331  
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTCAAGATGGGTACACTTTG 303  
DB 332 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGAGGAGAGACTACGCTGAGC 391  
QY 304 GAGCACT-----GGGGCCAGGGAAACCTGCTCAACCGTCTCCTCA 342  
DB 392 CACGACTTGTACTGAGTGGGGCCAGGAAACCTGCTCAACCGTCTCCTCA 438

RESULT 10  
LOCUS B0710488 904 bp mRNA linear EST 16-JUL-2002  
DEFINITION AGENCOURT 8352970 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6278137  
5', mRNA sequence.  
B0710488  
ACCESSION B0710488.1 GI:21849387  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 904)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LICM2465 row: k column: 02  
High quality sequence stop: 728.

FEATURES  
Source

1..904  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6278137"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_113"  
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

ORIGIN

Query Match 72.5%; Score 248; DB 5; Length 904;  
Best Local Similarity 84.5%; Pred. No. 8e-62;  
Matches 294; Conservative 0; Mismatches 45; Indels 9; Gaps 1;

QY 4 GAGTCTGAGCCAGGACTGTTGAAAGCCTTCACAGACCCCTGTCCTCCTGCTGCTCTCT 63  
DB 86 GAGTCTGAGCCAGGACTGTTGAAAGCCTTCACAGACCCCTGTCCTCCTGCTGCTCTCT 145  
QY 64 GGTGGCTCCATCCGACAGTGTGTATTATCTGAGTTGGATCCGCCAGCGTCCAGGGAG 123  
DB 146 GGTGGCTCCATCCGACAGTGTGTATTATCTGAGTTGGATCCGCCAGCGTCCAGGGAG 205  
QY 124 GGCCTGAGTGGATCGGCTATCTATTCACAGTGGCAACCTTCACAAACCCGTCCTC 183  
DB 206 GGCCTGAGTGGATCGGCTATCTATTCACAGTGGCAACCTTCACAAACCCGTCCTC 265  
QY 184 AAGAGTGAAGTTACCATGTAGTACAGCTCTAAGAACCTTCCTCCCTGAGGCTGAGC 243  
DB 266 AAGAGTGAAGTTACCATGTAGTACAGCTCTAAGAACCTTCCTCCCTGAGGCTGAGC 325  
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTCAAGATGGGTACACTTTG 294  
DB 326 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGAGGAGAGACTACGCTGAGC 385  
QY 295 TACACTTGGACAACCTGGGCGAGGAAACCTGCTCAACCGTCTCCTCA 342  
DB 386 CATTACTTCAGACACTGGGGCCAGGGCAACCTGCTCAACCGTCTCCTCA 433

RESULT 11  
LOCUS AM402200 447 bp mRNA linear EST 16-FEB-2000  
DEFINITION UI-HF-BKO-aat-d-09-0-UI.r1 NIH\_MGC\_36 Homo sapiens cDNA clone  
IMAGE:3054785 5', mRNA sequence.  
AM402200  
ACCESSION AM402200.1 GI:6920886  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 447)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares Lab  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
www-bio.llnl.gov/bdrip/image/image.html  
Seq primer: M13 Forward.

FEATURES  
Source

1..447  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:3054785"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LTI)"  
/clone\_lib="NIH\_MGC\_36"  
/note="Vector: pRT3-Pac; Site 1: NotI; Site 2: Eco RI;  
constructed from size fractionated cytoplasmic mRNA  
(0.5-1.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonafide, Ph.D. and M. Bento Soares, Ph.D."

## ORIGIN

Query Match 72.0%; Score 246.4; DB 2; Length 447;  
Best Local Similarity 84.2%; Pred. No. 2e-61;  
Matches 293; Conservative 0; Mismatches 46; Indels 9; Gaps 1;

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OY 4 GAGTCTGAGCCAGAGACTGTGTAAGCCTTCACAGACCTGTCTCTACCTGACCTGTCTCT
  |||
DB 47 GAGTCGGGCCCCAGAGACTGTGTAAGCCTTCGAGACCTGTCTCTCTCTGACCTGTCTCT
  |||
OY 64 GGTGGCTTCATCCAGCAGGTGTGTATTAATCTGAGATTGGATCCGCGACGCTCGAGGAAG
  |||
DB 107 GGTGCTTCATCCAGCAGGTGTGTATTAATCTGAGATTGGATCCGCGACGCTCGAGGAAG
  |||
OY 124 GGCCTGAGATGGATGGGATCATCTATCATGATGAGCAACCTTAACAACCCGCTCTC
  |||
DB 167 GGCCTGAGATGGATGGGATCATCTATCATGATGAGCAACCTTAACAACCCGCTCTC
  |||
OY 184 AAGAGTCAGATTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC
  |||
DB 227 AAGAGTCAGATTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC
  |||
OY 244 TCTGTACTGCGCGGACACGCGCTGTATTACTGTCTGAG-----GTCAAGATGG
  |||
DB 287 TCTGTACTGCGCGGACACGCGCTGTATTACTGTCTGAGAGAGGAGATGTGTATCT
  |||
OY 295 TAGACTTGGACAATGGGCGGACGAGGAACCTGTGACCGTCTCTCA 342
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DB 347 CACTGTGTGACCCCTGGGCGGACGAGGAACCTGTGACCGTCTCTCA 394
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## RESULT 12

LOCUS BG431274 725 bp mRNA linear EST 14-MAR-2001  
DEFINITION 602499844F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4613435 5',  
mRNA sequence.

ACCESSION BG431274  
VERSION BG431274.1 GI:13337780  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
Plate: LNCM1363 row: h column: 12  
High quality sequence stop: 716.

## FEATURES

## source

1. 725  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4613435"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH MGC 75"  
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:  
SfiI (ggcgctcgagc); Site 2: SfiI (ggcattatggc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTATGACC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGGAGCGGCGCATATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.65  
kb (range 0.5-4.0 kb). 15/15 clones contained inserts

## ORIGIN

Query Match 72.0%; Score 246.2; DB 4; Length 725;  
Best Local Similarity 82.9%; Pred. No. 2.6e-61;  
Matches 281; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

```
OY 4 GAGTCTGAGCCAGAGACTGTGTAAGCCTTCACAGACCTGTCTCTACCTGACCTGTCTCT
  |||
DB 109 GAGTCGGGCCCCAGAGACTGTGTAAGCCTTCGAGACCTGTCTCTCTGACCTGTCTCT
  |||
OY 64 GGTGGCTTCATCCAGCAGGTGTGTATTAATCTGAGATTGGATCCGCGACGCTCGAGGAAG
  |||
DB 169 GGTGCTTCATCCAGCAGGTGTGTATTAATCTGAGATTGGATCCGCGACGCTCGAGGAAG
  |||
OY 124 GGCCTGAGATGGATGGGATCATCTATCATGATGAGCAACCTTAACAACCCGCTCTC
  |||
DB 229 GGCCTGAGATGGATGGGATCATCTATCATGATGAGCAACCTTAACAACCCGCTCTC
  |||
OY 184 AAGAGTCAGATTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC
  |||
DB 289 GAGAGTCAGATTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC
  |||
OY 244 TCTGTACTGCGCGGACACGCGCTGTATTACTGTGAGAGTGTGATGAGTATCACTTTG
  |||
DB 349 CTTGTGACCCGCGGACACGCTGTATTACTGTGAGAGTGTGATGAGTATCACTTTG
  |||
OY 304 GACAACCTGGGCGGACGAGGAACCTGTGACCGTCTCTCA 342
  |||
DB 409 GACTATTGGGCGGACGAGGAACCTGTGACCGTCTCTCA 447
  |||
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## RESULT 13

LOCUS BUB99307 959 bp mRNA linear EST 17-OCT-2002  
DEFINITION AGENCOURT 8532130 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6280128  
5', mRNA sequence.

ACCESSION BUB99307  
VERSION BUB99307.1 GI:24081220  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
Plate: LNCM2470 row: n column: 01  
High quality sequence stop: 605.

## FEATURES

## source

1. 959  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6280128"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC\_113"  
/note="Organ: spleen; Vector: pDNR-LIB (Clontech); Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGGAG(G). Library constructed by Ling Hong in the

by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

## ORIGIN

laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

Query Match 72.0%; Score 246.2; DB 5; Length 959;  
Best Local Similarity 84.3%; Pred. No. 2.7e-61;  
Matches 291; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGTGTAAGCTTTCACAGACCTGTCCTCCTCAGCTGACTGTCT 63  
DB 86 GAGTCGGGCCAGGACTGTGTAAGCTTTCACAGACCTGTCCTCCTCAGCTGACTGTCT 145  
QY 64 GGTGGCTCCATCCGACAGTGTGTTATTACTGAGTTGATCCGCGACGCTCAGGGAG 123  
DB 146 GTGCTCCATCAGCAGAGTGTGATTTCTTCTGAGCTGATCCGCGACGCTCAGGGAG 205  
QY 124 GGCTGAGTGTGATCGGGTATCTATCAGAGTGGCAACACTTACAAACCCGTCCTC 183  
DB 206 GGCTGAGTGTGATCGGGTATCTATCAGAGTGGCAACACTTACAAACCCGTCCTC 265  
QY 184 AAGAGTGAAGTTACATGATGATGACACGCTTAAGAACACTTCTCCCTGAGGCTGAGC 243  
DB 266 AAGGCTGAGTTACATGATGATGACACGCTTAAGAACACTTCTCCCTGAGGCTGAGC 325  
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGAGGTGAG-----ATGGGTAC 297  
DB 326 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGAGGTGAGGTGAGGTGAGGT 385  
QY 298 ACTTGGACAACTGGGGCGAGGGAACCTGTGTCACCGTCTCTCA 342  
DB 386 GCTTTGATATCTGGGCGAAGGACATGTGTCAACCGTCTCTCA 430

## RESULT 14

LOCUS BQ710364 813 bp mRNA linear EST 16-JUL-2002  
DEFINITION AGENCOURT B351485 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6282412  
5', mRNA sequence.  
ACCESSION BQ710364  
VERSION BQ710364.1 GI:21849263  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgi.nci.nih.gov/.  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rudin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: LUCM2476 row: m column: 05  
High quality sequence stop: 529.

## FEATURES

source 1..813  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6282412"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 113"  
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:

## ORIGIN

GGCAGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

Query Match 71.9%; Score 246; DB 5; Length 813;  
Best Local Similarity 91.3%; Pred. No. 3e-61;  
Matches 261; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGGACTGTGTAAGCTTTCACAGACCTGTCCTCCTCAGCTGACTGTCT 63  
DB 82 GAGTCGGGCCAGGACTGTGTAAGCTTTCACAGACCTGTCCTCCTCAGCTGACTGTCT 141  
QY 64 GGTGGCTCCATCCGACAGTGTGTTATTACTGAGTTGATCCGCGACGCTCAGGGAG 123  
DB 142 GTGCTCCATCAGCAGAGTGTGATTTCTTCTGAGCTGATCCGCGACGCTCAGGGAG 201  
QY 124 GGCTGAGTGTGATCGGGTATCTATCAGAGTGGCAACACTTACAAACCCGTCCTC 183  
DB 202 GGCTGAGTGTGATCGGGTATCTATCAGAGTGGCAACACTTACAAACCCGTCCTC 261  
QY 184 AAGAGTGAAGTTACATGATGATGACACGCTTAAGAACACTTCTCCCTGAGGCTGAGC 243  
DB 262 AAGGCTGAGTTACATGATGATGACACGCTTAAGAACACTTCTCCCTGAGGCTGAGC 321  
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGAGGTGAG 289  
DB 322 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGAGGTGAG 367

## RESULT 15

LOCUS AM401348 582 bp mRNA linear EST 16-FEB-2000  
DEFINITION UI-HF-BK0-aaU-d-08-0-UI.r1 NIH\_MGC\_36 Homo sapiens cDNA clone  
IMAGE:3055142 5', mRNA sequence.  
ACCESSION AM401348  
VERSION AM401348.1 GI:6920130  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgi.nci.nih.gov/.  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Straut, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares lab  
CDNA Library Arrayed by: M.B. Soares lab  
DNA Sequencing by: M.B. Soares lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
www-bio.llnl.gov/bdrip/image/image.html  
Seq primer: M13 Forward.

## FEATURES

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3055142"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LTR)"  
/clone\_lib="NIH MGC 36"  
/note="Vector: pRT73-Pac; Site 1: NotI; Site 2: Eco RI; constructed from size fractionated cytoplasmic RNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis

## ORIGIN

M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonafido, Ph.D. and M. Bento Soares, Ph.D."

Query Match 71.9%; Score 245.8; DB 2; Length 582;  
Best Local Similarity 86.1%; Pred. No. 3.2e-61;  
Matches 297; Conservative 0; Mismatches 42; Indels 6; Gaps 2;

```
QY      4 GAGTCTGAGCCCGAGGACTGTGTAAGCCTTCACAGACCCCTGTCCTCACCCTGACATGTCCT 63
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      34 GAGTCGGGCCCCAGGACTGTGTGAAGCCTTCACAGACCCCTGTCCTCACCCTGACATGTCCT 93
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      64 GGTGGCTTCCA--TCCGAGTGTGTGTTATTACTGAGTTGATCCGCCAGCTCCAGGG 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      94 GGTGGCTTCCATCTTCAACAGTGTGATTACTTCTGSACTTGATCCGCCAGCACCAGGG 153
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      121 AAGGGCCTGAGTGGATGGGTATCATCTATCAAGTGGCAACACCTACAAACCCCTCC 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      154 AAGGGCCTGAGTGGATGGGTATCTATCTATTTACACTGGAGCACCTATTTACACCCCTCC 213
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      181 CTCAAGAGTCAGTTACCATGTCTAGTACACAGTCTAAGAACACTTCTCCCTGAGGCTG 240
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Db      214 CTCAAGAGTCAGTTTCCATATCACTGTGACACAGTCTAAGAACACTTCTCCCTGAACTG 273
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      241 AGCTCTGTACTGCCCGGAGACACGGCCGTGTATTACTGTGCGAGGTCAATGGGTAC--- 297
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      274 AGCTCTGTGACTGCCCGGAGACACGGCCGTGTATTACTGTGCGAGAGGTGCTTACTAT 333
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      298 ACTTTGACAACTGGGGGCCAGGGAAACCTGTGACCGTCTCTCA 342
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      334 GCTTTGATATCTGGGGCCAAGGACAATGGTCAACCGTCTCTCA 378
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 03:58:31 ; Search time 321.618 Seconds

(without alignments)  
6294.891 Million cell updates/sec

Title: US-10-027-725a-3

Perfect score: 342  
Sequence: 1.ctcgagctgcgcacagact.....ccctgctcacgcctctctca 342

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 0%

Listing first 45 summaries

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1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
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10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338.8	99.1	342	6	ABK89639 DNA encod
2	332.8	94.4	342	6	ABK89638 DNA encod
3	308.4	90.2	342	6	ABK89637 DNA encod
4	284.6	83.2	352	10	ADCC99786 Anti-huma
5	284.6	83.2	352	10	ADDO5390 Anti-MUC1
6	284.6	83.2	352	10	ADFO9828 Human ant
7	284.4	83.2	360	4	AAEF29076 Human HIV
8	276.6	80.9	354	13	ADs84403 Human ant
9	276.6	80.9	354	13	ADr68545 Anti-EPO-
10	276.6	80.9	1996	13	ADs84454 Human ant
11	276.6	80.9	1996	13	ADs84453 Human ant
12	276.6	80.9	1996	13	ADr68595 Human ant
13	276.6	80.9	1996	13	ADr68596 Human ant
14	275.8	80.6	663	10	ADJ32125 Human int
15	275	80.4	352	10	ADCC99778 Anti-huma
16	275	80.4	352	10	ADDO5382 Anti-MUC1
17	275	80.4	352	10	ADFO9820 Human ant
18	274.2	80.2	560	12	ADK52387 Human ant
19	273.8	80.1	369	4	AAEF29046 Human HIV
20	271.8	79.5	355	13	ADs84415 Human ant

21	271.8	79.5	355	13	ADr68557 Anti-EPO-
22	271.8	79.5	1996	13	ADs84472 Human ant
23	271.8	79.5	1996	13	ADs84471 Human ant
24	271.8	79.5	1996	13	ADr68614 Human ant
25	271.8	79.5	1996	13	ADr68613 Human ant
26	270.2	79.0	1838	10	ADP90705 Human hep
27	270	78.9	1338	12	ADK52355 Human ant
28	268.4	78.5	358	10	ADCC99798 Anti-huma
29	268.4	78.5	358	10	ADDO5402 Anti-MUC1
30	268.4	78.5	358	10	ADFO9840 Human ant
31	267.2	78.1	516	3	AA446876 DNA encod
32	264	77.2	366	4	AAEF29066 Human HIV
33	263.6	77.1	357	2	AAQ38670 MAB GAH v
34	262.8	76.8	352	10	ADCC99806 Anti-huma
35	262.8	76.8	352	10	ADDO5410 Anti-MUC1
36	262.8	76.8	352	10	ADFO9848 Human ant
37	261.4	76.4	741	3	AAZ28998 Anti-muri
38	258.6	75.6	1644	2	AAZ24434 Human bla
39	257	75.1	324	4	ABSA6332 Human liv
40	257	75.1	340	6	ABK84446 Human CDN
41	257	75.1	340	8	ACA64884 Human Ig
42	257	75.1	340	10	ADP90613 Human hep
43	257	75.1	384	12	ADP22095 Human ant
44	257	75.1	384	12	ADP22103 Human ant
45	257	75.1	384	12	ADP22123 Human ant

## ALIGNMENTS

RESULT 1	ABK89639	standard; DNA; 342 BP.
ID	ABK89639	
XX	ABK89639;	
AC	21-OCT-2002	(first entry)
DT		
XX	DNA encoding human Ige Fab clone 100 heavy chain.	
DE		
KW	Human; fab; ds; gene; anti-allergic; vaccine; grass pollen; phi p 2;	
KW	timothy grass pollen allergen; passive immunotherapy.	
XX		
OS	Homo sapiens.	
XX		
FH	Location/Qualifiers	
FT	CDS	1..342
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FT		/product= "Fab clone 100 heavy chain"
FT	misc_feature	7..78
FT		/tag= b
FT		/note= "FR1 region"
FT	misc_feature	79..99
FT		/tag= c
FT		/note= "CDR1 region"
FT	misc_feature	100..123
FT		/tag= d
FT		/note= "FR2 region"
FT	misc_feature	134..141
FT		/tag= e
FT		/note= "FR3 region"
FT	misc_feature	142..189
FT		/tag= f
FT		/note= "CDR2 region"
FT	misc_feature	190..285
FT		/tag= g
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FT	misc_feature	286..309
FT		/tag= h
FT		/note= "CDR3 region"
FT	misc_feature	310..342
FT		/tag= i
FT		/note= "FR4 region"

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XX PN WO200253595-A1.
XX PD 11-JUL-2002.
XX PF 27-DEC-2001; 2001WO-SE002908.
XX PR 29-DEC-2000; 2000SE-00004892.
XX PA (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX P-PSDB; ABG30447.
XX PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX PS Disclosure; Page 33; 45pp; English.
XX CC This invention relates to the DNA and protein sequences of group 2
XX CC allergen-specific human IgE Fabs and methods for their use. The proteins
XX CC of the invention may have antiallergic activities and may be used as a
XX CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
XX CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX CC 2 allergen-specific fabs of the invention may be useful for environmental
XX CC allergen detection and for standardisation of allergen extracts. The fabs
XX CC - or a vaccine against a type I allergy is useful for diagnosing a type
XX CC I allergy. The allergen-specific fabs of the invention are useful for
XX CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
XX CC also useful for identification of group 2 allergen-containing pollen and
XX CC may be used for blocking the binding of grass pollen allergic patients
XX CC IgE antibodies to Phi p 2. The present sequence represents the DNA
XX CC encoding the human IgE fab, clone 100 heavy chain protein of the
XX CC invention
XX SQ Sequence 342 BP; 69 A; 103 C; 94 G; 76 T; 0 U; 0 Other;
Query Match 99.1%; Score 338.8; DB 6; Length 342;
Best Local Similarity 99.4%; Pred. No. 1.6e-85;
Matches 340; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCAGCTGCACTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCAGCTGCACTGTC 60
QY 61 TCTGTGTGGCTTCATCCGAGTGTGTATTACTGAGATTGGATCCGCCAGCGTCCAGGG 120
Db 61 TCTGTGTGGCTTCATCCGAGTGTGTATTACTGAGATTGGATCCGCCAGCGTCCAGGG 120
QY 121 AAGGGCTGAGTGGATCGGTATCATCTATACAGTGGCAACCTTACAAACCCCGTCC 180
Db 121 AAGGGCTGAGTGGATCGGTATCATCTATACAGTGGCAACCTTACAAACCCCGTCC 180
QY 181 CTCGAAGTGGAGTTACCATGTCTAGTAGACAGTCTAAGAACCACTTCCCTGAGGCTG 240
Db 181 CTCGAAGTGGAGTTACCATGTCTAGTAGACAGTCTAAGAACCACTTCCCTGAGGCTG 240
QY 241 AGCTCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGTCCAGATGGTACACT 300
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QY 301 TTGGACAACCTGGGGCCAGGGAACTTGGTCAACCGTCTCTCTA 342
Db 301 TTGGACAACCTGGGGCCAGGGAACTTGGTCAACCGTCTCTCTA 342

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RESULT 2  
ABK89638

```

ID ABK89638 standard; DNA; 342 BP.
XX AC ABK89638;
XX DT 21-OCT-2002 (first entry)
XX DE DNA encoding human IgE Fab clone 60 heavy chain.
XX KW Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2,
XX OS timothy grass pollen allergen; passive immunotherapy.
XX OS Homo sapiens.
XX FT Key location/Qualifiers
XX FT CDS 1..342
XX FT /*tag= a
XX FT /product= "Fab clone 60 heavy chain"
XX FT /*tag= b
XX FT /note= "FR1 region"
XX FT /*tag= c
XX FT /note= "CDR1 region"
XX FT /*tag= d
XX FT /note= "FR2 region"
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XX FT /note= "FR3 region"
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XX FT /note= "FR3 region"
XX FT /*tag= h
XX FT /note= "CDR3 region"
XX FT /*tag= i
XX FT /note= "FR4 region"
XX PN WO200253595-A1.
XX PD 11-JUL-2002.
XX PF 27-DEC-2001; 2001WO-SE002908.
XX PR 29-DEC-2000; 2000SE-00004892.
XX PA (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX P-PSDB; ABG30446.
XX PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX PT variable region of group 2 allergen specific-human IgE Fabs, useful for
XX PT diagnosing or passive immunotherapy of type I allergy, for environmental
XX PT allergen detection.
XX PS Disclosure; Page 32; 45pp; English.
XX CC This invention relates to the DNA and protein sequences of group 2
XX CC allergen-specific human IgE Fabs and methods for their use. The proteins
XX CC of the invention may have antiallergic activities and may be used as a
XX CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
XX CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX CC 2 allergen-specific fabs of the invention may be useful for environmental
XX CC allergen detection and for standardisation of allergen extracts. The fabs
XX CC - or a vaccine against a type I allergy is useful for diagnosing a type
XX CC I allergy. It is also useful for diagnosing a type

```



CC I allergy. The allergen-specific fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the DNA  
 CC encoding the human IgE fab, clone 60 heavy chain protein of the invention  
 XX

Sequence 342 BP; 70 A; 105 C; 90 G; 77 T; 0 U; 0 Other;

Query Match 94.4%; Score 322.8; DB 6; Length 342;  
 Best Local Similarity 96.5%; Pred. No. 5.1e-81;  
 Matches 330; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 CTCGAGTCTGGCCCGAGAGCTGTGTAAGCCTTCAAGACCTTCCCTGACCTGCACTGTC 60  
 Db 1 CTCGAGTCTGGCCCGAGAGCTGTGTAAGCCTTCAAGACCTTCCCTGACCTGCACTGTC 60  
 Qy 61 TCTGAGTCTCCATCCGAGTGTGTATTATTAATGAGTTGAGTCCGACGCTCCAGGG 120  
 Db 61 TCTGAGTCTCCATCCGAGTGTGTATTATTAATGAGTTGAGTCCGACGCTCCAGGG 120  
 Qy 121 AAGGCTCTGAGTGTGATGAGTGTATATCAATGAGTGTGAGTGTGAGTGTGAGTGTG 180  
 Db 121 AAGGCTCTGAGTGTGATGAGTGTATATCAATGAGTGTGAGTGTGAGTGTGAGTGTG 180  
 Qy 181 CTCGAGTCTGAGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 240  
 Db 181 CTCGAGTCTGAGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 240  
 Qy 241 AGCTCTGTGACTGCGCGGAGACGCGCTGTATTACTGTGCGAGTGTGAGTGTGACT 300  
 Db 241 AGCTCTGTGACTGCGCGGAGACGCGCTGTATTACTGTGCGAGTGTGAGTGTGACT 300  
 Qy 301 TTGAGCACTGGGGCCAGGGAACCTTGTGACCGTCTCTCA 342  
 Db 301 TTGAGCACTGGGGCCAGGGAACCTTGTGACCGTCTCTCA 342

## RESULT 3

ABK89637  
 ID ABK89637 standard; DNA; 342 BP.

AC ABK89637;

DT 21-Oct-2002 (first entry)

XX DNA encoding human IgE Fab clone 94 heavy chain.

XX Human; fab; ds; gene; anti-allergic; vaccine; grass pollen; Phi p 2;

KM timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..342  
 FT /tag= a  
 FT /product= "Fab clone 94 heavy chain"

FT misc\_feature 7..78  
 FT /tag= b  
 FT /note= "FRI region"

FT misc\_feature 79..99  
 FT /tag= c  
 FT /note= "CDR1 region"

FT misc\_feature 100..123  
 FT /tag= d  
 FT /note= "FR2 region"

FT misc\_feature 134..141  
 FT /tag= e  
 FT /note= "FR3 region"

FT misc\_feature 142..189  
 FT /tag= f  
 FT /note= "CDR2 region"

FT misc\_feature 190..285

FT /tag= g  
 FT /note= "FR3 region"  
 FT misc\_feature 286..309  
 FT /tag= h  
 FT /note= "CDR3 region"  
 FT misc\_feature 310..342  
 FT /tag= i  
 FT /note= "FR4 region"

XX WO200253595-A1.

XX 11-JUL-2002.

XX 27-DEC-2001; 2001WO-SE002308.

XX 29-DEC-2000; 2000SE-00004892.

XX (PHAA ) PHARMACIA DIAGNOSTICS AB.

XX Flicker S, Steinberger P, Kraft D, Valenta R;

XX WPI; 2002-583604/62.

XX P-PSDB; ABG30445.

PT Group 2 allergen-specific immunoglobulins (Ig) E fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.

XX Disclosure; Page 31-32; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE fabs and methods for their use. The proteins  
 CC of the invention may have anti-allergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE  
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the DNA  
 CC encoding the human IgE fab, clone 94 heavy chain protein of the invention  
 XX

Sequence 342 BP; 69 A; 100 C; 98 G; 75 T; 0 U; 0 Other;

Query Match 90.2%; Score 308.4; DB 6; Length 342;  
 Best Local Similarity 93.9%; Pred. No. 5.9e-77;  
 Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CTCGAGTCTGGCCCGAGAGCTGTGTAAGCCTTCAAGACCTTCCCTGACCTGCACTGTC 60  
 Db 1 CTCGAGTCTGGCCCGAGAGCTGTGTAAGCCTTCAAGACCTTCCCTGACCTGCACTGTC 60  
 Qy 61 TCTGAGTCTCCATCCGAGTGTGTATTATTAATGAGTTGAGTCCGACGCTCCAGGG 120  
 Db 61 TCTGAGTCTCCATCCGAGTGTGTATTATTAATGAGTTGAGTCCGACGCTCCAGGG 120  
 Qy 121 AAGGCTCTGAGTGTGATGAGTGTATATCAATGAGTGTGAGTGTGAGTGTGAGTGTG 180  
 Db 121 AAGGCTCTGAGTGTGATGAGTGTATATCAATGAGTGTGAGTGTGAGTGTGAGTGTG 180  
 Qy 181 CTCGAGTCTGAGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 240  
 Db 181 CTCGAGTCTGAGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 240  
 Qy 241 AGCTCTGTGACTGCGCGGAGACGCGCTGTATTACTGTGCGAGTGTGAGTGTGACT 300  
 Db 241 AGCTCTGTGACTGCGCGGAGACGCGCTGTATTACTGTGCGAGTGTGAGTGTGACT 300

QY 301 TTGGACAATTGGGGCCAGGAAACCTTGTCACCGTCTCTCA 342  
DB 301 TTGGACAATTGGGGCCAGGAAACCTTGTCACCGTCTCTCA 342

RESULT 4  
ADCC9786  
ID ADCC9786 standard; DNA, 352 BP.  
XX  
XX ADCC9786;  
AC  
XX  
DT 01-JAN-2004 (first entry)  
XX  
XX Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 15.  
DE  
XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
XX cytostatic; melanoma; oesophageal; pancreatic; colorectal tumor;  
KM cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KM lung cancer; human; ds; gene.  
XX  
XX Homo sapiens.  
OS  
XX WO2003057838-A2.  
PN  
XX 17-JUL-2003.  
PD  
XX 26-DEC-2002; 2002WO-US041581.  
PF  
XX 28-DEC-2001; 2001US-0346299P.  
PR  
XX  
XX (ABGE-) ABGENIX INC.  
PA  
XX  
XX Gudas J;  
PI  
XX  
XX WPI: 2003-587113/55.  
DR P-PSDB; ADCC9784.  
XX  
PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
PT or condition associated with expression of MUC18 in a patient, e.g.  
PT tumors, cancers, and other malignancies.  
XX  
XX  
PS Claim 8; SEQ ID NO 15; 78pp; English.

CC The invention relates to a novel isolated monoclonal antibody comprising  
CC a heavy or light chain amino acid or a heavy or light chain variable  
CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
CC invention demonstrates cytostatic activity and may be useful for treating  
CC a disease or condition associated with the expression of MUC18 on the  
CC cell surface such as tumors, specifically melanoma, oesophageal,  
CC pancreatic or colorectal tumors, carcinomas, particularly cervical  
CC carcinomas and cervical intraepithelial neoplasia and cancers including  
CC colorectal, breast or lung cancer, as well as other malignancies. The  
CC current sequence is that of the anti-human MUC18 monoclonal antibody  
CC heavy chain variable domain DNA of the invention.  
XX  
XX  
SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match 83.2%; Score 284.6; DB 10; Length 352;  
Best Local Similarity 92.0%; Pred. No. 3.1e-70;  
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 4 GAGTCTGACCCAGAGACTGTGAAGCCTTGACAGACCTGTCTCCTGACTGTCTCT 63  
DB 16 GAGTCTGACCCAGAGACTGTGAAGCCTTGACAGACCTGTCTCCTGACTGTCTCT 75  
QY 64 GGTGGCTCCACATCCCAAGGTGTGTATTAATGAGATTGAGATCCCGACGTCAGGAG 123  
DB 76 GGTGGCTCCACATCCCAAGGTGTGTATTAATGAGATTGAGATCCCGACGTCAGGAG 135  
QY 124 GGCCTGAGTGAATCGGGTACATCATCAAGTGGACAACCTTCAACACCCGTCCTC 183  
DB 136 GGCCTGAGTGAATCGGGTACATCATTAACAGTGGAGCACTTACTACACCCGTCCTC 195

QY 184 AAGAGTGAATTACCATGTGTAGACAGCTTTAAGAACCACTTCTCCCTGAGCTGAGC 243  
DB 196 AAGAGTGAATTACCATGTGTAGACAGCTTTAAGAACCACTTCTCCCTGAGCTGAGC 255  
QY 244 TCTGTGACTGCGCGGACACAGCGCGGTATTAATGAGATTGAGATGGGTACACTTGG 303  
DB 256 TCTGTGACTGCGCGGACACAGCGCGGTATTAATGAGATTGAGATGGGTACACTTGG 312  
QY 304 GACAACTGGGGCCAGGAAACCTTGTCACCGTCTCTCA 342  
DB 313 GAACTAGTGGGGCCAGGAAACCTTGTCACCGTCTCTCA 351

RESULT 5  
ADD05390  
ID ADD05390 standard; DNA, 352 BP.  
XX  
XX ADD05390;  
AC  
XX 01-JAN-2004 (first entry)  
DT  
XX  
XX Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 15.  
DE  
XX monoclonal antibody; tumor; MUC18; proliferation; cytostatic; vaccine;  
KM antigen; tumor metastasis; melanoma; metastatic; human; heavy chain;  
KM gene; ds.  
XX  
XX Homo sapiens.  
OS  
XX WO2003057006-A2.  
PN  
XX 17-JUL-2003.  
PD  
XX 26-DEC-2002; 2002WO-US041582.  
PF  
XX 28-DEC-2001; 2001US-0346460P.  
PR  
XX  
XX (ABGE-) ABGENIX INC.  
PA  
XX  
XX Gudas J, Bar-El M;  
PI  
XX  
XX WPI: 2003-577496/54.  
DR P-PSDB; ADD05388.  
XX  
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
PT associated with melanoma, or increasing survival of an animal having a  
PT metastatic tumor.  
XX  
XX  
PS Disclosure; SEQ ID NO 15; 87pp; English.

CC The invention relates to a novel monoclonal antibody used for inhibiting  
CC tumor growth in an animal. The tumor inhibition process comprises  
CC selecting an animal in need of treatment for a tumor, providing a  
CC monoclonal antibody comprising a heavy chain amino acid, where the  
CC antibody consists of any one of 10 fully defined sequences of 117-123  
CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumor with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumors, inhibiting tumor growth (e.g. melanoma, lung tumor or  
CC tumor metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumor. This  
CC polynucleotide sequence represents the DNA encoding an anti-MUC18  
CC antibody heavy chain, variable region, protein of the invention.  
XX  
XX  
SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match 83.2%; Score 284.6; DB 10; Length 352;  
Best Local Similarity 92.0%; Pred. No. 3.1e-70;  
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGAGCTGTGTAAGCCCTTACAGACCCTGTCTCCCTGACCTGTGCTCT 63  
 DB 16 GAGTCGGGCCAGGAGCTGTGTAAGCCCTTACAGACCCTGTCTCCCTGACCTGTGCTCT 75  
 QY 64 GGTGGCTCCATCCGAGTGTGTGTTATTAATCTGAGATTGATCCGCCAGCGTCCAGGGAG 123  
 DB 76 GGTGGCTCCATCCGAGTGTGTGTTATTAATCTGAGATTGATCCGCCAGCGTCCAGGGAG 135  
 QY 124 GGCCTGGAGTGGAGTGGGATCATCTATCATAGTGGCAACCTTAACAACCCGCTCCCTC 183  
 DB 136 GGCCTGGAGTGGAGTGGGATCATCTATCATAGTGGCAACCTTAACAACCCGCTCCCTC 195  
 QY 184 AAGAGTCGAGTTACATATCATATGAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243  
 DB 196 AAGAGTCGAGTTACATATCATATGAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255  
 QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGGTGATGGGTACACTTTG 303  
 DB 256 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAG--AGAGGGAGATGGCTTT 312  
 QY 304 GACAACCTGGGGCCAGGGAACCCGTGTACCGCTCTCTCTCA 342  
 DB 313 GACTACTGGGGCCAGGGAACCCGTGTACCGCTCTCTCTCA 351

## RESULT 6

ADP09828 ID ADF09828 standard; DNA, 352 BP.

AC ADF09828;

DT 12-FEB-2004 (first entry)

DE Human anti-MUC18 monoclonal antibody heavy chain coding sequence #4.

XX cell proliferation inhibitor; MUC18 tumour antigen;

KM anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;

KW carcinoma; cancer; malignancy; heavy chain; human; de; gene.

XX Homo sapiens.

XX WO2003057837-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041580.

XX 28-DEC-2001; 2001US-0346414P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-598367/56.

XX P-PSDB; ADF09826.

XX Inhibiting cell proliferation associated with expression of MUC18 tumor

XX antigen, involves incubating and inhibiting cell by administering anti-

XX MUC18 monoclonal antibody.

XX Disclosure: SEQ ID NO 15; 83bp; English.

XX The invention comprises a method for inhibiting cell proliferation

XX associated with expression of MUC18 tumour antigen. The method involves

XX administering anti-MUC18 monoclonal antibody. The method of the invention

XX is useful for inhibiting cell (e.g. melanoma or tumour cell)

XX proliferation associated with the expression of MUC18 tumour antigen, the

XX method is preferably useful for inhibiting tumour metastasis. The method

XX is useful for inhibiting cell proliferation in patients with tumours,

XX carcinoma, cancer and other malignancies. The present DNA sequence

XX encodes a heavy chain from an MUC18 tumour antigen-specific monoclonal

XX antibody.

SEQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match 83.2%; Score 284.6; DB 10; Length 352;

Best Local Similarity 92.0%; Pred. No. 3,1e-70;

Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGAGCTGTGTAAGCCCTTACAGACCCTGTCTCCCTGACCTGTGCTCT 63  
 DB 16 GAGTCGGGCCAGGAGCTGTGTAAGCCCTTACAGACCCTGTCTCCCTGACCTGTGCTCT 75  
 QY 64 GGTGGCTCCATCCGAGTGTGTGTTATTAATCTGAGATTGATCCGCCAGCGTCCAGGGAG 123  
 DB 76 GGTGGCTCCATCCGAGTGTGTGTTATTAATCTGAGATTGATCCGCCAGCGTCCAGGGAG 135  
 QY 124 GGCCTGGAGTGGAGTGGGATCATCTATCATAGTGGCAACCTTAACAACCCGCTCCCTC 183  
 DB 136 GGCCTGGAGTGGAGTGGGATCATCTATCATAGTGGCAACCTTAACAACCCGCTCCCTC 195  
 QY 184 AAGAGTCGAGTTACATATCATATGAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243  
 DB 196 AAGAGTCGAGTTACATATCATATGAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255  
 QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGGTGATGGGTACACTTTG 303  
 DB 256 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAG--AGAGGGAGATGGCTTT 312  
 QY 304 GACAACCTGGGGCCAGGGAACCCGTGTACCGCTCTCTCTCA 342  
 DB 313 GACTACTGGGGCCAGGGAACCCGTGTACCGCTCTCTCTCA 351

## RESULT 7

AAF29076 ID AAF29076 standard; DNA, 360 BP.

AC AAF29076;

DT 03-APR-2001 (first entry)

DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 32.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;

XX envelope glycoprotein; gp120; diagnosis; de.

XX Homo sapiens.

XX WO200100678-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-US017327.

XX 30-JUN-1999; 99US-0141701P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Wackins BA, Reitz MS;

XX WPI; 2001-112438/12.

XX P-PSDB; AAB62775.

XX Novel human monoclonal antibody immunoreactive with human

XX immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

XX in biological sample and providing passive immunotherapy to HIV-1

XX infected mammal.

XX Claim 4; Page 45; 81bp; English.

XX The present invention provides the protein and coding sequences for the

XX variable regions of human monoclonal antibodies which are immunoreactive

XX with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.

XX These can be used in diagnosis and therapy of HIV-1 infection

Sequence 360 BP; 73 A; 104 C; 107 G; 76 T; 0 U; 0 Other;

Query Match 83.2%; Score 284.4; DB 4; Length 360;  
Best Local Similarity 91.5%; Pred. No. 3.5e-70;  
Matches 313; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 4 GAGCTGAGCCAGAGCTGTGAAGCTTTCACAGACCCCTGCTCCCTGACCTGACGTCTCT 63  
DB 19 GAGTGGGAGCCAGAGCTGTGAAGCTTTCACAGACCCCTGCTCCCTGACCTGACGTCTCT 78  
QY 64 GGTGGCTCCATCCGACGTGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 123  
DB 79 GGTGGCTCCATCCGACGTGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 138  
QY 124 GGCCTGAGTGTGATCGGGATCATTTATTCACAGTGGGCAACACCTTCAACACCCGCTCTC 183  
DB 139 GGCCTGAGTGTGATCGGGATCATTTATTCACAGTGGGCAACACCTTCAACACCCGCTCTC 198  
QY 184 AAGAGTGAAGTATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243  
DB 199 AAGAGTGAAGTATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 258  
QY 244 TCTGTGACTGCGCGGACACGCGCGGTATTAATTAATTAATTAATTAATTAATTAATTAAT 300  
DB 259 TCTGTGACTGCGCGGACACGCGCGGTATTAATTAATTAATTAATTAATTAATTAATTAAT 318  
QY 301 TTGGACAACTGGGGCCAGGGAAACCTGTGACCGCTCTCTCA 342  
DB 319 TTGGACAACTGGGGCCAGGGAAACCTGTGACCGCTCTCTCA 360

RESULT 8  
ADS84403  
ID ADS84403 standard; DNA; 354 BP.

ADS84403;

18-NOV-2004 (first entry)

Human anti-EPO-R antibody heavy chain variable region DNA SEQ ID NO:42.

human; erythropoietin receptor; EPO receptor;  
erythropoietin receptor binding antibody; EPO receptor binding antibody;  
antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;  
wound healing; neural cell damage protection;  
neural tissue damage protection; brain injury; spinal cord injury;  
stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;  
ds.

OS Homo sapiens.

PN WO2004035603-A2.

PD 29-APR-2004.

PF 14-OCT-2003; 2003WO-US032243.

PR 14-OCT-2002; 2002US-00269711.

PR 10-OCT-2003; 2003US-00684109.

PA (ABBO ) ABBOTT LAB.

PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wielek J;

DR WPI; 2004-348433/32.

DR P-PSDB; ADS84404.

PT New antibodies that bind to or activate an endogenous human  
erythropoietin receptor, useful for diagnosing, preventing or treating  
disorders associated with dysfunctional erythropoietin receptor, e.g.  
anemia.

PS Claim 47; SEQ ID NO 42; 192pp; English.

XX The present invention describes an antibody or its fragment that binds to  
CC or activates an endogenous activity of a human erythropoietin (EPO)  
CC receptor in a mammal, but does not interact with a peptide having a  
CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
CC methods of modulating or activating an endogenous activity of a human EPO  
CC receptor in a mammal, comprising administering to the mammal a  
CC therapeutic amount of the above antibody or its fragment to modulate or  
CC activate the receptor; (2) a method of treating a mammal suffering from  
CC aplasia, comprising administering to the mammal a therapeutic amount of  
CC the above antibody or its fragment to modulate or activate the receptor;  
CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
CC an isolated and purified polynucleotide sequence, and their fragments,  
CC complemented and degenerate codon equivalents; and (5) an isolated and  
CC purified amino acid sequence, and their fragments. The EPO receptor  
CC binding antibody has antianaemic, neuroprotective and vulnerary  
CC activities, and can be used in gene therapy. The compositions and methods  
CC from the present invention can be used for modulating an endogenous  
CC activity of a human EPO receptor or for treating mammals suffering from  
CC aplasia or anaemia. They may also be used for identifying mammals having  
CC a dysfunctional EPO receptor. The composition may also be used in  
CC promoting wound healing or in protecting against neural cell and/or  
CC tissue damage resulting from brain/spinal cord injury, stroke and the  
CC like. The present sequence encodes a human anti-EPO-R antibody heavy  
CC chain variable region, which is given in the exemplification of the  
CC present invention.

Sequence 354 BP; 76 A; 105 C; 97 G; 76 T; 0 U; 0 Other;

Query Match 80.9%; Score 276.6; DB 13; Length 354;  
Best Local Similarity 88.5%; Pred. No. 5.5e-66;  
Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 4 GAGCTGAGCCAGAGCTGTGAAGCTTTCACAGACCCCTGCTCCCTGACCTGACGTCTCT 63  
DB 16 GAGTGGGAGCCAGAGCTGTGAAGCTTTCACAGACCCCTGCTCCCTGACCTGACGTCTCT 75  
QY 64 GGTGGCTCCATCCGACGTGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 123  
DB 76 GGTGGCTCCATCCGACGTGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 135  
QY 124 GGCCTGAGTGTGATCGGGATCATTTATTCACAGTGGGCAACACCTTCAACACCCGCTCTC 183  
DB 136 GGCCTGAGTGTGATCGGGATCATTTATTCACAGTGGGCAACACCTTCAACACCCGCTCTC 195  
QY 184 AAGAGTGAAGTATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243  
DB 196 AAGAGTGAAGTATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 255  
QY 244 TCTGTGACTGCGCGGACACGCGCGGTATTAATTAATTAATTAATTAATTAATTAATTAAT 303  
DB 256 TCTGTGACTGCGCGGACACGCGCGGTATTAATTAATTAATTAATTAATTAATTAATTAAT 315  
QY 304 GACCACTGGGGCCAGGGAAACCTGTGACCGCTCTCTCA 342  
DB 316 GACCACTGGGGCCAGGGAAACCTGTGACCGCTCTCTCA 354

RESULT 9  
ADR68545  
ID ADR68545 standard; DNA; 354 BP.

ADR68545;

02-DEC-2004 (first entry)

Anti-EPO-R-antibody heavy chain variable region DNA seqid 42.

antianaemic; respiratory; vulnerary; gene therapy; vaccine;  
erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
wound healing; neural cell damage; tissue damage; brain injury;

KM spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;  
 KM variable region; ds.  
 OS Homo sapiens.  
 XX US2004175379-A1.  
 XX  
 PD 09-SEP-2004.  
 XX  
 PF 10-OCT-2003; 2003US-00684109.  
 XX  
 PR 14-OCT-2002; 2002US-0418031P.  
 XX  
 PA (DEVIR/) DEVIRIES P J.  
 PA (OSTRO/) OSTROW D H.  
 PA (REIL/) REILLY E B.  
 PA (GREEN/) GREEN L L.  
 PA (WIELER/) WIELER J.  
 XX  
 PI Deviries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;  
 XX  
 DR WPI; 2004-661369/64.  
 DR P-PSDB; ADR68546.  
 XX  
 PT New antibody or its antibody fragment that activates an endogenous  
 PT activity or is capable of binding to a human erythropoietin receptor in a  
 PT mammal, useful for treating a mammal suffering aplasia or anemia.  
 XX  
 PS Claim 47; SEQ ID NO 42; 156pp; English.  
 XX  
 XX The invention describes an antibody or its fragment that activates an  
 XX endogenous activity or capable of binding to a human erythropoietin  
 XX receptor in a mammal, or that comprises at least one heavy or light chain  
 XX variable region having a sequence comprising 116 or 107 amino acids (SEQ  
 XX ID NO: 3 or 5) given in the specification or its fragment, but does not  
 XX interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
 XX given in the specification. Also described are: a method of activating or  
 XX modulating an endogenous activity of a human erythropoietin receptor in a  
 XX mammal; a pharmaceutical composition comprising a therapeutic amount of  
 XX an antibody or antibody fragment above and a pharmaceutical excipient; an  
 XX isolated and purified polynucleotide sequence selected from 28 sequences  
 XX comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in  
 XX the specification, and their fragments, complements, and degenerate codon  
 XX equivalents; and an isolated and purified amino acid sequence selected  
 XX from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between  
 XX SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
 XX their fragments. The antibody or its antibody fragment that activates or  
 XX modulates the activity of the receptor is useful in a method of treating  
 XX a mammal suffering aplasia or anemia. The antibodies are also useful for  
 XX treating disorders characterised by decreased or subnormal levels of  
 XX oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
 XX hypoxia and/or diseases characterised by inadequate blood circulation or  
 XX reduced blood flow. They are also useful for promoting wound healing or  
 XX for protecting against neural cell and/or tissue damage, resulting from  
 XX brain/spinal cord injury, stroke and the like. The antibodies are also  
 XX useful for identifying or diagnosing mammals having dysfunctional  
 XX erythropoietin receptor. This sequence encodes an anti-EPO-R-antibody  
 XX heavy chain variable region.  
 XX  
 SQ Sequence 354 BP; 76 A; 105 C; 97 G; 76 T; 0 U; 0 Other;  
 XX  
 Query Match 80.9%; Score 276.6; DB 13; Length 354;  
 Best Local Similarity 88.5%; Fred. No. 5.5e-68;  
 Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
 OY 4 GAGTGTGGCCGAGGAGTGGTGAAGCTTACAGAGCCCTGCTCCCTACCTGACGTGTCTCT 63  
 DB 16 GAGTGTGGCCGAGGAGTGGTGAAGCTTACAGAGCCCTGCTCCCTACCTGACGTGTCTCT 75  
 OY 64 GGTGGCTTCATCCGAGTGGTGGTATTACTGAGAGTTGGATTCGCGACGCTTCCAGGAG 123  
 DB 76 GGTGGCTTCATCCGAGTGGTGGTATTACTGAGAGTTGGATTCGCGACGCGACGCGAGGAG 135

OY 124 GGCTGTGAGTGGATCGGCTACATCTATACAGTGGCAACACCTAACACCCGTCTC 183  
 DB 136 GGCTGTGAGTGGATTTGGGTATCATCTATTAAGAGACCTCTCTACCAACCCGCTCTC 195  
 OY 184 AAGAGTGAATTACCATGTCACTAGACACGCTTAAAGAACCTTCTCTGAGCTGAGC 243  
 DB 196 AAGAGTGAATTACCATGTCACTAGACACGCTTAAAGAACCTTCTCTGAGCTGAGC 255  
 OY 244 TCTGTGACTGCGCGGAGACAGCGCGCTGTATTACTGTGCGAGGTGAGATGGTACACTT 303  
 DB 256 TCTGTGACTGCGCGGAGACAGCGCGCTGTATTATTGTGAGAGATTAACCTGGGATTCGCG 315  
 OY 304 GACAACTGGGGCCGAGGAGAACCTGTGATCAACCTCTCTCTCA 342  
 DB 316 GACTACTGGGGCCGAGGAGAACCTGTGATCAACCTCTCTCTCA 354  
 XX  
 XX RESULT 10  
 XX ADS84454/C  
 XX ID ADS84454 standard; DNA; 1996 BP.  
 XX  
 XX ADS84454;  
 XX  
 XX 18-NOV-2004 (first entry)  
 XX  
 XX Human anti-EPO-R antibody Ab412 heavy chain complementary DNA SEQ ID:93.  
 XX  
 XX human; erythropoietin receptor; EPO receptor;  
 XX erythropoietin receptor binding antibody; EPO receptor binding antibody;  
 XX antianaemic; neuroprotective; vulnereary; gene therapy; aplasia; anaemia;  
 XX wound healing; neural cell damage protection;  
 XX neural tissue damage protection; brain injury; spinal cord injury;  
 XX stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;  
 XX ds.  
 XX  
 XX Homo sapiens.  
 XX  
 XX US2004035603-A2.  
 XX  
 XX 29-APR-2004.  
 XX  
 XX 14-OCT-2003; 2003WO-US032243.  
 XX  
 XX 14-OCT-2002; 2002US-00269711.  
 XX  
 XX 10-OCT-2003; 2003US-00684109.  
 XX  
 XX (ABBOTT LAB.  
 XX  
 XX Deviries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;  
 XX  
 XX WPI; 2004-348433/32.  
 XX  
 XX P-PSDB; ADS84455.  
 XX  
 XX New antibodies that bind to or activate an endogenous human  
 XX erythropoietin receptor, useful for diagnosing, preventing or treating  
 XX disorders associated with dysfunctional erythropoietin receptor, e.g.  
 XX anemia.  
 XX  
 XX Disclosure; SEQ ID NO 93; 192pp; English.  
 XX  
 XX The present invention describes an antibody or its fragment that binds to  
 XX or activates an endogenous activity of a human erythropoietin (EPO)  
 XX receptor in a mammal, but does not interact with a peptide having a  
 XX sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
 XX methods of modulating or activating an endogenous activity of a human EPO  
 XX receptor in a mammal, comprising administering to the mammal a  
 XX therapeutic amount of the above antibody or its fragment to modulate or  
 XX activate the receptor; (2) a method of treating a mammal suffering from  
 XX aplasia, comprising administering to the mammal a therapeutic amount of  
 XX the above antibody or its fragment to modulate or activate the receptor;  
 XX (3) a pharmaceutical composition comprising a therapeutic amount of the  
 XX above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
 XX an isolated and purified polynucleotide sequence, and their fragments,

CC complements and degenerate codon equivalents; and (5) an isolated and  
 CC purified amino acid sequence, and their fragments. The EPO receptor  
 CC binding antibody has antineutropenic, neuroprotective and vlnnerary  
 CC activities, and can be used in gene therapy. The compositions and methods  
 CC from the present invention can be used for modulating an endogenous  
 CC activity of a human EPO receptor or for treating mammals suffering from  
 CC aplasia or anaemia. They may also be used for identifying mammals having  
 CC a dysfunctional EPO receptor. The composition may also be used in  
 CC promoting wound healing or in protecting against neural cell and/or  
 CC tissue damage resulting from brain/spinal cord injury, stroke and the  
 CC like. The present sequence represents a human anti-EPO-R antibody heavy  
 CC chain complementary DNA sequence, which is given in the exemplification  
 CC of the present invention.

XX  
 XX Sequence 1996 BP; 351 A; 537 C; 686 G; 422 T; 0 U; 0 Other;  
 SQ

Query Match 80.9%; Score 276.6; DB 13; Length 1996;  
 Best Local Similarity 88.5%; Pred. No. 8.6e-68;  
 Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 4 GAGTCTGAGCCAGAGCTGTGAGACCTTACAGACCCCTGCTCCCTGACCTGCTCTCT 63  
 DB 1924 GAGTCGGGCCCCAGAGCTGTGAGACCTTACAGACCCCTGCTCCCTGACCTGCTCTCT 1865

QY 64 GGTGGCTCCATCCCGAGTGTGTATTATTAATCTGAGTTGATCCGCCAGCTCCAGGAG 123  
 DB 1864 GGTGCTCCATCCCGAGTGTGTATTATTAATCTGAGTTGATCCGCCAGCTCCAGGAG 1805

QY 124 GGCCTGAGTGTGATCGGGTATCATCTATCATAGTGGCAACCTTCAACCAACCCGCTCC 183  
 DB 1804 GGCCTGAGTGTGATCGGGTATCATCTATCATAGTGGCAACCTTCAACCAACCCGCTCC 1745

QY 184 AAGAGTGAAGTATTCATGTCAATGAGACAGCTTAAAGAACCACTTCTCCCTGAGGCTGAGC 243  
 DB 1744 AAGAGTGAAGTATTCATGTCAATGAGACAGCTTAAAGAACCACTTCTCCCTGAGGCTGAGC 1685

QY 244 TCTGTGACTCCCGGAGACAGCGCGGTATTAATCTGAGTTGATCCGCCAGCTCCAGGAG 303  
 DB 1684 TCTGTGACTCCCGGAGACAGCGCGGTATTAATCTGAGTTGATCCGCCAGCTCCAGGAG 1625

QY 304 GACAACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 342  
 DB 1624 GACAACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 1586

RESULT 11  
 ADS84453  
 ID ADS84453 standard; DNA; 1996 BP.  
 AC ADS84453;  
 DX 18-NOV-2004 (first entry)  
 DE Human anti-EPO-R antibody Ab412 heavy chain DNA SEQ ID NO:92.  
 XX  
 XX human; erythropoietin receptor; EPO receptor;  
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
 KW antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;  
 KW wound healing; neural cell damage protection;  
 KW neural tissue damage protection; brain injury; spinal cord injury;  
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;  
 KW db.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 PN NO2004035603-A2.  
 XX  
 PD 29-APR-2004.  
 XX  
 PF 14-OCT-2003; 2003WO-US032243.  
 XX  
 PR 14-OCT-2002; 2002US-00269711.  
 PR 10-OCT-2003; 2003US-00684109.

XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Devices PJ, Green IL, Ostrow DH, Reilly EB, Wieler J;  
 XX  
 DR WPI: 2004-348433/32.  
 DR P-PSDB; ADS84455.  
 XX  
 XX New antibodies that bind to or activate an endogenous human  
 PT erythropoietin receptor, useful for diagnosing, preventing or treating  
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
 PT anemia.  
 XX  
 XX Disclosure; SEQ ID NO 92; 192bp; English.  
 PS  
 XX  
 CC The present invention describes an antibody or its fragment that binds to  
 CC or activates an endogenous activity of a human erythropoietin (EPO)  
 CC receptor in a mammal, but does not interact with a peptide having a  
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
 CC methods of modulating or activating an endogenous activity of a human EPO  
 CC receptor in a mammal, comprising administering to the mammal a  
 CC therapeutic amount of the above antibody or its fragment to modulate or  
 CC activate the receptor; (2) a method of treating a mammal suffering from  
 CC aplasia, comprising administering to the mammal a therapeutic amount of  
 CC the above antibody or its fragment to modulate or activate the receptor;  
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
 CC an isolated and purified polynucleotide sequence; and (5) an isolated and  
 CC complements and degenerate codon equivalents; and (5) an isolated and  
 CC purified amino acid sequence, and their fragments. The EPO receptor  
 CC binding antibody has antineutropenic, neuroprotective and vulnerary  
 CC activities, and can be used in gene therapy. The compositions and methods  
 CC from the present invention can be used for modulating an endogenous  
 CC activity of a human EPO receptor or for treating mammals suffering from  
 CC aplasia or anaemia. They may also be used for identifying mammals having  
 CC a dysfunctional EPO receptor. The composition may also be used in  
 CC promoting wound healing or in protecting against neural cell and/or  
 CC tissue damage resulting from brain/spinal cord injury, stroke and the  
 CC like. The present sequence encodes a human anti-EPO-R antibody heavy  
 CC chain, which is given in the exemplification of the present invention.  
 XX  
 SQ Sequence 1996 BP; 422 A; 686 C; 537 G; 351 T; 0 U; 0 Other;

Query Match 80.9%; Score 276.6; DB 13; Length 1996;  
 Best Local Similarity 88.5%; Pred. No. 8.6e-68;  
 Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 4 GAGTCTGAGCCAGAGCTGTGAGACCTTACAGACCCCTGCTCCCTGACCTGCTCTCT 63  
 DB 73 GAGTCGGGCCCCAGAGCTGTGAGACCTTACAGACCCCTGCTCCCTGACCTGCTCTCT 132

QY 64 GGTGGCTCCATCCCGAGTGTGTATTATTAATCTGAGTTGATCCGCCAGCTCCAGGAG 123  
 DB 133 GGTGCTCCATCCCGAGTGTGTATTATTAATCTGAGTTGATCCGCCAGCTCCAGGAG 192

QY 124 GGCCTGAGTGTGATCGGGTATCATCTATCATAGTGGCAACCTTCAACCAACCCGCTCC 183  
 DB 193 GGCCTGAGTGTGATCGGGTATCATCTATCATAGTGGCAACCTTCAACCAACCCGCTCC 252

QY 184 AAGAGTGAAGTATTCATGTCAATGAGACAGCTTAAAGAACCACTTCTCCCTGAGGCTGAGC 243  
 DB 253 AAGAGTGAAGTATTCATGTCAATGAGACAGCTTAAAGAACCACTTCTCCCTGAGGCTGAGC 312

QY 244 TCTGTGACTCCCGGAGACAGCGCGGTATTAATCTGAGTTGATCCGCCAGCTCCAGGAG 303  
 DB 313 TCTGTGACTCCCGGAGACAGCGCGGTATTAATCTGAGTTGATCCGCCAGCTCCAGGAG 372

QY 304 GACAACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 342  
 DB 373 GACAACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 411

RESULT 12

ADR68595  
 ID ADR68595 standard; DNA; 1996 BP.  
 AC ADR68595;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Human antibody Ab412 heavy chain polynucleotide seqid 92.  
 XX  
 KM antihaemic; respiratory; vulnery; gene therapy; vaccine;  
 KM erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
 KM hypoxemia; chronic tissue hypoxia; blood circulation; blood flow;  
 KM wound healing; neural cell damage; tissue damage; brain injury;  
 KM spinal cord injury; stroke; human; anti-EPO-R-antibody; heavy chain;  
 KM AB412; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004175379-A1.  
 XX  
 PD 09-SEP-2004.  
 XX  
 PF 10-OCT-2003; 2003US-00684109.  
 XX  
 PR 14-OCT-2002; 2002US-0418031P.  
 XX  
 PA (DEVIR/) DEVRIES P J.  
 PA (OSTR/) OSTROW D H.  
 PA (REIL/) REILLY E B.  
 PA (GREE/) GREEN L L.  
 PA (WIEL/) WIELER J.  
 XX  
 PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;  
 DR WPI; 2004-661369/64.  
 DR P-PSDB; ADR68597, ADR68576, ADR68577.  
 XX  
 PT New antibody or its antibody fragment that activates an endogenous  
 PT activity or is capable of binding to a human erythropoietin receptor in a  
 PT mammal, useful for treating a mammal suffering aplasia or anemia.  
 PT  
 PS Disclosure; SEQ ID NO 92; 156pp; English.  
 XX  
 XX The invention describes an antibody or its fragment that activates an  
 CC endogenous activity or capable of binding to a human erythropoietin  
 CC receptor in a mammal, or that comprises at least one heavy or light chain  
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
 CC given in the specification. Also described are: a method of activating or  
 CC modulating an endogenous activity of a human erythropoietin receptor in a  
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
 CC isolated and purified polynucleotide sequence selected from 28 sequences  
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in  
 CC the specification, and their fragments, complements, and degenerate codon  
 CC equivalents; and an isolated and purified amino acid sequence selected  
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between  
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
 CC their fragments. The antibody or its antibody fragment that activates or  
 CC modulates the activity of the receptor is useful in a method of treating  
 CC a mammal suffering aplasia or anemia. The antibodies are also useful for  
 CC treating disorders characterised by decreased or subnormal levels of  
 CC oxygen in the blood or tissue such as hypoxemia or chronic tissue  
 CC hypoxia and/or diseases characterised by inadequate blood circulation or  
 CC reduced blood flow. They are also useful for promoting wound healing or  
 CC for protecting against neural cell and/or tissue damage, resulting from  
 CC brain/spinal cord injury, stroke and the like. The antibodies are also  
 CC useful for identifying or diagnosing mammals having dysfunctional  
 CC erythropoietin receptor. This sequence represents a human Ab412 antibody  
 CC heavy chain polynucleotide.  
 XX  
 SQ Sequence 1996 BP; 422 A; 686 C; 537 G; 351 T; 0 U; 0 Other;

Query Match 80.9%; Score 276.6; DB 13; Length 1996;  
 Best Local Similarity 88.5%; Pred. No. 8.66-68;  
 Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
 QY 4 GAGTCTGGCCCAAGAGCTGTGTAAGCCCTTCACAGACCTGTCTCCCTGCATGCTGTCT 63  
 DB 73 GAGTCTGGCCCAAGAGCTGTGTAAGCCCTTCACAGACCTGTCTCCCTGCATGCTGTCT 132  
 QY 64 GGTGCTCCATCCAGCTGCTGTGTAAGCCCTTCACAGACCTGTCTCCCTGCATGCTGTCT 123  
 DB 133 GGTGCTCCATCCAGCTGCTGTGTAAGCCCTTCACAGACCTGTCTCCCTGCATGCTGTCT 192  
 QY 124 GGCCTGAGTGTGATGCTGTGTAAGCCCTTCACAGACCTGTCTCCCTGCATGCTGTCT 183  
 DB 193 GGCCTGAGTGTGATGCTGTGTAAGCCCTTCACAGACCTGTCTCCCTGCATGCTGTCT 252  
 QY 184 AAGAGTGGAGTGTGATGCTGTGTAAGCCCTTCACAGACCTGTCTCCCTGCATGCTGTG 243  
 DB 253 AAGAGTGGAGTGTGATGCTGTGTAAGCCCTTCACAGACCTGTCTCCCTGCATGCTGTG 312  
 QY 244 TCTGTGACTGCGGCGGACACGCGCGTGTATTTGTCGAGATGATGATGATGATGATG 303  
 DB 313 TCTGTGACTGCGGCGGACACGCGCGTGTATTTGTCGAGATGATGATGATGATGATG 372  
 QY 304 GACAACCTGGGCGGCGGACACGCGCGTGTATTTGTCGAGATGATGATGATGATGATG 342  
 DB 373 GACTTCTGGGCGGCGGACACGCGCGTGTATTTGTCGAGATGATGATGATGATGATG 411  
 RESULT 13  
 ADR68596/c  
 ID ADR68596 standard; DNA; 1996 BP.  
 AC ADR68596;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Human antibody Ab412 heavy chain polynucleotide seqid 93.  
 XX  
 KM antihaemic; respiratory; vulnery; gene therapy; vaccine;  
 KM erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
 KM hypoxemia; chronic tissue hypoxia; blood circulation; blood flow;  
 KM wound healing; neural cell damage; tissue damage; brain injury;  
 KM spinal cord injury; stroke; human; anti-EPO-R-antibody; heavy chain;  
 KM AB412; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004175379-A1.  
 XX  
 PD 09-SEP-2004.  
 XX  
 PF 10-OCT-2003; 2003US-00684109.  
 XX  
 PR 14-OCT-2002; 2002US-0418031P.  
 XX  
 PA (DEVIR/) DEVRIES P J.  
 PA (OSTR/) OSTROW D H.  
 PA (REIL/) REILLY E B.  
 PA (GREE/) GREEN L L.  
 PA (WIEL/) WIELER J.  
 XX  
 PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;  
 DR WPI; 2004-661369/64.  
 XX  
 PT New antibody or its antibody fragment that activates an endogenous  
 PT activity or is capable of binding to a human erythropoietin receptor in a  
 PT mammal, useful for treating a mammal suffering aplasia or anemia.  
 PT  
 PS Disclosure; SEQ ID NO 93; 156pp; English.  
 XX



CC The invention describes an antibody or its fragment that activates an  
CC endogenous activity or capable of binding to a human erythropoietin  
CC receptor in a mammal, or that comprises at least one heavy or light chain  
CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
CC given in the specification. Also described are: a method of activating or  
CC modulating an endogenous activity of a human erythropoietin receptor in a  
CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
CC isolated and purified polynucleotide sequence selected from 28 sequences  
CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in  
CC the specification, and their fragments, complements, and degenerate codon  
CC equivalents; and an isolated and purified amino acid sequence selected  
CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between  
CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
CC their fragments. The antibody or its antibody fragment that activates or  
CC modulates the activity of the receptor is useful in a method of treating  
CC a mammal suffering aplasia or anaemia. The antibodies are also useful for  
CC treating disorders characterised by decreased or subnormal levels of  
CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
CC hypoxia and/or diseases characterised by inadequate blood circulation or  
CC reduced blood flow. They are also useful for promoting wound healing or  
CC for protecting against neural cell and/or tissue damage, resulting from  
CC brain/spinal cord injury, stroke and the like. The antibodies are also  
CC useful for identifying or diagnosing mammals having dysfunctional  
CC erythropoietin receptor. This sequence represents a human Ab412 antibody  
CC heavy chain polynucleotide.

XX Sequence 1996 BP; 351 A; 537 C; 686 G; 422 T; 0 U; 0 Other;

Query Match 80.9%; Score 276.6; DB 13; Length 1996;  
Best Local Similarity 88.5%; Pred. No. 8.6e-68;

Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 4 GAGCTGAGCCAGGACTGGTGAACCTTCACAGACCCGTGCTCCACCTGACGTCTCT 63  
DB 1924 GAGTCGGGCCAGGACTGGTGAACCTTCACAGACCCGTGCTCCACCTGACGTCTCT 1865  
QY 64 GGTGGCTCCATCCGACGTGTGTATTACTGAGTTGATCCGCCAGCGTCCAGGGAAG 123  
DB 1864 GGTGGCTCCATCCGACGTGTGTATTACTGAGTTGATCCGCCAGCGTCCAGGGAAG 1805  
QY 124 GGCTTGAGTGAATCGGATCATCTATCAGATGAGCAACCTTAACAACCCGTCCCTC 183  
DB 1804 GGCTTGAGTGAATCGGATCATCTATCAGATGAGCAACCTTAACAACCCGTCCCTC 1745  
QY 184 AAGAGTGAATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243  
DB 1744 AAGAGTGAATTAACATGATGATGATGATGATGATGATGATGATGATGATGATG 1685  
QY 244 TCTGTGACTGCGCGGACACGCGCGTATTAATTAATTAATTAATTAATTAATTAATTA 303  
DB 1684 TCTGTGACTGCGCGGACACGCGCGTATTAATTAATTAATTAATTAATTAATTAAT 1625  
QY 304 GACAACTGGGGCCAGGGAACCTTGATCAACCTGCTCTCA 342  
DB 1624 GACAACTGGGGCCAGGGAACCTTGATCAACCTGCTCTCA 1586

RESULT 14

ADJ32125 standard; DNA; 663 BP.

XX ADJ32125;

XX 22-APR-2004 (first entry)

DE Human interferon-gamma antibody heavy chain gene SeqID79.

XX antibody: antigen binding domain; interferon-gamma; INF-gamma;  
KM antigenic antibody; antiinflammatory; immunosuppressive;  
KW autoimmune disease; inflammatory condition; human; gene; ds; heavy chain.

XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH CDS 8..663  
FT /\*tag= a  
FT /product= "Human interferon-gamma antibody heavy chain"  
FT /partial  
FT /note= "No start or stop codon"

EN US2003099647-A1.

PD 29-MAY-2003.

XX 05-OCT-2001; 2001US-00972656.

XX 05-OCT-2001; 2001US-00972656.

XX (DESH/) DESHPANDE R V.

PA (TSAI/) TSAI M.

PI Deshpande RV, Tsai M;

XX WPI; 2003-696068/66.

DR P-PSDB; ADJ32126.

PT New antibody or antigen binding domain, or its fragment, variant or  
PT derivative, which binds to an interferon-gamma protein, useful for  
PT preparing a composition for preventing or treating inflammatory or  
PT autoimmune disorders.

XX Example 3; SEQ ID NO 79; 113bp; English.

CC This invention relates to a novel antibody or antigen binding domain, or  
CC its fragment, variant or derivative, which binds to an interferon-gamma  
CC (INF-gamma) protein, and is an antagonist antibody. The invention may be  
CC useful for the development of compounds with an antiinflammatory or  
CC immunosuppressive activity through action as interferon-gamma agonists. A  
CC composition containing the antibody is useful for preventing or treating  
CC an autoimmune disease and an inflammatory condition. The present sequence  
CC is that of a gene which encodes an antibody heavy chain of a human INF-  
CC gamma antibody which may be part of the invention.

XX Sequence 663 BP; 133 A; 216 C; 188 G; 126 T; 0 U; 0 Other;

Query Match 80.6%; Score 275.8; DB 10; Length 663;  
Best Local Similarity 89.0%; Pred. No. 1.1e-67;

Matches 298; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 4 GAGTGGGCCAGGACTGGTGAACCTTCACAGACCCGTGCTCCACCTGACGTCTCT 63  
DB 16 GAGTCGGGCCAGGACTGGTGAACCTTCACAGACCCGTGCTCCACCTGACGTCTCT 75  
QY 64 GGTGGCTCCATCCGACGTGTGTATTACTGAGTTGATCCGCCAGCGTCCAGGGAAG 123  
DB 76 GGTGGCTCCATCCGACGTGTGTATTACTGAGTTGATCCGCCAGCGTCCAGGGAAG 135  
QY 124 GGCTTGAGTGAATCGGATCATCTATCAGATGAGCAACCTTAACAACCCGTCCCTC 183  
DB 136 GGCTTGAGTGAATCGGATCATCTATCAGATGAGCAACCTTAACAACCCGTCCCTC 195  
QY 184 AAGAGTGAATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243  
DB 196 AAGAGTGAATTAACATGATGATGATGATGATGATGATGATGATGATGATGATG 255  
QY 244 TCTGTGACTGCGCGGACACGCGCGTATTAATTAATTAATTAATTAATTAATTAATTA 303  
DB 256 TCTGTGACTGCGCGGACACGCGCGTATTAATTAATTAATTAATTAATTAATTAATTA 315  
QY 304 GACAACTGGGGCCAGGGAACCTTGATCAACCTGCTCTC 338  
DB 316 GACAACTGGGGCCAGGGAACCTTGATCAACCTGCTCTC 350



RESULT 15  
 ADC97778  
 ID ADC97778 standard; DNA; 352 BP.  
 XX  
 AC ADC97778;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 7.  
 XX  
 KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 KW cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 KW lung cancer; human; ds; gene.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057838-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041581.  
 XX  
 PR 28-DEC-2001; 2001US-0346299P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudus J;  
 XX  
 DR WPI; 2003-587113/55.  
 DR P-PSDB; ADC99776.  
 XX  
 PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
 PT or condition associated with expression of MUC18 in a patient, e.g.  
 PT tumors, cancers, and other malignancies.  
 XX  
 PS Claim 8; SEQ ID NO 7; 78bp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody comprising  
 CC a heavy or light chain amino acid or a heavy or light chain variable  
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 CC invention demonstrates cytostatic activity and may be useful for treating  
 CC a disease or condition associated with the expression of MUC18 on the  
 CC cell surface such as tumours, specifically melanoma, oesophageal,  
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
 CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 CC colorectal, breast or lung cancer, as well as other malignancies. The  
 CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 CC heavy chain variable domain DNA of the invention.  
 CC  
 XX  
 SQ Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;  
 Query Match 80.4%; Score 275; DB 10; Length 352;  
 Best Local Similarity 90.3%; Pred. No. 1.6e-67;  
 Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;  
 QY 4 GAGTGTGCCCCAGACGCTGTAAGCCTTACACAGACCTGTCTCTCACTGCACTGTCT 63  
 DB 16 GAGTGGGCCCCAGAGCTGTGAAGCCTTACACAGACCTGTCTCTCACTGCACTGTCT 75  
 QY 64 GGTGCTTCATCCGAGAGGTGTATTAATGAGATTGATCCGACAGCTCCAGGAG 123  
 DB 76 GGTGCTTCATCCGAGAGGTGTATTAATGAGATTGATCCGACAGCTCCAGGAG 135  
 QY 124 GGCCTGAGTGGATCGGTATCATCTATCAAGTGGCAACCTTACAAACCCGTCCTC 183  
 DB 136 GGCCTGAGTGGATCGGTATCATCTATTAAGTGGAGACCTTACAAACCCGTCCTC 195  
 QY 184 AAGAGTCCAGTTACATGTCATAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243  
 DB 196 AAGAGTCCAGTTACATGTCATAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255

QY 244 TCTGTGACTGCGCCGCGACACGCGCGGTATTAATGAGAGTGGTACACTTGG 303  
 DB 256 TCTGTGACTGCGCCGCGACACGCGCGGTATTAATGAGAGTGGTACACTTGG 312  
 QY 304 GACAACTGCGGCGCGAGGGAACCTGTGTCACCGTCTCTCA 342  
 DB 313 AAGTACTGCGGCGCGAGGGAACCTGTGTCACCGTCTCTCA 351

Search completed: July 27, 2005, 05:59:45  
 Job time : 322.618 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: July 27, 2005, 09:08:49 ; Search time 512.827 Seconds  
(without alignments)  
4312.305 Million cell updates/sec

Title: US-10-027-725a-3

Perfect score: 342  
Sequence: 1 ctcgagctgcagccagac.....ccctgcacgcctcctca 342

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 7277826 seqs, 323339505 residues

Total number of hits satisfying chosen parameters: 14555652

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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24: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
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#### SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	342	100.0	342	14	US-10-027-725a-3
2	324.4	94.9	342	14	US-10-027-725a-2
3	310	90.6	342	14	US-10-027-725a-1
4	284.6	83.2	352	15	US-10-330-613-15
5	284.6	83.2	352	16	US-10-330-510-15
6	284.6	83.2	352	19	US-10-660-357-15
7	276.6	80.9	354	19	US-10-684-109-42

Query	Match	Score	DB	Length	Indels	Gaps
1	100.0%	342	14	342	0	0
2	94.9%	324.4	14	342	0	0
3	90.6%	310	14	342	0	0
4	83.2%	284.6	15	352	0	0
5	83.2%	284.6	16	352	0	0
6	83.2%	284.6	19	352	0	0
7	80.9%	276.6	19	354	0	0

#### ALIGNMENTS

US-10-027-725a-3  
Sequence 3, Appli  
Publication No. US20030082659A1  
GENERAL INFORMATION:  
APPLICANT: Flicker, Sabine  
TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
FILE REFERENCE: 25401-4  
CURRENT APPLICATION NUMBER: US/10/027,725A  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: US 60/259,436  
PRIOR FILING DATE: 2000-12-29  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 342  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-027-725a-3

Query	Match	Score	DB	Length	Indels	Gaps
1	100.0%	342	14	342	0	0
2	94.9%	324.4	14	342	0	0
3	90.6%	310	14	342	0	0
4	83.2%	284.6	15	352	0	0
5	83.2%	284.6	16	352	0	0
6	83.2%	284.6	19	352	0	0
7	80.9%	276.6	19	354	0	0

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Db      61 TCTGTCCTCCATCCGAGTCGTGTTATTACTGAGTTGGATCCGCCAGCTCCAGGG 120
Qy      121 AAGGCTCTGAGTGTGATCGGGTACATCTATACAGTGGCAACCTTACAAACCCGCTC 180
Db      121 AAGGCTCTGAGTGTGATCGGGTACATCTATACAGTGGCAACCTTACAAACCCGCTC 180
Qy      181 CTCAAGAGTCGAGTTACATGTCTAGTAGACACGCTTAAAGAACCTTCTCCCTGAGGCTG 240
Db      181 CTCAAGAGTCGAGTTACATGTCTAGTAGACACGCTTAAAGAACCTTCTCCCTGAGGCTG 240
Qy      241 AGCTCTGAGTGTGCGCGGACACGCGCTGTATTACTGTGCGAGTGCAGATGGGTACACT 300
Db      241 AGCTCTGAGTGTGCGCGGACACGCGCTGTATTACTGTGCGAGTGCAGATGGGTACACT 300
Qy      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA 342
Db      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA 342

RESULT 2
US-10-027-725a-2
; Sequence 2, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259, 436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725a-2

Query Match      94.9%; Score 324.4; DB 14; Length 342;
Best Local Similarity 96.8%; Pred. No. 8.3e-96;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy      1 CTCGAGTCTGGCCCAAGACCTGTGAAGCTTTCACAGACCTGTCTCCCTCACTGCACTGTC 60
Db      1 CTCGAGTCTGGCCCAAGACCTGTGAAGCTTTCACAGACCTGTCTCCCTCACTGCACTGTC 60
Qy      61 TCTGTCCTCCATCCGAGTCGTGTTATTACTGAGTTGGATCCGCCAGCTCCAGGG 120
Db      61 TCTGTCCTCCATCCGAGTCGTGTTATTACTGAGTTGGATCCGCCAGCTCCAGGG 120
Qy      121 AAGGCTCTGAGTGTGATCGGGTACATCTATACAGTGGCAACCTTACAAACCCGCTC 180
Db      121 AAGGCTCTGAGTGTGATCGGGTACATCTATACAGTGGCAACCTTACAAACCCGCTC 180
Qy      181 CTCAAGAGTCGAGTTACATGTCTAGTAGACACGCTTAAAGAACCTTCTCCCTGAGGCTG 240
Db      181 CTCAAGAGTCGAGTTACATGTCTAGTAGACACGCTTAAAGAACCTTCTCCCTGAGGCTG 240
Qy      241 AGCTCTGAGTGTGCGCGGACACGCGCTGTATTACTGTGCGAGTGCAGATGGGTACACT 300
Db      241 AGCTCTGAGTGTGCGCGGACACGCGCTGTATTACTGTGCGAGTGCAGATGGGTACACT 300
Qy      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA 342
Db      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA 342

RESULT 3
US-10-027-725a-1
; Sequence 1, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
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; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259, 436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725a-1

Query Match      90.6%; Score 310; DB 14; Length 342;
Best Local Similarity 94.2%; Pred. No. 4.3e-91;
Matches 322; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy      1 CTCGAGTCTGGCCCAAGACCTGTGAAGCTTTCACAGACCTGTCTCCCTCACTGCACTGTC 60
Db      1 CTCGAGTCTGGCCCAAGACCTGTGAAGCTTTCACAGACCTGTCTCCCTCACTGCACTGTC 60
Qy      61 TCTGTCCTCCATCCGAGTCGTGTTATTACTGAGTTGGATCCGCCAGCTCCAGGG 120
Db      61 TCTGTCCTCCATCCGAGTCGTGTTATTACTGAGTTGGATCCGCCAGCTCCAGGG 120
Qy      121 AAGGCTCTGAGTGTGATCGGGTACATCTATACAGTGGCAACCTTACAAACCCGCTC 180
Db      121 AAGGCTCTGAGTGTGATCGGGTACATCTATACAGTGGCAACCTTACAAACCCGCTC 180
Qy      181 CTCAAGAGTCGAGTTACATGTCTAGTAGACACGCTTAAAGAACCTTCTCTGAGGCTG 240
Db      181 CTCAAGAGTCGAGTTACATGTCTAGTAGACACGCTTAAAGAACCTTCTCTGAGGCTG 240
Qy      241 AGCTCTGAGTGTGCGCGGACACGCGCTGTATTACTGTGCGAGTGCAGATGGGTACACT 300
Db      241 AGCTCTGAGTGTGCGCGGACACGCGCTGTATTACTGTGCGAGTGCAGATGGGTACACT 300
Qy      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA 342
Db      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA 342

RESULT 4
US-10-330-613-15
; Sequence 15, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Guéas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330, 613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-15

Query Match      83.2%; Score 284.6; DB 15; Length 352;
Best Local Similarity 92.0%; Pred. No. 8.9e-83;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

Qy      4 GAGTCTGCCCCAGGAGTGTGAAGCTTTCACAGACCTGTCTCCCTCACTGCACTGCTCT 63
Db      16 GAGTCTGCCCCAGGAGTGTGAAGCTTTCACAGACCTGTCTCCCTCACTGCACTGCTCT 75
Qy      64 GGTGCTTCATCCGAGTGTGTTATTACTGAGTTGGATCCGCCAGCTCCAGGGAAG 123
```

```
Db      ||||| 76 GGTGGCTCCATCAGCAGGTGGTGTACTACTGAGCTGGAATCCGCCAGCAACCCAGGAG 135
Qy      ||||| 124 GGCCTGAGTGGATCGGGTACATCTATCAGAGTGGCAACCTTCAACAACCCGCTCC 183
Db      ||||| 136 GGCCTGAGTGGATGGGTTCATCTATTACGTGGAGCACTTCAACCCGCTCC 195
Qy      ||||| 184 AAGAGTGAAGTACCATGTCACTAGTACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 243
Db      ||||| 196 AAGAGTGAAGTACCATGTCACTAGTACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 255
Qy      ||||| 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGTCAAGATGGGTACACTTTG 303
Db      ||||| 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG---AGAGGAGATGGCTTT 312
Qy      ||||| 304 GACAACCTGGGGCCAGGAAACCTTGTCACCGCTCTCTCA 342
Db      ||||| 313 GACTACTGGGGCCAGGAAACCTTGTCACCGCTCTCTCA 351
```

## RESULT 5

```
US-10-330-530-15
; Sequence 15, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ARGENTIX.031A
; CURRENT APPLICATION NUMBER: US/10/330.530
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-530-15
```

```
Query Match      83.2%; Score 284.6; DB 16; Length 352;
Best Local Similarity 92.0%; Pred. No. 8.9e-83;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;
```

```
Qy      ||||| 4 GAGTCTGGCCCAAGAGACTGTGAAGCTTTCACAGAACCTTCCCTCACTGACTGTCTCT 63
Db      ||||| 16 GAGTGGGCCCCAGAGACTGTGAAGCTTTCACAGAACCTTCCCTCACTGACTGTCTCT 75
Qy      ||||| 64 GGTGGCTCCATCCGAGTGTGTATTACTGAGTGGATCCGCGACGTCAGAGGAG 123
Db      ||||| 76 GGTGGCTCCATCCGAGTGTGTATTACTGAGTGGATCCGCGACGTCAGAGGAG 135
Qy      ||||| 124 GGCCTGAGTGGATCGGGTACATCTATCAGAGTGGCAACCTTCAACAACCCGCTCC 183
Db      ||||| 136 GGCCTGAGTGGATGGGTTCATCTATTACGTGGAGCACTTCAACAACCCGCTCC 195
Qy      ||||| 184 AAGAGTGAAGTACCATGTCACTAGTACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 243
Db      ||||| 196 AAGAGTGAAGTACCATGTCACTAGTACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 255
Qy      ||||| 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGTCAAGATGGGTACACTTTG 303
Db      ||||| 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG---AGAGGAGATGGCTTT 312
Qy      ||||| 304 GACAACCTGGGGCCAGGAAACCTTGTCACCGCTCTCTCA 342
Db      ||||| 313 GACTACTGGGGCCAGGAAACCTTGTCACCGCTCTCTCA 351
```

```
RESULT 6
US-10-660-357-15
; Sequence 15, Application US/10660357
; Publication No. US20040115205A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ARGENTIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660.357
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-15
```

```
Query Match      83.2%; Score 284.6; DB 19; Length 352;
Best Local Similarity 92.0%; Pred. No. 8.9e-83;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;
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```
Qy      ||||| 4 GAGTCTGGCCCAAGAGACTGTGAAGCTTTCACAGAACCTTCCCTCACTGACTGTCTCT 63
Db      ||||| 16 GAGTGGGCCCCAGAGACTGTGAAGCTTTCACAGAACCTTCCCTCACTGACTGTCTCT 75
Qy      ||||| 64 GGTGGCTCCATCCGAGTGTGTATTACTGAGTGGATCCGCGACGTCAGAGGAG 123
Db      ||||| 76 GGTGGCTCCATCCGAGTGTGTATTACTGAGTGGATCCGCGACGTCAGAGGAG 135
Qy      ||||| 124 GGCCTGAGTGGATCGGGTACATCTATCAGAGTGGCAACCTTCAACAACCCGCTCC 183
Db      ||||| 136 GGCCTGAGTGGATGGGTTCATCTATTACGTGGAGCACTTCAACAACCCGCTCC 195
Qy      ||||| 184 AAGAGTGAAGTACCATGTCACTAGTACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 243
Db      ||||| 196 AAGAGTGAAGTACCATGTCACTAGTACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 255
Qy      ||||| 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGTCAAGATGGGTACACTTTG 303
Db      ||||| 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG---AGAGGAGATGGCTTT 312
Qy      ||||| 304 GACAACCTGGGGCCAGGAAACCTTGTCACCGCTCTCTCA 342
Db      ||||| 313 GACTACTGGGGCCAGGAAACCTTGTCACCGCTCTCTCA 351
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## RESULT 7

```
US-10-684-109-42
; Sequence 42, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989. US.02
; CURRENT APPLICATION NUMBER: US/10/684.109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-42
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Query Match      80.9%; Score 276.6; DB 19; Length 354;
```

Best Local Similarity 88.5%; Pred. No. 3.7e-80;  
Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

```
QY 4 GAGTCTGGCCCAAGACTGTGTGAAGCCCTTCAACAGCCCTGTCCCTCACTGTGACTGTCTCT 63
Db 16 GAGTCGGGCCCAAGACTGTGTGAAGCCCTTCAACAGCCCTGTCCCTCACTGTGACTGTCTCT 75
QY 64 GGTGGCTCCATCCGCACTGTGTGTATTACTGTGAGTTGATCCGCCAGCTCCAGGGAG 123
Db 76 GGTGGCTCCATCCGCACTGTGTGTATTACTGTGAGTTGATCCGCCAGCTCCAGGGAG 135
QY 124 GGCCTGAGTGAATCGGGTACATCTATCAAGTGGCAACCTTCAACAACCCGCTCCCTC 183
Db 136 GGCCTGAGTGAATCGGGTACATCTATCAAGTGAAGACTTCTCTACACACCCGCTCCCTC 195
QY 184 AAGAGTGAAGTTACCATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTGAAGTTACCATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGATC 255
QY 244 TCTGTGACTGCGCGGACAGCGCGGTGTATTACTGTGAGTTGATGAGTTGATGAGTTG 303
Db 256 TCTGTGACTGCGCGGACAGCGCGGTGTATTACTGTGAGTTGATGAGTTGATGAGTTG 315
QY 304 GACAACTGGGGCCAGGGAAACCTGTGACCGTCTCTCA 342
Db 316 GACTACTGGGGCCAGGGAAACCTGTGACCGTCTCTCA 354
```

## RESULT 8

```
US-10-684-109-92
; Sequence 92; Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wietler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989, US. 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-92
```

Query Match 80.9%; Score 276.6; DB 19; Length 1996;

Best Local Similarity 88.5%; Pred. No. 5.5e-80;  
Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

```
QY 4 GAGTCTGGCCCAAGACTGTGTGAAGCCCTTCAACAGCCCTGTCCCTCACTGTGACTGTCTCT 63
Db 73 GAGTCGGGCCCAAGACTGTGTGAAGCCCTTCAACAGCCCTGTCCCTCACTGTGACTGTCTCT 132
QY 64 GGTGGCTCCATCCGCACTGTGTGTATTACTGTGAGTTGATCCGCCAGCTCCAGGGAG 123
Db 133 GGTGGCTCCATCCGCACTGTGTGTATTACTGTGAGTTGATCCGCCAGCTCCAGGGAG 192
QY 124 GGCCTGAGTGAATCGGGTACATCTATCAAGTGGCAACCTTCAACAACCCGCTCCCTC 183
Db 193 GGCCTGAGTGAATCGGGTACATCTATCAAGTGAAGACTTCTCTACACACCCGCTCCCTC 252
QY 184 AAGAGTGAAGTTACCATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 253 AAGAGTGAAGTTACCATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGATC 312
```

```
QY 244 TCTGTGACTGCGCGGACAGCGCGGTGTATTACTGTGAGTTGATGAGTTGATGAGTTG 303
Db 313 TCTGTGACTGCGCGGACAGCGCGGTGTATTACTGTGAGTTGATGAGTTGATGAGTTG 372
QY 304 GACAACTGGGGCCAGGGAAACCTGTGACCGTCTCTCA 342
Db 373 GACTACTGGGGCCAGGGAAACCTGTGACCGTCTCTCA 411
```

## RESULT 9

```
US-10-684-109-93/c
; Sequence 93; Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wietler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989, US. 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-93
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Query Match 80.9%; Score 276.6; DB 19; Length 1996;

Best Local Similarity 88.5%; Pred. No. 5.5e-80;  
Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

```
QY 4 GAGTCTGGCCCAAGACTGTGTGAAGCCCTTCAACAGCCCTGTCCCTCACTGTGACTGTCTCT 63
Db 1924 GAGTCGGGCCCAAGACTGTGTGAAGCCCTTCAACAGCCCTGTCCCTCACTGTGACTGTCTCT 1865
QY 64 GGTGGCTCCATCCGCACTGTGTGTATTACTGTGAGTTGATCCGCCAGCTCCAGGGAG 123
Db 1864 GGTGGCTCCATCCGCACTGTGTGTATTACTGTGAGTTGATCCGCCAGCTCCAGGGAG 1805
QY 124 GGCCTGAGTGAATCGGGTACATCTATCAAGTGGCAACCTTCAACAACCCGCTCCCTC 183
Db 1804 GGCCTGAGTGAATCGGGTACATCTATCAAGTGAAGACTTCTCTACACACCCGCTCCCTC 1745
QY 184 AAGAGTGAAGTTACCATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 1744 AAGAGTGAAGTTACCATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGATC 1685
QY 244 TCTGTGACTGCGCGGACAGCGCGGTGTATTACTGTGAGTTGATGAGTTGATGAGTTG 303
Db 1684 TCTGTGACTGCGCGGACAGCGCGGTGTATTACTGTGAGTTGATGAGTTGATGAGTTG 1625
QY 304 GACAACTGGGGCCAGGGAAACCTGTGACCGTCTCTCA 342
Db 1624 GACTACTGGGGCCAGGGAAACCTGTGACCGTCTCTCA 1586
```

## RESULT 10

```
US-09-972-656-79
; Sequence 79; Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Teal, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
```

CURRENT APPLICATION NUMBER: US/09/972,656  
CURRENT FILING DATE: 2001-10-05  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 79  
LENGTH: 663  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(663)  
US-09-972-656-79

Query Match 80.6%; Score 275.8; DB 10; Length 663;  
Best Local Similarity 89.0%; Pred. No. 7.8e-80;  
Matches 298; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCCGAGAGCTGTGAAGCTTCAAGACCCCTGCTCACTGCACTGTCTCT 63  
DB 16 GAGTCGGGCGCCAGAGCTGTGAAGCTTCAAGACCCCTGCTCACTGCACTGTCTCT 75  
QY 64 GGTGGCTCATCCGAGAGTGTGTATTACTGATGGATCCGCGACGGTCCAGGGAG 123  
DB 76 GGTGGCTCATCCGAGAGTGTGTATTACTGATGGATCCGCGACGGTCCAGGGAG 135  
QY 124 GGCCTGGAGTGGATCGGTATCATCTATCAAGTGGCAACCTTCAACACCCGCTCCTC 183  
DB 136 GGCCTGGAGTGGATCGGTATCATCTATCAAGTGGCAACCTTCAACACCCGCTCCTC 195  
QY 184 AAGAGTCGAGTTACCATGTACGTAGACAGCGTTAAAGAACCTTCTCCCTGAAGCTGAGC 243  
DB 196 AAGAGTCGAGTTACCATGTACGTAGACAGCGTTAAAGAACCTTCTCCCTGAAGCTGAGC 255  
QY 244 TCTGTGACTGCGCGGAGACAGCGCGTGTATCTGTGAGAGTCAAGTGGTACACTTGG 303  
DB 256 TCTGTGACTGCGCGGAGACAGCGCGTGTATCTGTGAGAGTCAAGTGGTACACTTGG 315  
QY 304 GACAACCTGGGCGCAGGAGAACCTTGTCAACCGTCTC 338  
DB 316 GACTACTGGGCGCAGGAGAACCTTGTCAACCGTCTC 350

RESULT 11  
US-10-330-613-7  
Sequence 7, Application US/10330613  
Publication No. US20030147809A1  
GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
FILE REFERENCE: AGENIX.022A  
CURRENT FILING DATE: 2002-12-26  
CURRENT APPLICATION NUMBER: US/10/330,613  
PRIOR FILING DATE: 2001-12-18  
PRIOR APPLICATION NUMBER: 60/346299  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 352  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-10-330-613-7

Query Match 80.4%; Score 275; DB 15; Length 352;  
Best Local Similarity 90.3%; Pred. No. 1.2e-79;  
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCGAGAGCTGTGAAGCTTCAAGACCCCTGCTCACTGCACTGTCTCT 63  
DB 16 GAGTCGGGCGCCAGAGCTGTGAAGCTTCAAGACCCCTGCTCACTGCACTGTCTCT 75  
QY 64 GGTGGCTCATCCGAGAGTGTGTATTACTGATGGATCCGCGACGGTCCAGGGAG 123  
DB 76 GGTGGCTCATCCGAGAGTGTGTATTACTGATGGATCCGCGACGGTCCAGGGAG 135

QY 124 GGCCTGGAGTGGATCGGTATCATCTATCAAGTGGCAACCTTCAACACCCGCTCCTC 183  
DB 136 GGCCTGGAGTGGATCGGTATCATCTATCAAGTGGCAACCTTCAACACCCGCTCCTC 195  
QY 184 AAGAGTCGAGTTACCATGTACGTAGACAGCGTTAAAGAACCTTCTCCCTGAAGCTGAGC 243  
DB 196 AAGAGTCGAGTTACCATGTACGTAGACAGCGTTAAAGAACCTTCTCCCTGAAGCTGAGC 255  
QY 244 TCTGTGACTGCGCGGAGACAGCGCGTGTATCTGTGAGAGTCAAGTGGTACACTTGG 303  
DB 256 TCTGTGACTGCGCGGAGACAGCGCGTGTATCTGTGAGAGTCAAGTGGTACACTTGG 312  
QY 304 GACAACCTGGGCGCAGGAGAACCTTGTCAACCGTCTC 342  
DB 313 AAGTACTGGGCGCAGGAGAACCTTGTCAACCGTCTC 351

RESULT 12  
US-10-330-530-7  
Sequence 7, Application US/10330530  
Publication No. US20030152514A1  
GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
FILE REFERENCE: AGENIX.031A  
CURRENT FILING DATE: 2002-12-26  
CURRENT APPLICATION NUMBER: US/10/330,530  
PRIOR FILING DATE: 2001-12-18  
PRIOR APPLICATION NUMBER: 60/346414  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 352  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-10-330-530-7

Query Match 80.4%; Score 275; DB 16; Length 352;  
Best Local Similarity 90.3%; Pred. No. 1.2e-79;  
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCGAGAGCTGTGAAGCTTCAAGACCCCTGCTCACTGCACTGTCTCT 63  
DB 16 GAGTCGGGCGCCAGAGCTGTGAAGCTTCAAGACCCCTGCTCACTGCACTGTCTCT 75  
QY 64 GGTGGCTCATCCGAGAGTGTGTATTACTGATGGATCCGCGACGGTCCAGGGAG 123  
DB 76 GGTGGCTCATCCGAGAGTGTGTATTACTGATGGATCCGCGACGGTCCAGGGAG 135  
QY 124 GGCCTGGAGTGGATCGGTATCATCTATCAAGTGGCAACCTTCAACACCCGCTCCTC 183  
DB 136 GGCCTGGAGTGGATCGGTATCATCTATCAAGTGGCAACCTTCAACACCCGCTCCTC 195  
QY 184 AAGAGTCGAGTTACCATGTACGTAGACAGCGTTAAAGAACCTTCTCCCTGAAGCTGAGC 243  
DB 196 AAGAGTCGAGTTACCATGTACGTAGACAGCGTTAAAGAACCTTCTCCCTGAAGCTGAGC 255  
QY 244 TCTGTGACTGCGCGGAGACAGCGCGTGTATCTGTGAGAGTCAAGTGGTACACTTGG 303  
DB 256 TCTGTGACTGCGCGGAGACAGCGCGTGTATCTGTGAGAGTCAAGTGGTACACTTGG 312  
QY 304 GACAACCTGGGCGCAGGAGAACCTTGTCAACCGTCTC 342  
DB 313 AAGTACTGGGCGCAGGAGAACCTTGTCAACCGTCTC 351

RESULT 13  
US-10-660-357-7  
Sequence 7, Application US/10660357  
Publication No. US20040115205A1  
GENERAL INFORMATION:  
APPLICANT: Bar-El, Menashe

```

; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX .030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-7

Query Match      80.4%; Score 275; DB 19; Length 352;
Best Local Similarity 90.3%; Pred. No. 1.2e-79;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGAGCCAGAGCTGTGTAAGCCCTTACAGACCCCTGTCTCCTGACCTGTCTCT 63
    |||||
DB 16 GAGTCGGGCCCCAGAGCTGTGTAAGCCCTTACAGACCCCTGTCTCCTGACCTGTCTCT 75
    |||||

QY 64 GGTGGCTCCATCCGCAAGTGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTA 123
    |||||
DB 76 GGTGGCTCCATCCGCAAGTGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTA 135
    |||||

QY 124 GGCCTGAGAGTGAATCGGATCATCTATCAAGTGGCAACCTTCAACAAACCCGTCCTC 183
    |||||
DB 136 GGCCTGAGAGTGAATCGGATCATCTATCAAGTGGCAACCTTCAACAAACCCGTCCTC 195
    |||||

QY 184 AAGAGTCGAGTTACATGTCTAGTACAGACGCTTAAGAACCTTCTCTGAGGCTGAGC 243
    |||||
DB 196 AAGAGTCGAGTTACATGTCTAGTACAGACGCTTAAGAACCTTCTCTGAGGCTGAGC 255
    |||||

QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTAATTAATTAATTAATTAATTAATTAATTA 303
    |||||
DB 256 TCTGTGACTGCGCGGACACGCGCGTGTATTAATTAATTAATTAATTAATTAATTAATTA 312
    |||||

QY 304 GACAACCTGGGGCCAGGGAACCTGTGATCAACCTGTCTCTCA 342
    |||||
DB 313 AAGTACTGGGGCCAGGGAACCTGTGATCAACCTGTCTCTCA 351
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RESULT 14
US-10-644-277-93
; Sequence 93, Application US/10644277
; Publication No. US2005058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean M.
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Foord, Orit
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kiran
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; TITLE OF INVENTION: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
; FILE REFERENCE: ABGENIX.091A
; CURRENT APPLICATION NUMBER: US/10/644,277
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homosapien
US-10-644-277-93

Query Match      80.2%; Score 274.2; DB 21; Length 560;
Best Local Similarity 89.1%; Pred. No. 2.5e-79;
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Matches 311; Conservative 0; Mismatches 28; Indels 10; Gaps 1;

QY 4 GAGTCTGAGCCAGAGCTGTGTAAGCCCTTACAGACCCCTGTCTCCTGACCTGTCTCT 63
    |||||
DB 16 GAGTCGGGCCCCAGAGCTGTGTAAGCCCTTACAGACCCCTGTCTCCTGACCTGTCTCT 75
    |||||

QY 64 GGTGGCTCCATCCGCAAGTGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTA 123
    |||||
DB 76 GGTGGCTCCATCCGCAAGTGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTA 135
    |||||

QY 124 GGCCTGAGAGTGAATCGGATCATCTATCAAGTGGCAACCTTCAACAAACCCGTCCTC 183
    |||||
DB 136 GGCCTGAGAGTGAATCGGATCATCTATCAAGTGGCAACCTTCAACAAACCCGTCCTC 195
    |||||

QY 184 AAGAGTCGAGTTACATGTCTAGTACAGACGCTTAAGAACCTTCTCTGAGGCTGAGC 243
    |||||
DB 196 AAGAGTCGAGTTACATGTCTAGTACAGACGCTTAAGAACCTTCTCTGAGGCTGAGC 255
    |||||

QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTAATTAATTAATTAATTAATTAATTAATTA 293
    |||||
DB 256 TCTGTGACTGCGCGGACACGCGCGTGTATTAATTAATTAATTAATTAATTAATTAATTA 315
    |||||

QY 294 GTACACTTTGGAACAACTGGGGCCAGGGAACCTGTGACCCGTCTCTCA 342
    |||||
DB 316 CCACTGTTGACCCCTGTGGGCCAGGGAACCTGTGACCCGTCTCTCA 364
    |||||

RESULT 15
US-10-984-960A-19
; Sequence 19, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
; APPLICANT: Gallo, Michael
; APPLICANT: Chui, Daniel
; APPLICANT: Zhong, Haihong
; APPLICANT: Ary, Gulehan
; APPLICANT: LaRoche, William J.
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
; FILE REFERENCE: Cura 970
; CURRENT APPLICATION NUMBER: US/10/984,960A
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 60/518,275
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 19
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(366)
US-10-984-960A-19

Query Match      79.6%; Score 272.2; DB 22; Length 366;
Best Local Similarity 88.6%; Pred. No. 1e-78;
Matches 311; Conservative 0; Mismatches 28; Indels 12; Gaps 1;
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QY 244 TCTGTGACTGCCCGGACACGGCCGTATTTACTGTGGAG-----GTCAGAT 291  
 Db 256 TCTGTGACTGCCCGGACACGGCCGTATTTACTGTGGAGAGAGGGGAGTACTACGAT 315  
 QY 292 GGGTACACTTTGGACAACTGGGGCCAGGAACTGTGTCAACCTCTCTCA 342  
 Db 316 GAGGGGGGTTTGACTACTGGGGCCAGGAACTGTGTCAACCTCTCTCA 366

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 Job time : 512.827 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:42:26 ; Search time 95.3455 Seconds  
(without alignments)  
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Title: US-10-027-725a-2

Sequence: 1 ctcgagctcgcgcagact.....ccctgtcaccgtctctca 342

Scoring table: IDENTITY\_NUC  
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	251.2	73.5	516	US-09-472-087-33	Sequence 33, Appl
2	249.2	72.9	357	US-08-360-125-3	Sequence 3, Appl
3	249.2	72.9	357	US-08-450-578-3	Sequence 3, Appl
4	249.2	72.9	357	US-09-017-628-3	Sequence 3, Appl
5	249.2	72.9	357	US-09-014-880-3	Sequence 3, Appl
6	249.2	72.9	357	US-08-450-363-3	Sequence 3, Appl
7	249.2	72.9	357	US-09-467-903-3	Sequence 3, Appl
8	244.8	71.6	504	US-09-471-276-100	Sequence 100, App
9	243	70.1	450	US-09-582-337-13	Sequence 3, Appl
10	242.6	70.9	631	US-08-545-809A-31	Sequence 31, Appl
11	237.8	69.5	466	US-09-471-276-51	Sequence 51, Appl
12	237.4	69.4	1567	US-09-049-672A-17	Sequence 17, Appl
13	236.6	69.2	351	US-09-720-493-1	Sequence 1, Appl
14	236.6	68.2	351	US-09-720-493-21	Sequence 21, Appl
15	234.6	68.6	1543	US-09-800-729-74	Sequence 74, Appl
16	230.6	67.4	366	US-08-360-125-9	Sequence 9, Appl
17	230.6	67.4	366	US-08-450-578-9	Sequence 9, Appl
18	230.6	67.4	366	US-09-017-628-9	Sequence 9, Appl
19	230.6	67.4	366	US-09-014-880-9	Sequence 9, Appl
20	230.6	67.4	366	US-08-450-363-9	Sequence 9, Appl
21	230.6	67.4	366	US-09-467-903-9	Sequence 9, Appl
22	225	65.8	1212	US-08-545-809A-61	Sequence 61, Appl
23	223.4	65.3	800	US-08-545-809A-39	Sequence 39, Appl
24	216.2	63.2	392	US-09-471-276-52	Sequence 52, Appl
25	215.2	62.9	403	US-09-042-353-357	Sequence 357, App
26	215.2	62.9	403	US-08-758-417A-205	Sequence 205, App
27	215	62.9	840	US-09-260-527-4	Sequence 4, Appl

28	212.4	62.1	467	US-09-471-276-99	Sequence 99, Appl
29	212	62.0	524	US-09-042-353-419	Sequence 419, App
30	212	62.0	524	US-08-758-417A-219	Sequence 219, App
31	212	62.0	4926	US-09-042-353-418	Sequence 418, App
32	212	62.0	4926	US-08-758-417A-268	Sequence 268, App
33	209.2	61.2	417	US-09-203-768A-1	Sequence 1, Appl
34	209.2	61.2	469	US-09-471-276-58	Sequence 58, Appl
35	208	60.8	288	US-08-851-362D-7	Sequence 7, Appl
36	207.8	60.8	404	US-09-042-353-355	Sequence 355, App
37	207.8	60.8	404	US-08-758-417A-203	Sequence 203, App
38	207.8	60.8	800	US-08-545-809A-55	Sequence 55, Appl
39	207.6	60.7	351	US-08-477-553A-45	Sequence 45, Appl
40	206.8	60.5	360	US-09-424-840B-19	Sequence 19, Appl
41	206.6	60.4	291	US-08-851-362D-11	Sequence 11, Appl
42	205	59.9	357	US-08-652-816A-20	Sequence 20, Appl
43	204.2	59.7	354	US-08-652-816A-23	Sequence 23, Appl
44	204.2	59.7	624	US-08-545-809A-28	Sequence 28, Appl
45	203.8	59.6	369	US-08-793-450-3	Sequence 3, Appl

#### ALIGNMENTS

RESULT 1  
US-09-472-087-33  
Sequence 33, Application US/09472087  
Patent No. 6682736  
GENERAL INFORMATION:  
APPLICANT: HANSON, DOUGLAS C.  
APPLICANT: NEVEU, MARK J.  
APPLICANT: MUELLER, EILEEN E.  
APPLICANT: HANKE, JEFFREY H.  
APPLICANT: GILMAN, STEVEN C.  
APPLICANT: DAVIS, C. GEOFFREY  
APPLICANT: CORVALAN, JOSE R.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
FILE REFERENCE: ABX-PEI  
CURRENT APPLICATION NUMBER: US/09/472,087  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/113,647  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 33  
LENGTH: 516  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-472-087-33

Query Match 73.5%; Score 251.2; DB 4; Length 516;  
Best Local Similarity 85.7%; Pred. No. 8.6e-69;  
Matches 293; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

QY	7	TCCTGCGCAGAGCTGTGAAGCCCTTCACAGACCTGTCCCTGACCTGCTCTGGT	66
DB	1	TCGGGCCCAAGACGTGTGAAGCCCTTCACAGATCTCTGCCACCTGACGTCTCTGGT	60
QY	67	GGCTCCATCCGACGTGTGTTATTATTGAGTTGGTCCGCCAGCTCCAGGGAAGGCG	126
DB	61	GGCTCCATCCGACGTGTGTTATTATTGAGTTGGTCCGCCAGCTCCAGGGAAGGCG	120
QY	127	CTGAGTGGATCGGCAATCTTATCAACAGTGGCAACCTTCAACACCCCTCCCTGAG	186
DB	121	CTGAGTGGATCGGCAATCTTATCAACAGTGGCAACCTTCAACACCCCTCCCTGAG	180
QY	187	AGTGAATTACATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACTCT	246
DB	181	AGTGAATTACATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACTCT	240
QY	247	GTGATCGCCCGGACAGCGCGCTTATTACTGTGCGGGGTCAATGGG-----TAACT	300
DB	241	GTGATCGCCCGGACAGCGCGCTTATTACTGTGCGGGGTCAATGGG-----TAACT	300

QY 301 TTGACACCTGGGGCCAGGAAACCGCTGTCAACCGTCTCTCA 342  
Db 301 ATAGAGCTGTGGGGCCAGGAAACCGCTGTCTCTCA 342

## RESULT 2

US-08-360-125-3  
Sequence 3, Application US/08360125  
Patent No. 5767246  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5767246ihiko ITO  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Mordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360.125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL LINE: antibody G4H  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:

CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-3

Query Match 72.9%; Score 249.2; DB 1; Length 357;  
Best Local Similarity 85.1%; Pred. No. 3, 1e-68;  
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGCTTGGCCCGAGAGCTGTGAAGCCTTCACAGACCCCTGCTCACTGCTCT 63  
Db 16 GAGTCGGGCCCCAGAGCTGTGAAGCCTTCACAGACCCCTGCTCACTGCTCT 75  
QY 64 GGTGGCTTCCATCCGCACTGGTGTATTATTGAGTTGGTCCGCCAGCTCCAGGAG 123  
Db 76 GGTGGCTTCCATCCGCACTGGTGTATTATTGAGTTGGTCCGCCAGGAG 135  
QY 124 GGCCGTGAGTGAATCCGCAATCTATCAAGTGGCAACCTAACAACCCGCTC 183  
Db 136 GGCCGTGAGTGAATCCGCAATCTATCAAGTGGCAACCTAACAACCCGCTC 195  
QY 184 AAGAGTGAATTACATGTCAGTAGACACGCTTAAGAACCACTTCTCTGAGAC 243  
Db 196 AAGAGTGAATTACATGTCAGTAGACACGCTTAAGAACCACTTCTCTGAGAC 255  
QY 244 TCTGTACTGCCCGGACACAGCGCGTCTATTACTGTGCGGCTCAAGTGGTATCTTTG 303  
Db 256 TCTGTACTGCCCGGACACAGCGCGTCTATTACTGTGCGGCTCAAGTGGTATCTTTG 315  
QY 304 ---GACAACTGGGGCCAGGAAACCGCTGTCAACCGTCTCTCA 342  
Db 316 GCTGACTACTGGGGCCAGGAAACCGCTGTCAACCGTCTCTCA 357

## RESULT 3

US-08-450-578-3  
Sequence 3, Application US/08450578  
Patent No. 5837845  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845ihiko ITO  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL LINE: antibody GAH  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
PUBLICATION DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-3

Query Match 72.9%; Score 249.2; DB 2; Length 357;  
Best Local Similarity 85.1%; Pred. No. 3.1e-68;  
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCAAGACTGTTGAAAGCCCTTCACAGACCTGTCCCTACCTGACTGTCTCT 63  
DB 16 GAGTCGGGGCCCAAGACTGTTGAAAGCCCTTCACAGACCTGTCCCTACCTGACTGTCTCT 75  
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTGAGTTGGTCCGCGACCGCTCCAGGAG 123  
DB 76 GGTGGCTCCATCCGAGTGGTGGTTATTGAGTTGGTCCGCGACCGCTCCAGGAG 135  
QY 124 GGCCTGAGTGAATCCGCAATCTATACAGTGGCAACACTAACAACCCGTCCTC 183  
DB 136 GGCCTGAGTGAATCCGCAATCTATACAGTGGCAACACTAACAACCCGTCCTC 195  
QY 184 AAGAGTGAATTAACATGATGATGACAGCGTCTAAGAACCACTTCTCTGAGCTGAC 243  
DB 196 AAGAGTGAATTAACATGATGATGACAGCGTCTAAGAACCACTTCTCTGAGCTGAC 255  
QY 244 TCTGTGACTGCGCGGACAGCGCGTCTATTACTGTGCGGGGTCAAGTGGTATCTTTG 303  
DB 256 TCTGTGACTGCGCGGACAGCGCGTCTATTACTGTGCGGGGTCAAGTGGTATCTTTG 315  
QY 304 ---GACAACCTGGGGCCAGGGAACCGTGTACCGTCTCTCA 342  
DB 316 GCTGACTACTGGGGCCAGGGAACCAATGTCAACCGTCTCTCA 357

RESULT 4  
US-09-017-628-3  
Sequence 3, Application US/09017628  
Patent No. 5990287  
GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saiko  
APPLICANT: TAGAWA, Toshiaki  
APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITO, No. 5990287:hiko  
APPLICANT: NAGAIKE, Kazuhiro  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
FILE REFERENCE: 177/527361KH  
CURRENT APPLICATION NUMBER: US/09/017,628  
CURRENT FILING DATE: 1998-02-02  
EARLIER APPLICATION NUMBER: 08/360,125  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 357  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody GAH  
US-09-017-628-3

Query Match 72.9%; Score 249.2; DB 2; Length 357;  
Best Local Similarity 85.1%; Pred. No. 3.1e-68;  
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCAAGACTGTTGAAAGCCCTTCACAGACCTGTCCCTACCTGACTGTCTCT 63  
DB 16 GAGTCGGGGCCCAAGACTGTTGAAAGCCCTTCACAGACCTGTCCCTACCTGACTGTCTCT 75  
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTGAGTTGGTCCGCGACCGCTCCAGGAG 123  
DB 76 GGTGGCTCCATCCGAGTGGTGGTTATTGAGTTGGTCCGCGACCGCTCCAGGAG 135  
QY 124 GGCCTGAGTGAATCCGCAATCTATACAGTGGCAACACTAACAACCCGTCCTC 183  
DB 136 GGCCTGAGTGAATCCGCAATCTATACAGTGGCAACACTAACAACCCGTCCTC 195  
QY 184 AAGAGTGAATTAACATGATGATGACAGCGTCTAAGAACCACTTCTCTGAGCTGAC 243  
DB 196 AAGAGTGAATTAACATGATGATGACAGCGTCTAAGAACCACTTCTCTGAGCTGAC 255  
QY 244 TCTGTGACTGCGCGGACAGCGCGTCTATTACTGTGCGGGGTCAAGTGGTATCTTTG 303

Db 256 TCTGTGACTGCGGACACGGCCGTATTACTGTGAGAGTCTTACCCGACTAGGGGG 315  
Qy 304 ---GACAACTGGGGCCAGGAAACCTGTGTCACCGTCTCTCA 342  
Db 316 GGTGACTACTGGGGCCAGGAAACATGTGTACCGTCTCTTCA 357

RESULT 5  
US-09-014-880-3  
; Sequence 3, Application US/09014880  
; Patent No. 5990297  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA et al.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
; STREET: 2033 K Street, N.W., #800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/014,880  
; FILING DATE: January 28, 1998  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/450,578  
; FILING DATE: May 25, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/360,125  
; FILING DATE: December 20, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-721-8200  
; TELEFAX: 202-721-8250  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 357 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; CELL TYPE: Hybridoma producing human  
; CELL TYPE: antibody G4H  
; US-09-014-880-3

Query Match 72.9%; Score 249.2; DB 2; Length 357;  
Best Local Similarity 85.1%; Pred. No. 3.1e-68;  
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

Qy 4 GAGTGTGGCCCAAGAGACTGTGAAGCTTCAAGACCTGTCTTCACTGACTGTCTCT 63  
Db 16 GAGTGTGGCCCAAGAGACTGTGAAGCTTCAAGACCTGTCTTCACTGACTGTCTCT 75  
Qy 64 GGTGGCTCCATCCGACAGGTGTTATATGAGATTGGGGCCGACACCTCCAGAGAG 123  
Db 76 GGTGGCTCCATCCGACAGGTGTTATATGAGATTGGGGCCGACACCTCCAGAGAG 135

Qy 124 GGCCTGAGTGGATGGCAACATCTATACAGTGGCAACCTTAAACAAACCCGTCCTC 183  
Db 136 GGCCTGAGTGGATGGGATCATCTATTAACATGGAGACCTTAAACCCGTCCTC 195  
Qy 184 AAGAGTGAATTAACATGTCAGTAAAGACAGTCTTAAAGAACACTTCCCTGAGCTAAC 243  
Db 196 AAGAGTGAATTAACATGTCAGTAAAGACAGTCTTAAAGAACACTTCCCTGAGCTAAC 255  
Qy 244 TCTGTGACTGCGGACACGGCCGTATTACTGTGCGGTCAGATGGGTATACCTTTG 303  
Db 256 TCTGTGACTGCGGACACGGCCGTATTACTGTGCGGTCAGATGGGTATACCTTTG 315  
Qy 304 ---GACAACTGGGGCCAGGAAACCTGTGTCACCGTCTCTCA 342  
Db 316 GGTGACTACTGGGGCCAGGAAACATGTGTACCGTCTCTTCA 357

RESULT 6  
US-08-450-363-3  
; Sequence 3, Application US/08450363  
; Patent No. 6436434  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki ITRAMA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 6436434Ihiko ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,363  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/360,125  
; FILING DATE: December 20, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 357 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:

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ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-3

Query Match 72.9%; Score 249.2; DB 3; Length 357;
Best Local Similarity 85.1%; Pred. No. 3,le-68;
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1

QY 4 GAGTCTGGCCAGGAGCTGTGTAAGCCTTCACAGACCCCTGCTCACCCTGCACTGCTCT 63
Db 16 GAGTCTGGCCAGGAGCTGTGTAAGCCTTCACAGACCCCTGCTCACCCTGCACTGCTCT 75
QY 64 GGTGGCTTCATCCGCACTGTGTGTTATTATTTGAGTTGGGTTCCGCAAGCTTCAGGAAG 123
Db 76 GGTGGCTTCATCCGCACTGTGTGTTATTATTTGAGTTGGGTTCCGCAAGCTTCAGGAAG 135
QY 124 GGCTCGAGTGGATGGGCAACATCTATCACTGAGGCAACACTTACACAAACCCGTCCTC 183
Db 136 GGCTCGAGTGGATGGGCAACATCTATTTACAGTGGGAGCACTTACACAAACCCGTCCTC 195
QY 184 AAGAGTGAATTACATGTCAGTACAGACGCTTAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTGAATTACATGTCAGTACAGACGCTTAGAACCACTTCTCCCTGAGACTGAGC 255
QY 244 TCTGGACTGCGCGAGACAGGCGCTCTATTACTGTGCGGGTCAGATGGGTACTTTG 303
Db 256 TCTGGACTGCGCGAGACAGGCGCTCTATTACTGTGCGAGGTCTAACCCGACTACGGGGG 315
QY 304 --GACAACTGGGGCCAGGAAACCTTGTCACCGTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGAAACATGTGTCACCGTCTCTCA 357

RESULT 7
US-09-467-903-3
; Sequence 3, Application US/09467903
; Patent No. 6787153
; GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
Toshiaki TAGAWA
Yoko HIRAKAWA

```

No. 6787153jshiko ITO  
 Kazuhiro NAGAIKE  
 TITLE OF INVENTION: Human Monoclonal Antibody  
 Specifically Binding to Surface Antigen of Cancer  
 Cell Membrane  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Wenderoth, Lind & Ponack  
 STREET: 203 K Street, N.W., #800  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/467,903  
 FILING DATE: 21-Dec-1999  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/450,363  
 FILING DATE: May 25, 1995  
 APPLICATION NUMBER: 08/360,125  
 FILING DATE: December 20, 1994  
 APPLICATION NUMBER: 07/905,534  
 FILING DATE: June 29, 1992  
 APPLICATION NUMBER: JP158859/1991  
 FILING DATE: June 28, 1991  
 APPLICATION NUMBER: JP158860/1991  
 FILING DATE: June 28, 1991  
 APPLICATION NUMBER: JP158861/1991  
 FILING DATE: June 28, 1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek Jr.  
 REGISTRATION NUMBER: 33,367  
 REFERENCE/DOCKET NUMBER: <Unknown>  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-721-8200  
 TELEFAX: <Unknown>  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 357 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: <Unknown>  
 ANTI-SENSE: <Unknown>  
 ORIGINAL SOURCE:  
 ORGANISM: <Unknown>  
 STRAIN: <Unknown>  
 INDIVIDUAL ISOLATE: <Unknown>  
 DEVELOPMENTAL STAGE: <Unknown>  
 HAPLTYPE: <Unknown>  
 TISSUE TYPE: <Unknown>  
 CELL TYPE: Hybridoma producing human  
 antibody G4H  
 CELL LINE: <Unknown>  
 ORGANELLE: <Unknown>  
 IMMEDIATE SOURCE:  
 LIBRARY: <Unknown>  
 CLONE: <Unknown>  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT: <Unknown>  
 MAP POSITION: <Unknown>  
 UNITS: <Unknown>  
 FEATURE:  
 NAME/KEY:  
 LOCATION:

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IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-09-467-903-3

Query Match      72.9%; Score 249.2; DB 4; Length 357;
Best Local Similarity 85.1%; Pred. No. 3.1e-68;
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGGACTGTGTAAGCCCTTCAACAGACCCCTGCTCCCTGACCTGCTCTCT 63
DB 16 GAGTCCGCCCCAGGACTGTGTAAGCCCTTCAACAGACCCCTGCTCCCTGACCTGCTCTCT 75
QY 64 GGTGGCTCCATCCGCACTGCTGTTATTATTGAGTTGGTCCGCCAGCCTCCAGGGAG 123
DB 76 GGTGGCTCCATCCGCACTGCTGTTATTATTGAGTTGGTCCGCCAGCCTCCAGGGAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATACAGTGGCAACCTTCAACAAACCCGCTCC 183
DB 136 GGCCTGGAGTGGATCGGCAACATCTATACAGTGGCAACCTTCAACAAACCCGCTCC 195
QY 184 AAGAGTGAATTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTGAATTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 255
QY 244 TCTGTACTGCCCCGAGACGCGCGCTATTACTGTGCGCGCTCAAGTGGTATACCTTTG 303
DB 256 TCTGTACTGCCCCGAGACGCGCGCTATTACTGTGCGCGCTCAAGTGGTATACCTTTG 315
QY 304 ---GACAACTGGGGCGAGGGAACCTGTGTCACCGTCTCCCTCA 342
DB 316 GCTGACTACTGGGGCGAGGGAACATGTGTCACCGTCTCCCTCA 357

RESULT 8
US-09-471-276-100
; Sequence 100, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CPI
; CURRENT APPLICATION NUMBER: US/09/471.276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057.719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069.047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 100
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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LOCATION: 39..503
NAME/KEY: sig_peptide
LOCATION: 39..95
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 9.3000019073486
OTHER INFORMATION: seq FULLVAGPRWVLS/QV
US-09-471-276-100

Query Match      71.6%; Score 244.8; DB 4; Length 504;
Best Local Similarity 83.4%; Pred. No. 8.6e-67;
Matches 287; Conservative 3; Mismatches 51; Indels 3; Gaps 1;

QY 1 CTGAGCTTGGCCCCAGGACTGTGTAAGCCCTTCAACAGACCCCTGCTCCCTGACCTGCTCTC 60
DB 108 SDKAGTCCGCCCCAGGACTGTGTAAGCCCTTCAACAGACCCCTGCTCCCTGACCTGCTCTC 167
QY 61 TCTGTGGCTCCATCCGCACTGCTGTTATTATTGAGTTGGTCCGCCAGCCTCCAGGG 120
DB 168 TCTGTGGCTCCATCCGCACTGCTGTTATTATTGAGTTGGTCCGCCAGCCTCCAGGG 227
QY 121 AAGGCGCTGGAGTGGATCGGCAACATCTATACAGTGGCAACCTTCAACAAACCCGCTCC 180
DB 228 AAGGCGCTGGAGTGGATCGGCAACATCTATACAGTGGCAACCTTCAACAAACCCGCTCC 287
QY 181 CTGAAGTGAATTACATGTCACTAGTACAGTGAACAGCTTCAAGAACCTTCCCTGAGACTG 240
DB 288 CTGAAGTGAATTACATGTCACTAGTACAGTGAACAGCTTCAAGAACCTTCCCTGAGACTG 347
QY 241 ACCCTGTGACTCGCGGAGACGCGCGCTATTACTGTGCGCGTCAAGTGGGTATACCT 300
DB 348 AGCTGTGACTACCGGAGACGCGCGCTATTACTGTGCGCGTCAAGTGGGTATACCT 407
QY 301 ---TTGCAACACTGGGGCGAGGGAACCTGTGTCTCTC 341
DB 408 TATTGACCCCTGGGGCGAGGGAACCTGTGTCTCTC 451

RESULT 9
US-09-582-337-13
; Sequence 13, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/09/582.337
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(450)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(58)
; NAME/KEY: V region
; LOCATION: (59)..(353)
US-09-582-337-13

Query Match      71.1%; Score 243; DB 4; Length 450;
Best Local Similarity 84.9%; Pred. No. 3e-66;
Matches 303; Conservative 0; Mismatches 35; Indels 19; Gaps 2;

QY 4 GAGTCTGCCCCAGGACTGTGTAAGCCCTTCAACAGACCCCTGCTCCCTGACCTGCTCTCTCT 63
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Db 74 GAGTCGGCCAGAGCTGTGAAGCCTTTCACAGACCTCTGT-CCTACCTGCACTGTCTCT 132  
QY 64 GGTGCTCCATCCGACAGTGGTGTATTATTGAGTGGGTCCGACAGCTCCAGGGAG 123  
Db 133 GGTGGCTCCATCCGACAGTGGTGTATTATTGAGTGGGTCCGACAGCTCCAGGGAG 192  
QY 124 GGCCTGAGTGAATCGGCAACATCTATACAGTGGCAACCTAACAAACCCGTCTC 183  
Db 193 GGCCTGAGTGAATGGGTATCATCTATTACAGTGGCAACCTAACAAACCCGTCTC 252  
QY 184 AAGAGTGAATTCATGTCATGTCAGTGAACAGCTTAAGAACCACTTCTCCCTGAGACTGAC 243  
Db 253 AAGAGTGAATTCATGTCATGTCAGTGAACAGCTTAAGAACCACTTCTCCCTGAGACTGAC 312  
QY 244 TCTGTGACTGCGCGGACAGCGCGCTATTACTGTGCGGGTCACTGGGTACT--- 300  
Db 313 TCTGTGACTGCGCGGACAGCGCGCTATTACTGTGCGGGTCACTGGGTACTGGT 372  
QY 301 -----TTGACAACTGGGCGCAGGAAACCTGTGTCACCGTCTCCTCA 342  
Db 373 GGTATTAGACTACTTGTGACTACTGGGGCAGGAAACCTGTGTCACCGTCTCCTCA 429

RESULT 10  
US-08-545-809A-31  
; Sequence 31, Application US/08545809A  
; Patent No. 6096878

GENERAL INFORMATION:

APPLICANT: Honjo, Tsukuru

APPLICANT: Matsuda, Fumihiko

TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

NUMBER OF SEQUENCES: 145

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/545,809A

FILING DATE: 27-MAR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00603

FILING DATE: 10-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 06501/004001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 631 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

CELL TYPE: human lymphoblast

CELL LINE: CEM1

Query Match 70.9%; Score 242.6; DB 3; Length 631;

Best Local Similarity 91.5%; Pred. No. 4,6e-66;  
Matches 257; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 4 GAGTCGGCCAGAGCTGTGAAGCCTTTCACAGACCTCTGT-CCTACCTGCACTGTCTCT 63  
Db 305 GAGTCGGCCAGAGCTGTGAAGCCTTTCACAGACCTCTGT-CCTACCTGCACTGTCTCT 364  
QY 64 GGTGCTCCATCCGACAGTGGTGTATTATTGAGTGGGTCCGACAGCTCCAGGGAG 123  
Db 365 GGTGCTCCATCCGACAGTGGTGTATTATTGAGTGGGTCCGACAGCTCCAGGGAG 424  
QY 124 GGCCTGAGTGAATCGGCAACATCTATACAGTGGCAACCTAACAAACCCGTCTC 183  
Db 425 GGCCTGAGTGAATGGGTATCATCTATTACAGTGGCAACCTAACAAACCCGTCTC 484  
QY 184 AAGAGTGAATTCATGTCATGTCAGTGAACAGCTTAAGAACCACTTCTCCCTGAGACTGAC 243  
Db 485 AAGAGTGAATTCATGTCATGTCAGTGAACAGCTTAAGAACCACTTCTCCCTGAGACTGAC 544  
QY 244 TCTGTGACTGCGCGGACAGCGCGCTATTACTGTGCGGG 284  
Db 545 TCTGTGACTGCGCGGACAGCGCGCTATTACTGTGCGAG 585

RESULT 11  
US-09-471-276-51  
; Sequence 51, Application US/09471276  
; Patent No. 6822072

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclest A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6822072

FILE REFERENCE: GENSET.025CPI

CURRENT APPLICATION NUMBER: US/09/471,276

CURRENT FILING DATE: 1999-12-21

EARLIER APPLICATION NUMBER: 09/057,719

EARLIER FILING DATE: 1998-04-09

EARLIER APPLICATION NUMBER: 09/069,047

EARLIER FILING DATE: 1998-04-28

EARLIER APPLICATION NUMBER: PCT/IB99/00712

EARLIER FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 1622

SOFTWARE: Patent.pm

SEQ ID NO 51

LENGTH: 466

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 38..466

NAME/KEY: sig\_peptide

LOCATION: 38..94

OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 10.8999996185303

OTHER INFORMATION: seq FLVLVAAPRWLS/QV

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 423

OTHER INFORMATION: n=a, g, c or t

OTHER INFORMATION: Oligonucleotide

US-09-471-276-51

Query Match 69.5%; Score 237.8; DB 4; Length 466;  
Best Local Similarity 81.2%; Pred. No. 1.3e-64;  
Matches 281; Conservative 7; Mismatches 51; Indels 7; Gaps 1;  
QY 4 GAGTCGGCCAGAGCTGTGAAGCCTTTCACAGACCTCTGT-CCTACCTGCACTGTCTCT 63  
Db 110 GAGTCGGCCAGAGCTGTGAAGCCTTTCACAGACCTCTGT-CCTACCTGCACTGTCTCT 169  
QY 64 GGTGCTCCATCCGACAGTGGTGTATTATTGAGTGGGTCCGACAGCTCCAGGGAG 123

Db 170 GGTGGCTCCATCAGCACTGTTGTTACTTCTGAGTTGGATCCGCGACCCAGGCGG 229  
Qy 124 GGCCTGAGTGAATCGGCAACATCTATCAGATGGCAACCTAACAAACCCGTCCTC 183  
Db 230 GGCCTGAGTGAATCGGCAACATCTATCAGATGGCAACCTAACAAACCCGTCCTC 289  
Qy 184 AAGAGTCGAGTTCACATGTCATAGACACGCTTAAAGAACCTTCTCCCTGAGTAC 243  
Db 290 AAGAGTCGAGTTCACATGTCATAGACACGCTTAAAGAACCTTCTCCCTGAGTAC 349  
Qy 244 TCTGTGACTCCCGGACGCGGCTTATTAATGTCGCGG-----GTCAATGGGTA 236  
Db 350 TCTGTGACTCCCGGACGCGGCTTATTAATGTCGCGG-----GTCAATGGGTA 409  
Qy 297 TACTTGGACAACCTGGGCGGAGAACCTGTGTCACGCTCTCTCA 342  
Db 410 TGGTCAASHMCTNNGGGMCAAGGACCAAGTCAACGCTCTCA 455

RESULT 12  
US-09-049-672A-17  
; Sequence 17, Application US/09049672A  
; Patent No. 6135941

## GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Young, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baughn, Marian R.  
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,672A  
FILING DATE: HEREWITH  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1567 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PANTCUT01  
CLONE: 1513264  
US-09-049-672A-17

Query Match 69.4%; Score 237.4; DB 3; Length 1567;  
Best Local Similarity 82.1%; Pred. No. 2,9e-64;  
Matches 293; Conservative 0; Mismatches 46; Indels 18; Gaps 1;  
Qy 4 GAGTCTGGCCAGAGTGTGAAGCCTTCAAGACCCCTGTCTCTCACTGTCTCT 63  
Db 150 GAGTCTGGCCAGAGTGTGAAGCCTTCAAGACCCCTGTCTCTCACTGTCTCT 209  
Qy 64 GGTGGCTCCATCCGACGTGTGTTATTTATGAGTTGGTCCGCAAGCTTCAAG 123  
Db 210 GGTGGCTCCATCCGACGTGTGTTATTTATGAGTTGGTCCGCAAGCTTCAAG 269  
Qy 124 GGCCTGAGTGAATCGGCAACATCTATCAGATGGCAACCTAACAAACCCGTCCTC 183  
Db 270 GGCCTGAGTGAATCGGCAACATCTATCAGATGGCAACCTAACAAACCCGTCCTC 329  
Qy 184 AAGAGTCGAGTTCACATGTCATAGACACGCTTAAAGAACCTTCTCCCTGAGTAC 243  
Db 330 AAGAGTCGAGTTCACATGTCATAGACACGCTTAAAGAACCTTCTCCCTGAGTAC 389  
Qy 244 TCTGTGACTCCCGGACGCGGCTTATTAATGTCGCGG-----GTCAATGGGTA 232  
Db 390 TCTGTGACTCCCGGACGCGGCTTATTAATGTCGCGG-----GTCAATGGGTA 449  
Qy 293 -----GTATCTTGGACAACCTGGGCGGAGAACCCGTGTCACCTCTCTCA 342  
Db 450 GGGGGAACCTACGATGAGAGCTGTGGGCGGAGAACCCGTGTCACCTCTCTCA 506

## RESULT 13

US-09-720-493-1  
; Sequence 1, Application US/09720493  
; Patent No. 6827925

## GENERAL INFORMATION:

APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Williams, Andrew J  
APPLICANT: Tempest, Philip R  
APPLICANT: Holte, Thor L  
APPLICANT: Main, Sarah H  
APPLICANT: Jackson, Helen  
APPLICANT: Darmon, Oleksan  
TITLE OF INVENTION: Improvements relating to antibodies  
FILE REFERENCE: AHB/CP577533  
CURRENT APPLICATION NUMBER: US/09/720,493  
CURRENT FILING DATE: 2002-10-23  
PRIOR APPLICATION NUMBER: GB 9814383.7  
PRIOR FILING DATE: 1998-07-02  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 351  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(351)  
US-09-720-493-1

Query Match 69.2%; Score 236.6; DB 4; Length 351;  
Best Local Similarity 83.2%; Pred. No. 2.7e-64;  
Matches 282; Conservative 0; Mismatches 54; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGAGTGTGAAGCCTTCAAGACCCCTGTCTCTCACTGTCTCT 63  
Db 16 GAGTCTGGCCAGAGTGTGAAGCCTTCAAGACCCCTGTCTCTCACTGTCTCT 75  
Qy 64 GGTGGCTCCATCCGACGTGTGTTATTTATGAGTTGGTCCGCAAGCTTCAAG 123  
Db 76 GGTGGCTCCATCCGACGTGTGTTATTTATGAGTTGGTCCGCAAGCTTCAAG 132  
Qy 124 GGCCTGAGTGAATCGGCAACATCTATCAGATGGCAACCTAACAAACCCGTCCTC 183  
Db 133 GGCCTGAGTGAATCGGCAACATCTATCAGATGGCAACCTAACAAACCCGTCCTC 192

QY 184 AAGAGTGAATTACATGTCAGTAGACAGCTTAAGAACACTTCTCCCTGAGACTGACC 243  
| | | | |  
Db 193 AAGAGTGAAGTACACCATATCATGATGACACGCTCAAGAACAGCTGCTCCCTGAACTGAGC 252  
| | | | |  
QY 244 TCTGTGACTGCGCGGAGACAGCGCGCTCATATCTGTGGCGCGGTGAGATGGTATACCTTTG 303  
| | | | |  
Db 253 TCTGTGACCGCGCGGAGACAGCGCGCTGTATTAATCTGTGCMAAGGAGAGTGTGCAAGTTT 312  
| | | | |  
QY 304 GACAACCTGGGGGCGAGGAAACCTGTGTCACCGTCTCTCA 342  
| | | | |  
Db 313 GACTATTGGGGCGCAAGGACCCCTGTGTACCGTCTCTTCA 351  
| | | | |

## RESULT 14

US-09-720-493-21/c  
; Sequence 21. Application US/09720493  
; Patent No. 6827925  
; GENERAL INFORMATION:  
; APPLICANT: Cambridge Antibody Technology Limited  
; APPLICANT: Williams, Andrew J  
; APPLICANT: Tempest, Philip R  
; APPLICANT: Holter, Thor L  
; APPLICANT: Main, Sarah H  
; APPLICANT: Jackson, Helen  
; APPLICANT: Daromola, Olalekan  
; TITLE OF INVENTION: Improvements relating to antibodies  
; FILE REFERENCE: AHB/CP5775333  
; CURRENT APPLICATION NUMBER: US/09/720,493  
; CURRENT FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: GB 9814383.7  
; PRIOR FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 351  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-720-493-21

Query Match 69.2%; Score 236.6; DB 4; Length 351;  
Best Local Similarity 83.2%; Pred. No. 2.7e-64;  
Matches 282; Conservative 0; Mismatches 54; Indels 3; Gaps 1;  
QY 4 GAGCTGGCCCGAGAGCTGTGTAAGCTTCAAGACCCCTGCTCACTGAGCTGCTCT 63  
| | | | |  
Db 336 GAGTCCGCGCCAGAGACTGTGTAAGCTTGGAGACCCCTGCTCACTGAGCTGCTCT 277  
| | | | |  
QY 64 GGTGGCTCCATCCGAGTGTGTTAATTAATGAGTTGGTCCGCGAGCTCCAGGGAG 123  
| | | | |  
Db 276 GGTACTCTCATCAACA---GTGGTTACTACTGGGGCTGGATTCCGGACGCCCGAGGAG 220  
| | | | |  
QY 124 GGCCTGAGTGGATCGGCAACATCTATCAAGTGGCAACACCTTCAACACACCGTCCCTC 183  
| | | | |  
Db 219 GGGCTGAGTGGATGGAGATGATCATATGATGGAGACCTTACTACACCCGTCCTC 160  
| | | | |  
QY 184 AAGAGTGAATTACATGTCAGTAGACAGCTTAAGAACCTTCTCCCTGAGACTGACC 243  
| | | | |  
Db 159 AAGAGTGAAGTACCATATATCATGTAGACAGCTTCAAGAACCAAGTTCTCCCTGAACTGAGC 100  
| | | | |  
QY 244 TCTGTGACTGCGCGGAGACAGCGCGTCTAATTAATGAGTGGCGCGGTGAGATGGTATACCTTTG 303  
| | | | |  
Db 99 TCTGTGACCGCGCGGAGACAGCGCGGTGTATTAATGAGTGGAGAGGAGAGTGTGCAAGTTT 40  
| | | | |  
QY 304 GACAACCTGGGGGCGAGGAAACCTGTGTCACCGTCTCTCA 342  
| | | | |  
Db 39 GACTATTGGGGCGCAAGGACCCCTGTGTACCGTCTCTTCA 1  
| | | | |

RESULT 15  
US-09-800-729-74  
; Sequence 74. Application US/09800729  
; Patent No. 6605592

; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: P2044P1  
; CURRENT APPLICATION NUMBER: US/09/800,729  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 74  
; LENGTH: 1543  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-800-729-74

Query Match 68.6%; Score 234.6; DB 4; Length 1543;  
Best Local Similarity 81.0%; Pred. No. 2.2e-63;  
Matches 273; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 4 GAGTCTGGCCCGAGAGCTGTGTAAGCTTCAAGACCCCTGCTCACTGAGCTGCTCT 63  
| | | | |  
Db 90 GAGTCCGCGCCAGAGACTGTGTAAGCTTCAAGACCCCTGCTCACTGAGCTGCTCT 149  
| | | | |  
QY 64 GGTGGCTCCATCCGAGTGTGTTAATTAATGAGTTGGTCCGCGAGCCCTCCAGGGAG 123  
| | | | |  
Db 150 GGTGGCTCCATCCAGAGTGTGTTAATTAATGAGTTGGTCCGCGAGCCCTCCAGGGAG 209  
| | | | |  
QY 124 GGCCTGAGTGGATCGGCAACATCTATCAAGTGGCAACACTTCAACACCCGTCCTC 183  
| | | | |  
Db 210 GGCCTGAGTGGATGGGTGATCTCTTACATGGGGTCACTACTACATTCGTCCTC 269  
| | | | |  
QY 184 AAGAGTGAATTACATGTCAGTAGACAGCTTAAGAACCTTCTCCCTGAGACTGACC 243  
| | | | |  
Db 270 AAGAGTGAAGTACCATATCTGTAGACAGCTTCAAGAACCAAGTTCTCCCTGAGGCTGAGC 329  
| | | | |  
QY 244 TCTGTGACTGCGCGGAGACAGCGCGTCTAATTAATGAGTGGCGCGGTGAGATGGTATACCTTTG 303  
| | | | |  
Db 330 TCTGTGACTGCGCGGAGACAGCGCGTCTAATTAATGAGTGGCGCGGTGAGATGGTATACCTTTG 389  
| | | | |  
QY 304 GACAACCTGGGGGCGAGGAAACCTGTGTCACCGTCTCTCA 340  
| | | | |  
Db 390 GACCGTACCAAGCTGGAATACCAAGGCTTGTGACTACT 426  
| | | | |

Search completed: July 27, 2005, 12:41:20  
Job time : 95.3455 secs

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:42:26 ; Search time 95.3455 Seconds

(without alignments)  
5869.253 Million cell updates/sec

Title: US-10-027-725A-1

Perfect score: 342

Sequence: 1 cctcgagctcggccagagact.....ccctggtcaccgtctcctca 342

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PTCUS.COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	260.8	76.3	516 4	US-09-472-087-33 Sequence 33, Appl
2	255.6	74.7	357 1	US-08-360-125-3 Sequence 3, Appl
3	255.6	74.7	357 2	US-08-450-578-3 Sequence 3, Appl
4	255.6	74.7	357 2	US-09-017-628-3 Sequence 3, Appl
5	255.6	74.7	357 2	US-09-014-880-3 Sequence 3, Appl
6	255.6	74.7	357 3	US-08-450-363-3 Sequence 3, Appl
7	255.6	74.7	357 3	US-09-467-903-3 Sequence 3, Appl
8	249	72.8	631 3	US-08-545-809A-31 Sequence 31, Appl
9	248.6	72.7	1567 3	US-09-049-672A-17 Sequence 17, Appl
10	247.8	72.5	450 4	US-09-582-317-13 Sequence 13, Appl
11	241	70.5	466 4	US-09-471-276-51 Sequence 51, Appl
12	241	70.5	1543 4	US-09-800-729-74 Sequence 74, Appl
13	240	70.2	504 4	US-09-471-276-100 Sequence 100, App
14	237	69.3	366 1	US-08-360-125-9 Sequence 9, Appl
15	237	69.3	366 2	US-08-450-578-9 Sequence 9, Appl
16	237	69.3	366 2	US-09-017-628-9 Sequence 9, Appl
17	237	69.3	366 2	US-09-014-880-9 Sequence 9, Appl
18	237	69.3	366 4	US-08-450-363-9 Sequence 9, Appl
19	236.6	69.2	366 4	US-09-467-903-9 Sequence 9, Appl
20	236.6	69.2	351 4	US-09-720-493-1 Sequence 21, Appl
21	236.6	69.2	351 4	US-09-720-493-21 Sequence 21, Appl
22	228.2	66.7	1212 3	US-08-545-809A-61 Sequence 39, Appl
23	225	65.8	800 3	US-08-545-809A-39 Sequence 39, Appl
24	219.2	64.1	288 3	US-08-851-362D-7 Sequence 7, Appl
25	218.4	63.9	403 3	US-09-042-353-357 Sequence 205, App
26	218.4	63.9	403 3	US-08-758-417A-205 Sequence 4, Appl
27	218.2	63.8	840 3	US-09-260-527-4 Sequence 4, Appl

28	217.8	63.7	291 3	US-08-851-362D-11 Sequence 11, Appl
29	213	62.3	357 2	US-08-652-816A-20 Sequence 20, Appl
30	212	62.0	291 3	US-08-851-362D-9 Sequence 9, Appl
31	211	61.7	800 3	US-08-545-809A-55 Sequence 55, Appl
32	209.6	61.3	294 3	US-08-851-362D-3 Sequence 3, Appl
33	209.2	61.2	417 4	US-09-203-768A-1 Sequence 1, Appl
34	209	61.1	624 3	US-08-545-809A-28 Sequence 28, Appl
35	208.8	61.1	524 3	US-09-042-353-419 Sequence 429, Appl
36	208.8	61.1	524 3	US-08-758-417A-219 Sequence 219, App
37	208.8	61.1	4926 3	US-09-042-353-418 Sequence 418, App
38	208.8	61.1	4926 3	US-08-758-417A-268 Sequence 268, App
39	208.6	61.0	392 4	US-09-471-276-52 Sequence 52, Appl
40	208.4	60.9	360 4	US-09-424-840B-19 Sequence 19, Appl
41	207.8	60.8	404 3	US-09-042-353-355 Sequence 355, App
42	207.8	60.8	404 3	US-08-758-417A-203 Sequence 203, App
43	206.2	60.3	622 3	US-08-545-809A-59 Sequence 59, Appl
44	205	59.9	291 3	US-08-851-362D-5 Sequence 5, Appl
45	204.8	59.9	467 4	US-09-471-276-99 Sequence 99, Appl

#### ALIGNMENTS

RESULT 1

US-09-472-087-33 Application US/09472087

Patent No. 6682736

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: NEVEU, MARK J.

APPLICANT: MUELLER, ELLEN E.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GLIMAN, STEVEN C.

APPLICANT: DAVIS, C. GEOFFREY

APPLICANT: CORVALAN, JOSE R.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PPI

CURRENT APPLICATION NUMBER: US/09/472,087

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/113,647

PRIOR FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 33

LENGTH: 516

TYPE: DNA

ORGANISM: Homo sapiens

US-09-472-087-33

Query Match

Best Local Similarity 87.4%; Pred. No. 2.5e-72;

Matches 299; Conservative 37; Indels 6; Gaps 1;

Qy	7	TCGCGCCAGAGAGCTGAGAGCCCTGACAGACCTGTCCTGAGCTGCTGAC	66
Db	1	TCGCGCCAGAGAGCTGAGAGCCCTGACAGACCTGTCCTGAGCTGCTGAC	60
Qy	67	GGCTCCATCCGACAGTGTGTTACTGAGAGTTGATCCGCCAACCCAGGAGGCG	126
Db	61	GGCTCCATCCGACAGTGTGTTACTGAGAGTTGATCCGCCAACCCAGGAGGCG	120
Qy	127	CTGAGAGGATGGGTGATCTATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG	186
Db	121	CTGAGAGGATGGGTGATCTATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG	180
Qy	187	AGTGAATTCGACATGCTGAGAGCCTGAGAGGAGGAGGAGGAGGAGGAGGAG	246
Db	181	AGTGAATTCGACATGCTGAGAGCCTGAGAGGAGGAGGAGGAGGAGGAGGAG	240
Qy	247	GTCAGTCCCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	300
Db	241	GTCAGTCCCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	300

QY 301 TTGGACATCTGGGGCCAGGAGACCCCTGTGACCGTCTCTCA 342  
DB 301 ATAGACGCTGGGGCCAGGAGACCGTCAACCGTCTCTCA 342

## RESULT 2

US-08-360-125-3

/ Sequence 3, Application US/08360125  
/ Patent No. 5767246  
/ GENERAL INFORMATION:  
/ APPLICANT: Saiko HOSOKAWA  
/ APPLICANT: Tohiaki TAGAWA  
/ APPLICANT: Yoko HIRAKAWA  
/ APPLICANT: No. 5767246ihiko ITO  
/ APPLICANT: Kazuhiro NAGAIKE  
/ TITLE OF INVENTION: Human Monoclonal Antibody  
/ TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
/ TITLE OF INVENTION: Cell Membrane  
/ NUMBER OF SEQUENCES: 42  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Wenderoth, Lind & Ponack  
/ STREET: 805 Fifteenth Street, N.W., #700  
/ CITY: Washington  
/ STATE: D.C.  
/ COUNTRY: U.S.A.  
/ ZIP: 20005  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: MS-DOS  
/ SOFTWARE: Wordperfect 5.1  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/360,125  
/ FILING DATE:  
/ CLASSIFICATION: 424  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 07/905,534  
/ FILING DATE: June 29, 1992  
/ APPLICATION NUMBER:  
/ FILING DATE:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Warren M. Cheek, Jr.  
/ REGISTRATION NUMBER: 33,367  
/ REFERENCE/DOCKET NUMBER:  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-371-8850  
/ TELEFAX:  
/ TELEX:  
/ INFORMATION FOR SEQ ID NO: 3:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 357 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: double  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: cDNA  
/ HYPOTHEICAL:  
/ ANTI-SENSE:  
/ FRAGMENT TYPE:  
/ ORIGINAL SOURCE:  
/ ORGANISM:  
/ STRAIN:  
/ INDIVIDUAL ISOLATE:  
/ DEVELOPMENTAL STAGE:  
/ HAPLOTYPE:  
/ TISSUE TYPE:  
/ CELL TYPE: Hybridoma producing human  
/ CELL TYPE: antibody G4H  
/ CELL LINE:  
/ ORGANELLER:  
/ IMMEDIATE SOURCE:  
/ LIBRARY:  
/ CLONE:  
/ POSITION IN GENOME:

/ CHROMOSOME/SEGMENT:  
/ MAP POSITION:  
/ UNITS:  
/ FEATURE:  
/ NAME/KEY:  
/ LOCATION:  
/ IDENTIFICATION METHOD:  
/ OTHER INFORMATION:  
/ PUBLICATION INFORMATION:  
/ AUTHORS:  
/ TITLE:  
/ JOURNAL:  
/ VOLUME:  
/ ISSUE:  
/ PAGES:  
/ DATE:  
/ DOCUMENT NUMBER:  
/ FILING DATE:  
/ PUBLICATION DATE:  
/ RELEVANT RESIDUES IN SEQ ID NO:  
/ US-08-360-125-3

Query Match 74.7%; Score 255.6; DB 1; Length 357;

Best Local Similarity 86.3%; Pred. No. 9,2e-71;  
Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 4 GAAGTCGGCCAGGAGCTGTGAAGCCTGACAGACCCCTGCTCAGCTGGCTGTCT 63  
DB 16 GAATCGGGCCAGGAGCTGTGAAGCCTTACAGACCCCTGCTCAGCTGTCTCT 75  
QY 64 GCGGCTCCATCCGCGAGTGTGTACTACTGAGTTGATTCGCGCAAGCCAGGGAAG 123  
DB 76 GGTGGCTCCATCAGAGTGTGTGTCTACTGAACTGAGTCCGCGAGCCAGGGAAG 135  
QY 124 GGCCTGAGTGAATGGGTATCATCAAGTGGGAACACTACAAACCCGCTCC 183  
DB 136 GGCCTGAGTGAATGGGTATCATCAAGTGGGAACACTACAAACCCGCTCC 195  
DB 184 AAGAGTCGAATGCCATGTGCTAGACACGCTGTGAGAACAAATGTTCCCTGAGGCTGAAC 243  
DB 196 AAGAGTCGAATGCCATGTGCTAGACACGCTGTGAGAACAAATGTTCCCTGAGGCTGAAC 255  
QY 244 TCTGTGATCGCCCGGACAGGCGCGTATTAATGTCGAGGTTAATGCTACACTT 303  
DB 256 TCTGTGATCGCCCGGACAGGCGCGTATTAATGTCGAGGTTAATGCTACACTT 315  
QY 304 ---GACATCTGGGGCCAGGAGACCCGTCAACCGTCTCTCA 342  
DB 316 GCTGACTACTGGGGCCAGGAGACCAATGTCACCGTCTCTCA 357

## RESULT 3

US-08-450-578-3

/ Sequence 3, Application US/08450578  
/ Patent No. 5837845  
/ GENERAL INFORMATION:  
/ APPLICANT: Saiko HOSOKAWA  
/ APPLICANT: Tohiaki TAGAWA  
/ APPLICANT: Yoko HIRAKAWA  
/ APPLICANT: No. 5837845ihiko ITO  
/ APPLICANT: Kazuhiro NAGAIKE  
/ TITLE OF INVENTION: Human Monoclonal Antibody  
/ TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
/ TITLE OF INVENTION: Cell Membrane  
/ NUMBER OF SEQUENCES: 42  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Wenderoth, Lind & Ponack  
/ STREET: 805 Fifteenth Street, N.W., #700  
/ CITY: Washington  
/ STATE: D.C.  
/ COUNTRY: U.S.A.  
/ ZIP: 20005  
/ COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/450,578  
 FILING DATE: May 25, 1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/360,125  
 FILING DATE: December 20, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/905,534  
 FILING DATE: June 29, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek, Jr.  
 REGISTRATION NUMBER: 33,367  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-8850  
 TELEFAX:  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 357 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHEetical:  
 ANTI-SENSE:  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM:  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL TYPE: Hybridoma producing human  
 CELL LINE: antibody GAH  
 CELL TYPE:  
 ORGANELLE:  
 IMMEDIATE SOURCE:  
 LIBRARY:  
 CLONE:  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT:  
 MAP POSITION:  
 UNITS:  
 FEATURES:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:  
 VOLUME:  
 ISSUE:  
 PAGES:  
 DATE:  
 DOCUMENT NUMBER:  
 FILING DATE:  
 PUBLICATION DATE:  
 RELEVANT RESIDUES IN SEQ ID NO:  
 US-08-450-578-3

Query Match 74.7%; Score 255.6; DB 2; Length 357;  
 Best Local Similarity 86.3%; Pred. No. 9.2e-71;  
 Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Query 4  
 Db 16  
 QY 64  
 Db 76  
 QY 124  
 Db 136  
 QY 184  
 Db 196  
 QY 244  
 Db 256  
 QY 304  
 Db 316

4 GAGTCTGCCCCAGAGACTGTGAAGCCCTGCACAGACCCTGTCTCTCACTGCTCTCT  
 16 GAGTCTGCCCCAGAGACTGTGAAGCCCTGCACAGACCCTGTCTCTCTCACTGCTCTCT  
 64 GCGGCTTCATCCGAGTGTGTACTTACTGAGTTGATTCGCGCAACCCAGGAG  
 76 GGTGCTTCATCAGCACTGTGTGTCTTACTGGAACCTGATTCGCGCAACCCAGGAG  
 124 GGCCTGAGTGAATTGGGTATCTATCAAGTGGGGAACCTTAAACACCCGCTC  
 136 GGCCTGAGTGAATTGGGTATCTATCAAGTGGGGAACCTTAAACACCCGCTC  
 184 AAGAGTGAATTGGGTATCTATCAAGTGGGGAACCTTAAACACCCGCTC  
 196 AAGAGTGAATTGGGTATCTATCAAGTGGGGAACCTTAAACACCCGCTC  
 244 TCTGTGACTGCGCGGACACGCGCGTATTAATGTCGAGGTTAGATGCTACATT  
 256 TCTGTGACTGCGCGGACACGCGCGTATTAATGTCGAGGTTAGATGCTACATT  
 304 ---GACATCTGGGGCCAGGGAACCTTGTCAACCTTCTCTCA 342  
 316 GCTGACTACTGGGGCCAGGGAACCTTGTCAACCTTCTCTCA 357

RESULT 4  
 US-09-017-628-3  
 Sequence 3, Application US/09017628  
 Patent No. 5990287  
 GENERAL INFORMATION:  
 APPLICANT: HOSOKAWA, Saiko  
 APPLICANT: TAGAWA, Toshiaki  
 APPLICANT: HIRAKAWA, Yoko  
 APPLICANT: ITO, No. 5990287hiko  
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
 TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
 FILE REFERENCE: 177/527361KH  
 CURRENT APPLICATION NUMBER: US/09/017,628  
 CURRENT FILING DATE: 1998-02-02  
 EARLIER APPLICATION NUMBER: 08/360,125  
 EARLIER FILING DATE: 1994-12-20  
 NUMBER OF SEQ ID NOS: 42  
 SOFTWARE: Patent In Ver. 2.0  
 SEQ ID NO 3  
 LENGTH: 357  
 TYPE: DNA  
 ORGANISM: Unknown  
 FEATURES:  
 OTHER INFORMATION: Hybridoma producing human antibody GAH  
 US-09-017-628-3

Query Match 74.7%; Score 255.6; DB 2; Length 357;  
 Best Local Similarity 86.3%; Pred. No. 9.2e-71;  
 Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 4  
 Db 16  
 QY 64  
 Db 76  
 QY 124  
 Db 136  
 QY 184  
 Db 196  
 QY 244

4 GAGTCTGCCCCAGAGACTGTGAAGCCCTGCACAGACCCTGTCTCTCTCACTGCTCTCT  
 16 GAGTCTGCCCCAGAGACTGTGAAGCCCTGCACAGACCCTGTCTCTCTCACTGCTCTCT  
 64 GCGGCTTCATCCGAGTGTGTACTTACTGAGTTGATTCGCGCAACCCAGGAG  
 76 GGTGCTTCATCAGCACTGTGTGTCTTACTGGAACCTGATTCGCGCAACCCAGGAG  
 124 GGCCTGAGTGAATTGGGTATCTATCAAGTGGGGAACCTTAAACACCCGCTC  
 136 GGCCTGAGTGAATTGGGTATCTATCAAGTGGGGAACCTTAAACACCCGCTC  
 184 AAGAGTGAATTGGGTATCTATCAAGTGGGGAACCTTAAACACCCGCTC  
 196 AAGAGTGAATTGGGTATCTATCAAGTGGGGAACCTTAAACACCCGCTC  
 244 TCTGTGACTGCGCGGACACGCGCGTATTAATGTCGAGGTTAGATGCTACATT

Db 256 TCCTGCTGCTGCGGACAGCGCCGTGTATTAAGTGTACCCGACTACGGGGG 315  
Qy 304 ---GACATCTGGGGCCAGGGAACCTGTGTCACCGTCTCCCTCA 342  
Db 316 GCTGACTACTGGGGCCAGGGAACAATGTCACCGTCTCTTCA 357

## RESULT 5

US-09-014-880-3

; Sequence 3, Application US/09014880  
; Patent No. 590297

; GENERAL INFORMATION:

; APPLICANT: Saiko HOSOKAWA et al.

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY

; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind &amp; Ponack, L.L.P.

; STREET: 2033 K Street, N.W., #800

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/014,880

; FILING DATE: January 28, 1998

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/450,578

; FILING DATE: May 25, 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/360,125

; FILING DATE: December 20, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/905,534

; FILING DATE: June 29, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-721-8200

; TELEFAX: 202-721-8250

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 357 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; CELL TYPE: Hybridoma producing human

; US-09-014-880-3

Query Match 74.7%; Score 255.6; DB 2; Length 357;

Best Local Similarity 86.3%; Pred. No. 9.2e-71;

Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Qy 4 GAGTCTGCCCCAGAGTGTGTAGACCTGACAGACCCCTGTCCTCAAGCTGCTGTCT 63  
Db 16 GAGTCGGGGCCAGAGCTGTGTAAACCTTCACAGACCCCTGTCCTCAAGCTGTCTCT 75  
Qy 64 GGGGGCTCCATCCGACATGTGTGTACTACATGAGATTGAGATCCGCAACCCAGGAG 123  
Db 76 GGTGGCTCCATCAGACAGTGTGTGTCTTACTGTGAATCGATCCGCAACCCAGGAG 135

Qy 124 GGCTGAGTGTGATTTGGGTACATCTATCAAGTGGGAACACTTAAACAACCCGTCCCTC 183  
Db 136 GGCTGAGTGTGATTTGGGTACATCTATCAAGTGGGAACACTTAAACAACCCGTCCCTC 195  
Qy 184 AAGATCGAATTTGCCATGTGTGTAGACAGCTGTGAGAACAAATTTCTCCCTGAGGCTGAG 243  
Db 196 AAGATCGAATTTGCCATGTGTGTAGACAGCTGTGAGAACAAATTTCTCCCTGAGGCTGAG 255  
Qy 244 TCCTGACTGCGCCGACAGCGCCGTGTATTAAGTGTACCGGACTTACACTTTG 303  
Db 256 TCCTGACTGCGCCGACAGCGCCGTGTATTAAGTGTACCGGACTTACACTTTG 315  
Qy 304 ---GACATCTGGGGCCAGGGAACCTGTGTCACCGTCTCCCTCA 342  
Db 316 GCTGACTACTGGGGCCAGGGAACAATGTCACCGTCTCTTCA 357

## RESULT 6

US-08-450-363-3

; Sequence 3, Application US/08450363  
; Patent No. 6436434

; GENERAL INFORMATION:

; APPLICANT: Saiko HOSOKAWA

; APPLICANT: Toshiaki TAGAWA

; APPLICANT: Yoko HIRAKAWA

; APPLICANT: No. 6436434Ihiko ITO

; APPLICANT: Kazuhiro NAGAIKE

; TITLE OF INVENTION: Human Monoclonal Antibody

; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind &amp; Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/450,363

; FILING DATE: May 25, 1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/360,125

; FILING DATE: December 20, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/905,534

; FILING DATE: June 29, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8850

; TELEFAX:

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 357 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL:

; ANTI-SENSE:

; FRAGMENT TYPE:

; ORIGINAL SOURCE:



ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-363-3

Query Match 74.7%; Score 255.6; DB 3; Length 357;  
Best Local Similarity 86.3%; Pred. No. 9.2e-71;  
Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;  
QY 4 GAGTCTGGCCGAGAGCTGTGAGACCTGACAGACCCCTGTCTCTGAGTGGCTGTCTCT 63  
DB 16 GAGTCTGGCCGAGAGCTGTGAGACCTGACAGACCCCTGTCTCTGAGTGGCTGTCTCT 75  
QY 64 GCGCGCTTCACCTCCGAGTGTGTTACTGAGTGGATCCGCAACCCAGGGAG 123  
DB 76 GGTGGCTTCACCTCCGAGTGTGTTACTGAGTGGATCCGCAACCCAGGGAG 135  
QY 124 GCGCTGAGTGGATGGGTACATCTATGACAGTGGGAAACCTTCAACCAACCGTCCCTC 183  
DB 136 GCGCTGAGTGGATGGGTACATCTATGACAGTGGGAAACCTTCAACCAACCGTCCCTC 195  
QY 184 AAGAGTCGAATTGCGCATGTCGGTAGACACGTCTGAGAACAGTTCTCCCTGAGGCTGAC 243  
DB 196 AAGAGTCGAATTGCGCATGTCGGTAGACACGTCTGAGAACAGTTCTCCCTGAGGCTGAC 255  
QY 244 TCTGTACTGCGCGGAGACCGCGGTGATTACTGTGCGAGGTAGATGCTTACACTTTG 303  
DB 256 TCTGTACTGCGCGGAGACCGCGGTGATTACTGTGCGAGGTAGATGCTTACACTTTG 315  
QY 304 ---GACATCTGGGGCGAGGAAACCTGTGTCACCGTCTCTCA 342  
DB 316 GCTGACTACTGGGGCGAGGAAACAGTGTGTCACCGTCTCTCA 357

RESULT 7  
US-09-467-903-3  
Sequence 3, Application US/09467903  
Patent No. 6787153  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
Toshiaki TAGAWA  
Yoko HIRAKAWA

No. 6787153hiko ITO  
Kazuhiko NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
Specifically Binding to Surface Antigen of Cancer  
Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Menderoth, Lind & Ponack  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/467,903  
FILING DATE: 21-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,363  
FILING DATE: May 25, 1995  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER: JP158859/1991  
FILING DATE: June 28, 1991  
APPLICATION NUMBER: JP158860/1991  
FILING DATE: June 28, 1991  
APPLICATION NUMBER: JP158861/1991  
FILING DATE: June 28, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: <Unknown>  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: <Unknown>  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: Hybridoma producing human  
antibody GAH  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:

```
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-09-467-903-3

Query Match      74.7%; Score 255.6; DB 4; Length 357;
Best Local Similarity 86.3%; Pred. No. 9.2e-71;
Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 4 GAGTCTGAGCCAGAGAGTGTGAAGCCCTGACAGACAGACCCCTGCTGCTCT 63
    |||||
DB 16 GAGTCGGGGCCAGAGAGTGTGAAGCCCTGCTGCTGCTGCTGCTGCTGCT 75
    |||||
QY 64 GCGCGCTCCATCCGAGTGTGTACTGAGTGTGATCCGCCAACCAGGAG 123
    |||||
DB 76 GGTGGCTCCATCAGCAGTGTGTGTCTGACTGAACTGATCCGCCAGAG 135
    |||||
QY 124 GGCCTGAGAGGATTTGGGTATCTATCAAGTGGGAACCTTCAACACCCCTCC 183
    |||||
DB 136 GGCCTGAGAGGATTTGGGTATCTATCAAGTGGGAACCTTCAACACCCCTCC 195
    |||||
QY 184 AAGAGTCGAATTGCGATGCGTAGACACGCTGAGAACAGATTCTCCCTGAGGCTG 243
    |||||
DB 196 AAGAGTCGAATTGCGATGCGTAGACACGCTGAGAACAGATTCTCCCTGAGGCTG 255
    |||||
QY 244 TCTGTACTGCGCGGACACGCGCGTATTACTGTGCGAGTTAGATGCTACACTTTG 303
    |||||
DB 256 TCTGTACTGCGCGGACACGCGCGTATTACTGTGCGAGTTAGATGCTACACTTTG 315
    |||||
QY 304 ---GACATCTGGGGCGAGGGAACCGTGTCACCGCTCTCTCA 342
    |||||
DB 316 GCTGACTACTGGGGCGAGGGAACAGTGTCACCGCTCTCTCA 357
    |||||

RESULT 8
US-08-545-809A-31
; Sequence 31, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545, 809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
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FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: GM1
US-08-545-809A-31

Query Match      72.8%; Score 249; DB 3; Length 631;
Best Local Similarity 92.9%; Pred. No. 1.4e-68;
Matches 261; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 4 GAGTCTGAGCCAGAGAGTGTGAAGCCCTGACAGACAGACCCCTGCTGCTCT 63
    |||||
DB 305 GAGTCGGGGCCAGAGAGTGTGAAGCCCTGCTGCTGCTGCTGCTGCTGCT 364
    |||||
QY 64 GCGCGCTCCATCCGAGTGTGTACTGAGTGTGATCCGCCAACCAGGAG 123
    |||||
DB 365 GGTGGCTCCATCAGCAGTGTGTGTCTGACTGAACTGATCCGCCAGAG 424
    |||||
QY 124 GGCCTGAGAGGATTTGGGTATCTATCAAGTGGGAACCTTCAACACCCCTCC 183
    |||||
DB 425 GGCCTGAGAGGATTTGGGTATCTATCAAGTGGGAACCTTCAACACCCCTCC 484
    |||||
QY 184 AAGAGTCGAATTGCGATGCGTAGACACGCTGAGAACAGATTCTCCCTGAGGCTG 243
    |||||
DB 485 AAGAGTCGAATTGCGATGCGTAGACACGCTGAGAACAGATTCTCCCTGAGGCTG 544
    |||||
QY 244 TCTGTACTGCGCGGACACGCGCGTATTACTGTGCGAG 284
    |||||
DB 545 TCTGTACTGCGCGGACACGCGCGTATTACTGTGCGAG 585
    |||||

RESULT 9
US-09-049-672A-17
; Sequence 17, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,672A  
FILING DATE: HERWITH  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1567 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PANTU01  
CLONE: 1513264  
US-09-049-672A-17

Query Match 72.7%; Score 248.6; DB 3; Length 1567;  
Best Local Similarity 84.0%; Pred. No. 2.8e-68;  
Matches 300; Conservative 0; Mismatches 39; Indels 18; Gaps 1;

QY 4 GAGTCTGGCCAGAGCTGTGAAGCCCTGACAGACCCCTGCTCAGTGGCTGTCT 63  
DB 150 GAGTGGGCCCCAGAGCTGTGAAGCCCTGCGAGACCCCTGCTCAGTGGCTGTCT 209  
QY 64 GCGCGCTCCATCCCGAGTGTGTTACTGAGTGGATCCGCGCAACCCAGGGAG 123  
DB 210 GGTGGCTCCATCAGTGGTGTGTTACTGAGTGGATCCGCGCAACCCAGGGAG 269  
QY 124 GCGCTGAGTGTGTTGGTATCATCTATCAAGTGGAGAACCTTCAACACCCGCTC 183  
DB 270 GCGCTGAGTGTGTTGGTATCATCTATCAAGTGGAGAACCTTCAACACCCGCTC 329  
QY 184 AAGAGTGAATGGCATGTGCTGAGACAGCTGTAGAACAGTTCCTGAGCTGAC 243  
DB 330 AAGAGTGAATGGCATGTGCTGAGACAGCTGTAGAACAGTTCCTGAGCTGAC 389  
QY 244 TCTGTGACTGCGCGGAGACAGCGCGGTGTTACTGTGCGAGTTAGATG----- 292  
DB 390 TCTGTGACTGCGCGGAGACAGCGCGGTGTTACTGTGCGAGTTAGATG----- 449  
QY 293 -----GCTACACTTGTGACATCTGGGCGCAGGGAACCTGTGACCGTCTCTCA 342  
DB 450 GGGGGAACCTACGATGAGACGTCTGGGCGCAGGGAACCTGTGACCGTCTCTCA 506

RESULT 10  
US-09-582-337-13  
Sequence 13, Application US/09582337  
Patent No. 6562618  
GENERAL INFORMATION:  
APPLICANT: Japan Tobacco, Inc.  
TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor  
FILE REFERENCE: J1-009PCT  
CURRENT APPLICATION NUMBER: US/09/582,337  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: JP P1997-367699  
PRIOR FILING DATE: 1997-12-25  
PRIOR APPLICATION NUMBER: JP P1998-356183  
PRIOR FILING DATE: 1998-12-15  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentl Ver. 2.0

SEQ ID NO 13  
LENGTH: 450  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(450)  
NAME/KEY: sig\_peptide  
LOCATION: (1)..(58)  
NAME/KEY: V\_region  
LOCATION: (59)..(353)  
US-09-582-337-13

Query Match 72.5%; Score 247.8; DB 4; Length 450;  
Best Local Similarity 85.7%; Pred. No. 2.9e-68;  
Matches 306; Conservative 0; Mismatches 32; Indels 19; Gaps 2;

QY 4 GAGTCTGGCCAGAGCTGTGAAGCCCTGACAGACCCCTGCTCAGTGGCTGTCT 63  
DB 74 GAGTGGGCCCCAGAGCTGTGAAGCCCTTCAAGACCTGT-CTTCACTGCACTGTCTCT 132  
QY 64 GCGCGCTCCATCCCGAGTGTGTTACTGAGTGGATCCGCGCAACCCGCTCCTC 123  
DB 133 GGTGGCTCCATCAGTGGTGTGTTACTGAGTGGATCCGCGCAACCCGCTCCTC 192  
QY 124 GCGCTGAGTGTGTTGGTATCATCTATCAAGTGGAGAACCTTCAACACCCGCTC 183  
DB 193 GCGCTGAGTGTGTTGGTATCATCTATCAAGTGGAGAACCTTCAACACCCGCTC 252  
QY 184 AAGAGTGAATGGCATGTGCTGAGACAGCTGTAGAACAGTTCCTGAGCTGAC 243  
DB 253 AAGAGTGAATGGCATGTGCTGAGACAGCTGTAGAACAGTTCCTGAGCTGAC 312  
QY 244 TCTGTGACTGCGCGGAGACAGCGCGGTGTTACTGTGCGAGT----- 286  
DB 313 TCTGTGACTGCGCGGAGACAGCGCGGTGTTACTGTGCGAGTATTAATGATGATGT 372  
QY 287 -TAGATGCTACACTTGTGACATCTGGGCGCAGGGAACCTGTGACCGTCTCTCA 342  
DB 373 GGTATTACGACATCTTGTGACTAGTGGGCGCAGGGAACCTGTGACCGTCTCTCA 429

RESULT 11  
US-09-471-276-51  
Sequence 51, Application US/09471276  
Patent No. 6822072  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert A.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6822072  
FILE REFERENCE: GENSET.025CP1  
CURRENT APPLICATION NUMBER: US/09/471,276  
PRIOR FILING DATE: 1999-12-21  
EARLIER APPLICATION NUMBER: 09/057,719  
EARLIER FILING DATE: 1998-04-09  
EARLIER APPLICATION NUMBER: 09/069,047  
EARLIER FILING DATE: 1998-04-28  
EARLIER APPLICATION NUMBER: PCT/IB99/00712  
NUMBER OF SEQ ID NOS: 1622  
SOFTWARE: Patent .pm  
SEQ ID NO 51  
LENGTH: 466  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 38..466  
NAME/KEY: sig\_peptide  
LOCATION: 38..94  
OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 10.899996185303  
OTHER INFORMATION: seq FLVLAAPRWLS/QV  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 423  
OTHER INFORMATION: n=a, g, c or t  
OTHER INFORMATION: Oligonucleotide  
US-09-471-276-51

Query Match 70.5%; Score 241; DB 4; Length 466;  
Best Local Similarity 81.8%; Pred. No. 4,1e-66;  
Matches 283; Conservative 7; Mismatches 49; Indels 7; Gaps 1;

QY 4 GAGTGTGCCCCAGAGCTGTGAAGCTGTGACAGACCCCTGTCCCTAGCTGGCTGTCT 63  
DB 110 GAGTCGGGCCCAAGAGCTGTGAAGCTGTGACAGACCCCTGTCCCTAGCTGTCTCT 169  
QY 64 GGCGGCTCCCAATCCGAGTGTGTGTTACTACTGAGATTGAGATCCGCCAACCAGGAG 123  
DB 170 GGTGGCTCCCAATCAGAGTGTGTGTTACTCTGAGATTGAGATCCGCCAACCAGGAG 229  
QY 124 GGCGTGAAGTGAATTGGGTATCATATCAAGTGGAAACACTTCAACAACCCGCTCC 183  
DB 230 GGCGTGAAGTGAATTGGGTATCATATCAATGAGACACTTCAACAACCCGCTCC 289  
QY 184 AAGAGTCGAATTGCCATGTCTGGTAGACACGTCTGAACAAGATTCTCCCTGAGGCTGAAC 243  
DB 290 AGGAGTCGAGTTACCATATGTCATGAGACACGCTTAAGAACCAAGTTCTCCCTGAACCTGAAC 349  
QY 244 TCTGTGACTGCCGGGAGACACGCGGTATATCTGTGGAGATTAGATGCTAC----- 297  
DB 350 TCTGTACTGTCCGGGAGACACGCGSCATGTATTACTGTGSASAGGTCCGGAGCGCTTGGC 409  
QY 298 -ACTTTGACATCTGGGGCCAGGAACCTGTGTACCGTCTCTCA 342  
DB 410 TGGTTCAASHMCTTNGGGGCMAGGACCCAGGTACCGCTCTCATCA 455

RESULT 12  
US-09-800-729-74  
Sequence 74, Application US/09800729  
Patent No. 6605592  
GENERAL INFORMATION:  
APPLICANT: NI et al.  
TITLE OF INVENTION: 32 Human secreted proteins  
FILE REFERENCE: P2044P1  
CURRENT APPLICATION NUMBER: US/09/800,729  
CURRENT FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: PCT/US00/26013  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 60/155,709  
NUMBER OF SEQ ID NOS: 217  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 74  
LENGTH: 1543  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-800-729-74

Query Match 70.5%; Score 241; DB 4; Length 1543;  
Best Local Similarity 82.2%; Pred. No. 7e-66;  
Matches 277; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GAGTGTGCCCCAGAGCTGTGAAGCTGTGACAGACCCCTGTCCCTAGCTGGCTGTCT 63  
DB 90 GAGTGTGCCCCAGAGCTGTGAAGCTGTGACAGACCCCTGTCCCTAGCTGTCTCT 149  
QY 64 GGCGGCTCCCAATCCGAGTGTGTGTTACTACTGAGATTGAGATCCGCCAACCAGGAG 123  
DB 150 GGTGGCTCCCAATCAGAGTGTGTGTTACTACTGAGATTGAGATCCGCCAACCAGGAG 209  
QY 124 GGCGTGAAGTGAATTGGGTATCATATCAAGTGGAAACACTTCAACAACCCGCTCC 183

DB 210 GGCGTGAAGTGAATTGGGTATCATATCTTCAACAAGGGGTCACTTAACAATCCGCTCC 269  
QY 184 AAGAGTCGAATTGCCATGTGTGAGACAGCTGTGAACAAGTTTCCCTGAGGCTGAAC 243  
DB 270 AAGAGTCGAATTGCCATGTGTGAGACAGCTGTGAACAAGTTTCCCTGAGGCTGAAC 329  
QY 244 TCTGTGACTGCCGGGAGACACGCGGTATATCTGTGCGAGATTAGATGAGCTACATT 303  
DB 330 TCTGTGACTGCCGGGAGACACGCGGTATATCTGTGCGAAGATATCGAGGACGAGA 389  
QY 304 GACATCTGGGGCCAGGGAACCTGTGTACCGTCTCT 340  
DB 390 GACGGGTACCACTGGAATTACCAAGGCTTGAATCACT 426

RESULT 13  
US-09-471-276-100  
Sequence 100, Application US/09471276  
Patent No. 6822072  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: GENSET.025CP1  
CURRENT APPLICATION NUMBER: US/09/471,276  
CURRENT FILING DATE: 1999-12-21  
EARLIER APPLICATION NUMBER: 09/057,719  
EARLIER FILING DATE: 1998-04-09  
EARLIER APPLICATION NUMBER: 09/069,047  
EARLIER FILING DATE: 1998-04-28  
EARLIER APPLICATION NUMBER: PCT/IB99/00712  
NUMBER OF SEQ ID NOS: 1622  
SOFTWARE: Patent.pm  
SEQ ID NO 100  
LENGTH: 504  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 39..503  
NAME/KEY: sig\_peptide  
LOCATION: 39..95  
OTHER INFORMATION: Von Heijne matrix  
OTHER INFORMATION: score 9.30000019073486  
OTHER INFORMATION: seq FLVLAAPRWLS/QV  
US-09-471-276-100

Query Match 70.2%; Score 240; DB 4; Length 504;  
Best Local Similarity 82.6%; Pred. No. 8,9e-66;  
Matches 284; Conservative 3; Mismatches 54; Indels 3; Gaps 1;

QY 1 CTCGAGTCTGCCCCAGAGCTGTGAAGCTGTGACAGACCCCTGTCCCTAGCTGGCTGTCT 60  
DB 108 SDKAGTCGGGCCCAAGAGCTGTGAAGCTGTGACAGACCCCTGTCCCTAGCTGTCT 167  
QY 61 TCTGGCGGCTCCCAATCCGAGTGTGTGTTACTACTGAGATTGAGATCCGCCAACCAGG 120  
DB 168 TCTGGCGGCTCCCAATCCGAGTGTGTGTTACTACTGAGATTGAGATCCGCCAACCAGG 227  
QY 121 AAGGCTGAAGTGAATTGGGTATCATATCAAGTGGAAACACTTCAACAACCCGCTCC 180  
DB 228 AAGGCTGAAGTGAATTGGGTATCATATCAAGTGGAAACACTTCTCAACCCGCTCC 287  
QY 181 CTCGAAGTCGAATTGCCATGTGTGAGACACGCTGTGAACAAGTTCTCTCGAGGCTG 240  
DB 288 CTCGAAGTCGAATTAACTATATCAATGACACGCTTAAGATGATGATGCTCCCTGAACCTG 347  
QY 241 AACTGTGACTGCCGGGAGACAGGCGGTATATCTGTGCGAGATTAGATGCTTACTACT 300

Db 348 AGGCTGTGTACTACCGCGGACAGCGCCGTCTATTACTGTGGAGAGACCAATTGCATCTT 407  
QY 301 ---TTGACATCTGGGGCGAGGAACTGTGACCTGCTTCCTC 341  
Db 408 TACTTGACCCCTGGGGCGAGGAACCTGTGTCACCGTCTTCCTC 451

RESULT 14  
US-08-360-125-9  
Sequence 9, Application US/08360125  
Patent No. 5767246  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Tohiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5767246ihiko ITO  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
City: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,125  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 366 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:

POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
JOURNAL:  
TITLE:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-9

Query Match 69.3%; Score 237; DB 1; Length 366;  
Best Local Similarity 82.3%; Pred. No. 6, 8e-65;  
Matches 289; Conservative 0; Mismatches 50; Indels 12; Gaps 1;

QY 4 GAGCTGTGCGCCAGAGCTGTGAAGCCTGACAGACCTGTCTCTGCTGCTCT 63  
Db 16 GAGTCGGGGCCAGAGCTGTGAAGCCTGCGAGACCTGTCTCTGCTGCTCT 75  
QY 64 GGGGCTTCATCCGCACTGTGTGTTACTGAGTTGATTCGGCCAAACCCAGGAG 123  
Db 76 GGTGCTCCATCAGCACTGTGTGTTACTGAGTTGATTCGGCCAAACCCAGGAG 135  
QY 124 GGCCTGAGTGAATGGGTATCTATCAAGTGGGAAACCTGACCAACACCGTCCCTC 183  
Db 136 GGGCTGAGTGAATGGGTATCTATCAAGTGGGAAACCTGACCAACACCGTCCCTC 195  
QY 184 AAGAGTCGAATTCATGTCGTAGACACGTCGTGAAGAACTTCTCCGTGAGCTGAGC 243  
Db 196 AAGAGTCGAATTCATGTCGTAGACACGTCGTGAAGAACTTCTCCGTGAGCTGAGC 255  
QY 244 TCTGTGACTCCCGCGGACAGGCGCGTATTACTGTGCGA-----GGTTGAT 291  
Db 256 TCTGTGACTCCCGCGGACAGGCGCGTATTACTGTGCGA-----GGTTGAT 315  
QY 292 GGCTACACTTGGACATCTGGGGCCAGGAAACCTGTGACCGTCTCTCTCA 342  
Db 316 TACTACGTAATGACGTCGTGGGGCCAGGAAACCGTCTCTCTCTCA 366

RESULT 15  
US-08-450-578-9  
Sequence 9, Application US/08450578  
Patent No. 5837845  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Tohiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845ihiko ITO  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
City: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 366 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-9

Query Match 69.3%; Score 237; DB 2; Length 366;  
Best local Similarity 82.3%; Pred. No. 6,8e-65;  
Matches 289; Conservative 0; Mismatches 50; Indels 12; Gaps 1;

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QY      4 GAATCTGGCCCAAGACTGAGTGAAGCCTGCACAGACCCTGTCTCTCACTGCGCTGTCTCT 63
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Db       16 GAGTCGGGCCCAAGACTGAGTGAAGCCTTCCGAGACCCTGTCTCTCACTGCTCTCT 75
QY      64 GGGGGCTCCATCCGCACTGGTGGTTACTACTGAGTTGATTCGGCCAAACCCAGGGAAG 123
        |||
Db       76 GGTGGCTCCATCAGCAGTAGTAGTACTACTGAGGGCTGGATCCGCCAGCCCCAGGGGAAG 135
QY      124 GGCCTGGAGTGAATTGGGTACATCTATCAAGTGGGAAACCTAACAAACCCGTCCTC 183
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Db       136 GGGCTGGAGTGAATTGGGAGTATCTATTAAGTGGAGACCTACTAACAAACCCGTCCTC 195
QY      184 AAGAGTCGAATTGCCATGTCTGTTAGACACGCTCTGAGAACAGTTCTCTGAGGCTGAAC 243
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Db       196 AAGAGTCGAGTCAACATATCTCGTAGACACGTCCAAAGAACAGTTCTCTGAGGCTGAGC 255
QY      244 TCTGTACTGCGCCGCAACGCGCTGTATTACTGTGCCA-----GTTAGAT 291
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Db       256 TCTGTACCGCGCCAGACACGCGCTGTATTACTGTGCGAGGGGAGCTAACGGGGGCTAC 315
QY      292 GGCTACACTTTGGACATCTGGGGCCAGGAAACCTGCTCACCGTCTCTCA 342
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Db       316 TACTACGGTATGACGCTCTGGGGCCAAAGGACCAACGCTCACCGTCTCTCA 366
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Job time : 96.3455 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:09:06 ; Search time 1956.83 Seconds  
(without alignments)  
8468.649 Million cell updates/sec

Title: US-10-027-725A-2  
Perfect score: 342  
Sequence: 1 ctcgagctctgcccagagact.....ccctgctcacgcctctctca 342

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb da:\*  
2: gb bta:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	324.4	94.9	342	9	HSA458384
3	297.2	86.9	342	9	HSA458382
4	286.2	83.7	355	9	AY640487
5	284.6	83.2	355	9	AY640580
6	281.4	82.3	355	9	AY640509
7	281.4	82.3	355	9	AY640579
8	279.8	81.8	355	9	AY640564
9	275	80.4	355	9	AY640507
10	273.4	79.9	432	9	HSA491911
11	271.8	79.5	354	9	HSA491912
12	271.8	79.5	354	9	HSA491912
13	270.8	79.2	411	9	AF062112
14	270.8	79.2	411	9	HST22X1
15	269	78.7	403	12	AF452917
16	268.6	78.5	351	9	HSA245020
17	268.4	78.5	358	9	HSA244930
18	268.4	78.5	358	9	AF021954
19	268.4	78.5	360	6	AX061463

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21	267	78.1	360	9	HSU80130	U80130 Human immun
22	266	77.8	354	9	HSA244955	AJ244955 Homo sapi
23	266	77.8	355	9	AY640551	AY640551 Homo sapi
24	265.8	77.7	341	9	AY607380	AY607380 Homo sapi
25	265.8	77.7	400	12	AF452909	AF452909 Synthetic
26	265.6	77.7	357	9	HSA244949	AJ244949 Homo sapi
27	265.4	77.6	354	9	HSA579125	AJ579125 Homo sapi
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30	264	77.2	363	9	HSU80131	U80131 Human immun
31	263	76.9	412	12	AF452912	AF452912 Synthetic
32	262.8	76.8	411	9	HST14X10	Z75363 H. sapiens m
33	262.4	76.7	409	12	AF452947	AF452947 Synthetic
34	262	76.6	357	9	HSA279523	AJ279523 Homo sapi
35	261.8	76.5	362	9	HSU80166	U80166 Human immun
36	261.4	76.4	351	9	AY607364	AY607364 Homo sapi
37	260.8	76.2	363	9	HSU80128	U80128 Human immun
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39	260.4	76.1	357	9	HSA279541	AJ279541 Homo sapi
40	259.6	75.9	417	9	HST14X9	Z75383 H. sapiens m
41	259	75.7	339	9	AY607360	AY607360 Homo sapi
42	259	75.7	340	9	AY607366	AY607366 Homo sapi
43	259	75.7	384	9	AY640529	AY640529 Homo sapi
44	258.8	75.7	357	9	HSA244934	AJ244934 Homo sapi
45	258.8	75.7	357	9	HSA244964	AJ244964 Homo sapi

#### ALIGNMENTS

RESULT 1	HS458383	342 bp	mRNA	linear	PRI 30-APR-2002
LOCUS	HS458383				
DEFINITION	Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 60.				
ACCESSION	AJ458383				
VERSION	AJ458383.1	GI:20387065			
KEYWORDS	IGHV gene; immunoglobulin heavy chain; variable region.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1				
AUTHORS	Flicker, S., Steinberger, P., Nordberg, L., Sperr, W.R., Majlesi, Y., Valent, P., Kratt, D. and Valente, R.				
TITLE	Conversion of grass allergen-specific human IgB into a protective IgG1 antibody				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 342)				
AUTHORS	Flicker, S.				
TITLE	Direct Submission				
JOURNAL	Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA				
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CDs	/mol_type="mRNA"				
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	/product="immunoglobulin heavy chain"				
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	/db_xref="GI:20387065"				
	/translation="LESGPGLVPSQTLILCTVSGSIRGGYMSWVRPPGKLE				
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	NWGGTLVTVSS"				

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/product="immunoglobulin heavy chain variable region"

ORIGIN

Query Match 99.5%; Score 340.4; DB 9; Length 342;  
Best Local Similarity 99.7%; Pred. No. 1.9e-89;  
Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCCGCAGAGCTGTGTAAGCCTTCACAGACCCCTGTCCCTCACCTGCAGCTGC 60  
Db 1 CTGAGTCTGGCCCGCAGAGCTGTGTAAGCCTTCACAGACCCCTGTCCCTCACCTGCAGCTGC 60  
QY 61 TCTGTGGCTCCATCCGACGTGTGTATTATTGAGTTGGGTCCGCGACCTCCAGGG 120  
Db 61 TCTGTGGCTCCATCCGACGTGTGTATTATTGAGTTGGGTCCGCGACCTCCAGGG 120  
QY 121 AAGGCGCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACCTTACAAACCCGTCC 180  
Db 121 AAGGCGCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACCTTACAAACCCGTCC 180  
QY 181 CTCAGAGTGGATTTACATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTG 240  
Db 181 CTCAGAGTGGATTTACATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTG 240  
QY 241 ACCTCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGGAGTCAGATGGGTATACT 300  
Db 241 ACCTCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGGAGTCAGATGGGTATACT 300  
QY 301 TTGGACAACCTGGGGCCAGGGAACCCCTGTCAACCGTCTCCCTCA 342  
Db 301 TTGGACAACCTGGGGCCAGGGAACCCCTGTCAACCGTCTCCCTCA 342

RESULT 2  
HSA458384 342 bp mRNA linear PRI 30-APR-2002  
LOCUS HSA458384  
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 100.  
ACCESSION AJ458384.1 GI:20387067  
VERSION IGHV gene; immunoglobulin heavy chain; variable region.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Flicker S., Steinberger P., Norderhaug L., Sperr W.R., Majlesi Y., Valent P., Kraft D. and Valenta R.  
TITLE Conversion of grass allergen-specific human IGE into a protective Igl1 antibody  
JOURNAL Unpublished  
AUTHORS Flicker S.  
REFERENCE Direct Submission  
TITLE Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA  
JOURNAL Location/Qualifiers  
FEATURES  
source 1..342  
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V\_region 1..342  
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ORIGIN

Query Match 94.9%; Score 324.4; DB 9; Length 342;  
Best Local Similarity 96.8%; Pred. No. 1e-84;  
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCCGCAGAGCTGTGTAAGCCTTCACAGACCCCTGTCCCTCACCTGCAGCTGC 60  
Db 1 CTGAGTCTGGCCCGCAGAGCTGTGTAAGCCTTCACAGACCCCTGTCCCTCACCTGCAGCTGC 60  
QY 61 TCTGTGGCTCCATCCGACGTGTGTATTATTGAGTTGGGTCCGCGACCTCCAGGG 120  
Db 61 TCTGTGGCTCCATCCGACGTGTGTATTATTGAGTTGGGTCCGCGACCTCCAGGG 120  
QY 121 AAGGCGCTGGAGTGGATCGGCAACATCTATACAGTGGCAACCTTACAAACCCGTCC 180  
Db 121 AAGGCGCTGGAGTGGATCGGCAACATCTATACAGTGGCAACCTTACAAACCCGTCC 180  
QY 181 CTCAGAGTGGATTTACATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTG 240  
Db 181 CTCAGAGTGGATTTACATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTG 240  
QY 241 ACCTCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGGAGTCAGATGGGTATACT 300  
Db 241 ACCTCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGGAGTCAGATGGGTATACT 300  
QY 301 TTGGACAACCTGGGGCCAGGGAACCCCTGTCAACCGTCTCCCTCA 342  
Db 301 TTGGACAACCTGGGGCCAGGGAACCCCTGTCAACCGTCTCCCTCA 342

RESULT 3  
HSA458382 342 bp mRNA linear PRI 30-APR-2002  
LOCUS HSA458382  
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 94.  
ACCESSION AJ458382.1 GI:20387063  
VERSION IGHV gene; immunoglobulin heavy chain; variable region.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Flicker S., Steinberger P., Norderhaug L., Sperr W.R., Majlesi Y., Valent P., Kraft D. and Valenta R.  
TITLE Conversion of grass allergen-specific human IGE into a protective Igl1 antibody  
JOURNAL Unpublished  
AUTHORS Flicker S.  
REFERENCE Direct Submission  
TITLE Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA  
JOURNAL Location/Qualifiers  
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## ORIGIN

Query Match 86.9%; Score 297.2; DB 9; Length 342;  
Best Local Similarity 91.8%; Pred. No. 1.1e-76;  
Matches 314; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGAGACTGTGTAAGCTTCACAGACCTCTGCTCACTGACATGTC 60  
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QY 61 TCTGTGGTCCATCCGAGTGTGTATTATTGAGATTGAGTCCGCGCAGCTCCAGGG 120  
DB 61 TCTGTGGTCCATCCGAGTGTGTATTATTGAGATTGAGTCCGCGCAGCTCCAGGG 120  
QY 121 AAGGCTGTGAGTGTGCAATCTATCAAGTGGCAACACTTACCAACCCGCTCC 180  
DB 121 AAGGCTGTGAGTGTGCAATCTATCAAGTGGCAACACTTACCAACCCGCTCC 180  
QY 181 CTCAAGAGTGAATTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTG 240  
DB 181 CTCAAGAGTGAATTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTG 240  
QY 241 ACCCTGTGACTGCGCGGAGCAACGCGCTATTACTGTGCGGCTCAAGTGGATTA 300  
DB 241 AACTGTGTGACTGCGCGGAGCAACGCGCTATTACTGTGCGGCTCAAGTGGATTA 300  
QY 301 TTGGACAACCTGGGCGCAGGGAACCTGTGTACCCGCTCTCTCA 342  
DB 301 TTGGACAACCTGGGCGCAGGGAACCTGTGTACCCGCTCTCTCA 342

RESULT 4 355 bp mRNA linear PRI 03-JUL-2004  
AY640487  
LOCUS Homo sapiens clone AP immunoglobulin E variable region mRNA,  
partial cds.  
ACCESSION AY640487.1 GI:49354726  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VHS IGE+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK

FEATURES  
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CDS

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/product="immunoglobulin heavy chain variable region"

## ORIGIN

Query Match 83.7%; Score 286.2; DB 9; Length 355;  
Best Local Similarity 90.3%; Pred. No. 1.9e-73;  
Matches 306; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 GAGTGTGCCCCAGAGACTGTGTAAGCTTCACAGACCTGTCTCCTGACCTGCTCT 63  
DB 16 GAGTGTGCCCCAGAGACTGTGTAAGCTTCACAGACCTGTCTCCTGACCTGCTCT 75  
QY 64 GTGTGCTTCATCCGCACTGTGTATTATTATTGAGTGGTGGCGCCAGCTCCAGGAG 123  
DB 76 GTGTGCTTCATCCGCACTGTGTATTATTATTGAGTGGTGGCGCCAGCTCCAGGAG 135  
QY 124 GACCTGTGAGTGTGCAATCTATCAAGTGGCAACCTTCTCTGAGACTGAC 183  
DB 136 GACCTGTGAGTGTGCAATCTATCAAGTGGCAACCTTCTCTGAGACTGAC 195  
QY 184 AAGAGTGAATTACATGTCACTAGACACGCTTAAGAACCACTTCTCTGAGACTGAC 243  
DB 196 AAGAGTGAATTACATGTCACTAGACACGCTTAAGAACCACTTCTCTGAGACTGAC 255  
QY 244 TCTGTGACTGCGCGGAGCAACGCGCTATTACTGTGCGGCTCAAGTGGATTA 303  
DB 256 TCTGTGACTGCGCGGAGCAACGCGCTATTACTGTGCGGCTCAAGTGGATTA 315  
QY 304 GACAACCTGGGCGCAGGGAACCTGTGTACCCGCTCTCTCA 342  
DB 316 GACTACTGGGCGCAGGGAACCTGTGTACCCGCTCTCTCA 354

RESULT 5 355 bp mRNA linear PRI 03-JUL-2004  
AY640580  
LOCUS Homo sapiens clone RU immunoglobulin E variable region mRNA,  
partial cds.  
ACCESSION AY640580  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VHS IGE+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK

FEATURES  
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CDS

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ORIGIN YPDPYMGQGLTVTVSS"

Query Match 83.2%; Score 284.6; DB 9; Length 355;  
Best Local Similarity 90.0%; Pred. No. 5,8e-73;  
Matches 305; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGACTGTGTAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63  
DB 16 GAGTCGGGCCCAAGAGACTGTGTAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 75  
QY 64 GGTGGCTCCATCCGACAGTGTGTTATTATTTAGTTGGGTGGGCGGCAAGCCCTCCAGGGAG 123  
DB 76 GGTGGCTCCATCCGACAGTGTGTTATTATTTAGTTGGGTGGGCGGCAAGCCCTCCAGGGAG 135  
QY 124 GGCTGGAGTGGATCGGCAACATCTATTCACAGTGGCAACACCTTCAACACCCGCTCCCTC 183  
DB 136 GGCTGGAGTGGATTTGGGTAGTCTATTACAGTGGGAACACTTCAACACCCGCTCCCTC 195  
QY 184 AAGAGTGAATTACCATGTCACTAGTACAGCTGTAAAGAACACTTCTCTGAGACTGACC 243  
DB 196 AAGAGTGAATTACCATGTCACTAGTACAGCTGTAAAGAACACTTCTCTGAGACTGACC 255  
QY 244 TCTGTGACTGCCGGGACAGCGCCGTATTTACTGTGCGGCTCAGATGGGTATATCTTG 303  
DB 256 TCTGTGACTGCCGGGACAGCGCCGTATTTACTGTGCGGCTCAGATGGGTATATCTTG 315  
QY 304 GACAACCTGGGGCCAGGGAACCCCTGTGTCACCGTCTCTCA 342  
DB 316 GACTACTGGGGCCAGGGAACCCCTGTGTCACCGTCTCTCA 354

RESULT 6 355 bp mRNA linear PRI 03-JUL-2004  
LOCUS AY640509  
DEFINITION Homo sapiens clone BM immunoglobulin E variable region mRNA,  
partial cds.  
ACCESSION AY640509  
VERSION AY640509.1 GI:49354765  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE 1 (bases 1 to 355)  
BIOSOURCE Biased use of VHS IGB+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE 2 (bases 1 to 355)  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK

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ORIGIN  
Query Match 82.3%; Score 281.4; DB 9; Length 355;

Best Local Similarity 89.4%; Pred. No. 5.1e-72;  
Matches 303; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGACTGTGTAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63  
DB 16 GAGTCGGGCCCAAGAGACTGTGTAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 75  
QY 64 GGTGGCTCCATCCGACAGTGTGTTATTATTTAGTTGGGTGGGCGGCAAGCCCTCCAGGGAG 123  
DB 76 GGTGGCTCCATCCGACAGTGTGTTATTATTTAGTTGGGTGGGCGGCAAGCCCTCCAGGGAG 135  
QY 124 GGCTGGAGTGGATCGGCAACATCTATTCACAGTGGCAACACCTTCAACACCCGCTCCCTC 183  
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QY 184 AAGAGTGAATTACCATGTCACTAGTACAGCTGTAAAGAACACTTCTCTGAGACTGACC 243  
DB 196 AAGAGTGGGTTACCATGTCACTAGTACAGCTGTAAAGAACACTTCTCTGAGACTGACC 255  
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DB 256 TCTGTGACTGCCGGGACAGCGCCGTATTTACTGTGCGGCTCAGATGGGTATATCTTG 315  
QY 304 GACAACCTGGGGCCAGGGAACCCCTGTGTCACCGTCTCTCA 342  
DB 316 GACTACTGGGGCCAGGGAACCCCTGTGTCACCGTCTCTCA 354

RESULT 7 355 bp mRNA linear PRI 03-JUL-2004  
LOCUS AY640579  
DEFINITION Homo sapiens clone RT immunoglobulin E variable region mRNA,  
partial cds.  
ACCESSION AY640579  
VERSION AY640579.1 GI:49354899  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE 1 (bases 1 to 355)  
BIOSOURCE Biased use of VHS IGB+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE 2 (bases 1 to 355)  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK

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WTFDYGQGLTVTVSS"

ORIGIN  
Query Match 82.3%; Score 281.4; DB 9; Length 355;  
Best Local Similarity 89.4%; Pred. No. 5.1e-72;  
Matches 303; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGACTGTGTAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63

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Db 16 GAGTCGGAGCCAGAGATCGTGTAAACCTTCACAGACCCCTGCTCCTCAGCTGCTCT 75  
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Oy 244 TCTGTGACTGCGCGGACAGCGCCGTCTATCTGTGCGGGGTGAGATGGGTATACCTTTG 303  
Db 256 TCTGTGACTGCGCGGACAGCGCCGTCTATCTGTGCGGGGTGAGATGGGTATACCTTTT 315  
Oy 304 GACAACCTGGGGCCAGGAAACCTGTGTCACCGCTCTCTCA 342  
Db 316 GACTACTGGGGCCAGGAAACCTGTGTCACCGCTCTCTCA 354  
RESULT 8 355 bp mRNA linear PRI 03-JUL-2004  
AY640564  
LOCUS Homo sapiens clone RE immunoglobulin E variable region mRNA,  
DEFINITION partial cds.  
ACCESSION AY640564  
VERSION AY640564.1 GI:49354872  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VH5 IGE+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2. (bases 1 to 355)  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK  
FEATURES  
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WTFPDMQCGTLIVTSS"

## ORIGIN

Query Match 81.8%; Score 279.8; DB 9; Length 355;  
Best Local Similarity 89.1%; Pred. No. 1.5e-71;  
Matches 302; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Oy 4 GAGTCTGGCCAGAGATCGTGTAAACCTTCACAGACCCCTGCTCCTCAGCTGCTCT 63  
Db 16 GAGTCGGAGCCAGAGATCGTGTAAACCTTCACAGACCCCTGCTCCTCAGCTGCTCT 75  
Oy 64 GGTGGCTCCATCCGACAGTGGTGTATATGAGATTGGGTCGCGCAGCCCTCCAGGGAG 123

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Db 76 GGTGGCTCCATCCGACAGTGGTGTATATGAGATTGGGTCGCGCAGCCCTCAGGGAG 135  
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Db 196 AAGAGTGAATTACCATGTCTAGTACACGCTCTAAGAACCACTTCTCTCTGAGACTGACC 255  
Oy 244 TCTGTGACTGCGCGGACAGCGCCGTCTATCTGTGCGGGGTGAGATGGGTATACCTTTG 303  
Db 256 TCTGTGACTGCGCGGACAGCGCCGTCTATCTGTGCGGGGTGAGATGGGTATACCTTTT 315  
Oy 304 GACAACCTGGGGCCAGGAAACCTGTGTCACCGCTCTCTCA 342  
Db 316 GACTACTGGGGCCAGGAAACCTGTGTCACCGCTCTCTCA 354

RESULT 9 355 bp mRNA linear PRI 03-JUL-2004  
AY640507  
LOCUS Homo sapiens clone BK immunoglobulin E variable region mRNA,  
DEFINITION partial cds.  
ACCESSION AY640507  
VERSION AY640507.1 GI:49354762  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VH5 IGE+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2. (bases 1 to 355)  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK  
FEATURES  
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WTFPDMQCGTLIVTSS"

## ORIGIN

Query Match 80.4%; Score 275; DB 9; Length 355;  
Best Local Similarity 88.2%; Pred. No. 4e-70;  
Matches 299; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Oy 4 GAGTCTGGCCAGAGATCGTGTAAACCTTCACAGACCCCTGCTCCTCAGCTGCTCT 63  
Db 16 GAGTCGGAGCCAGAGATCGTGTAAACCTTCACAGACCCCTGCTCCTCAGCTGCTCT 75  
Oy 64 GGTGGCTCCATCCGACAGTGGTGTATATGAGATTGGGTCGCGCAGCCCTCCAGGGAG 123  
Db 76 GGTGGCTCCATCCGACAGTGGTGTATATGAGATTGGGTCGCGCAGCCCTCCAGGGAG 135  
Oy 124 GGCCTGGAGTGGATCGGCAACATCTATCACTAGTGGCAACCTTCAACACCCCTCCCTC 183

Db	Qy	Db	Qy	Db	Qy	RESULT 10
136	GGCGTGAAGTGGATTGGAATACATCTATTACAGGGGGAGCACTTACATCAACCCGTCCTC	195				
184	AAGATCGAATTACCATCTCAGTACAGACGTCCTAAGAACCACTTCTCCCTGAGACTGACC	243				
196	AGGATCGAATAATCAATGTCATTAATGACACGTCCTGCAATCAGTTCTCCCTGAGGCTGACC	255				
244	TTCTGTGACTGCGCGGGACACAGCGCGCTCATTAATCATGTGGCGGCTCAGATGGGTAATCTTGG	303				
256	TTCTGTGACTGCGCGGACAGACGCGCGCTGATTAATTTCTGTGCGGCTCTAAGATGGGTACAGTTTG	315				
304	GACAACTGGGGCCACAGGAACCTCGGTACCGCTCTCTCA	342				
316	GACTACTGGGCGCAGGGAACCTCGGTACCGCTCTCTCA	354				
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LOCUS	HS4491911					
ACCESSION	AF491911					
VERSION	AF491911.1	GI:24415808				
KEYWORDS	constant region; epsilon chain; IGH gene; immunoglobulin heavy chain; variable region.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1					
AUTHORS	Coker H.A., Durham S.R. and Gould H.J.					
TITLE	Local somatic hypermutation and class switch recombination in the nasal mucosa of allergic rhinitis patients					
JOURNAL	J. Immunol. 171 (10), 5602-5610 (2003)					
MEDLINE	22970235					
PUBMED	14607969					
REFERENCE	2 (bases 1 to 432)					
AUTHORS	Coker H.A.					
TITLE	Direct Submision					
JOURNAL	Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall Centre, King's College London, Guy's Campus, London, SE1 1UL, UNITED KINGDOM					
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Oy	64 GGTGGCTCCCAACCCAGTGCGTGTATTATATGTGAGTGGGTGCGCCAGCCTCCAGGAG	123
Db	76 GTGGCCGCATCACTAATGAGTGTTACTACTGAGCTGGATTCGCCAGACCCAGGAG	135
Oy	124 GGCTGTGAGTGTATCGGCACATCATCACTACAGTGGCAACCTACAAACCCGTCCTC	183
Db	136 GGCTGTGAGTGTATGTATCATCTATTACAGGGGAGACCTACATCAACCCGTCCTC	195
Oy	184 AAGATCGAATTACCATGTCTAGTAGACAAGTCTTAAGAACCACTTCTCCCTGAGACTGAC	243
Db	196 AGGATCGAATAATCATGTCAATTGACACGCTCTCAATTCAGTTCTCCCTGAGGCTGAC	255
Oy	244 TCTGTGACTGCGCGGAGACAGGCCGCTCATTAATCTGTGCGGCTCAGATGGGTACTTTG	303
Db	256 TCTGTGACTGCGCGGAGACAGGCCGCTCATTAATCTGTGCGGCTCAGATGGGTACTTTG	315
Oy	304 GACAACCTGGGCGCAGGGAACCTGTGTCAACCGTCTCCCTCA	342
Db	316 GACTACTGGGCGCAGGGAACCTGTGTCAACCGTCTCCCTCA	354
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LOCUS DEFINITION	Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region (Clone HD17 C37).	
ACCESSION	AJ491912	
VERSION	AJ491912.1 GI:24415810	
KEYWORDS	constant region; epsilon chain; IGH gene; immunoglobulin heavy chain; variable region.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	1 Coker,H.A., Durham,S.R. and Gould,H.J.	
TITLE	Local somatic hypermutation and class switch recombination in the nasal mucosa of allergic rhinitis patients	
JOURNAL	J. Immunol. 171 (10), 5602-5610 (2003)	
MEDLINE	22970235	
PUBMED	14607969	
REFERENCE	2 (bases 1 to 432)	
AUTHORS	Coker,H.A.	
TITLE	Direct Submission	
JOURNAL	Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall Centre, King's College London, Guy's Campus, London, SE1 1UL, UNITED KINGDOM	
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Best Local Similarity 87.9%; Pred. No. 1.2e-69;
Matches 298; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGCTGTGAAGCCTTCAAGACCCGTGCTCCACCTGACGTCTCT 63
DB 16 GAGTCGGGCCAGAGCTGTGAAGCCTTCAAGACCCGTGCTCCACCTGACGTCTCT 75
QY 64 GGTGGCTCATCCGACAGTGTGTTATTATTGAGTTGGTCCGCCAGCCTCCAGGAG 123
DB 76 GGTGGCCCATCATATGTTGGTTACTACTGAGCTGGAATCCGCCAGACCCAGGAG 135
QY 124 GGCCTGAGTGAATGGCAATCTATCAAGTGGCAACACTTAACAACCCGTCCTC 183
DB 136 GGCCTGAGTGAATGGCAATCTATCAAGTGGCAACACTTAACAACCCGTCCTC 195
QY 184 AAGAGTGAATTATCATGTGATGAGACACGCTTAAGAACCTTCTCCCTGAGACTAGC 243
DB 196 AAGAGTGAATTATCATGTGATGAGACACGCTTCAATCAATCCTTCTCCCTGAGACTAGC 255
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DB 316 GACTACTGGGGCCAGGGAACCTTGTCACCGTCTCCCTCA 354
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DEFINITION Homo sapiens mRNA for immunoglobulin gamma heavy chain variable
region, partial, clone 2-D123.
ACCESSION AJ245064
VERSION AJ245064.1 GI:4995589
KEYWORDS IGG; Igg heavy chain; immunoglobulin gamma heavy chain; variable
region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Dono, M., Zupo, S., Chiocazzi, N. and Ferrarini, M.
TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 354)
AUTHORS Dono, M.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
ITALY

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Matches 297; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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QY 64 GGTGGCTCATCCGACAGTGTGTTATTATTGAGTTGGTCCGCCAGCCTCCAGGAG 123
DB 76 GGTGGCCCATCATATGTTGGTTACTACTGAGCTGGAATCCGCCAGACCCAGGAG 135
QY 124 GGCCTGAGTGAATGGCAATCTATCAAGTGGCAACACTTAACAACCCGTCCTC 183
DB 136 GGCCTGAGTGAATGGCAATCTATCAAGTGGCAACACTTAACAACCCGTCCTC 195
QY 184 AAGAGTGAATTATCATGTGATGAGACACGCTTAAGAACCTTCTCCCTGAGACTAGC 243
DB 196 AAGAGTGAATTATCATGTGATGAGACACGCTTCAATCAATCCTTCTCCCTGAGACTAGC 255
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QY	244	TCCTGACGTGCGGGGACAGGGCCGCTATCTACTGTGCGGGTCAAGATGGTATACTTGG	303
Db	256	TCCTGACGTGCGGGACAGACGCGCCGTGATTAATGTGTGCAGGGGGATTAGTACTACTT	315
QY	304	GACAACTGGGGCCACAGGAACCTGTGTCAACCGTCTCTCA	342
Db	316	GACTACTGGGGCCAGGAGACCTGTGTCAACCGTCTCTCA	354
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ACCESSION		region (IGH) mRNA, partial cds.	
VERSION		AF062112	
KEYWORDS		AF062112.1	GI:3170686
SOURCE			
ORGANISM		Homo sapiens (human)	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
TITLE		1 (bases 1 to 414)	
JOURNAL		Immunoglobulin VH gene expression in human aging	
MEDLINE		Clin. Immunol. 93 (2), 132-142 (1999)	
PUBMED		99459182	
REFERENCE		10527689	
AUTHORS		2 (bases 1 to 414)	
TITLE		Wang, X. and Stollar, B.D.	
JOURNAL		Submitted (22-APR-1998) Biochemistry Department, Tufts University	
FEATURES		School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA	
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QY	124	GGCCTGGAGTGGATGGCAACATCTATACAGTGGCAACCTTACACAAACCCGTCCTC	183

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Db	253	AAGATCGAGTTACCATATCATAGTACAGACCGTCCAAAGAACGATTCTCCCTGAAGCTGAGC	312
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Db	373	GACTACTGGGCGACGGAGACCTGTGTACCGTTCCTCA	411
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ACCESSION	275385		
VERSION	275385.1	GI:2062048	
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SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 411)		
TITLE	Tonnelle,C., D'Ercole,C., Depaeetere,V., Meltras,D., Boublil,L. and Fougereau,M.		
JOURNAL	Human thymic B cells largely overexpress the VH4 Ig gene family. A possible role in the control of tolerance in situ?		
MEDLINE	Int. Immunol. 9 (3), 407-414 (1997)		
REFERENCE	9724170		
AUTHORS	2 (bases 1 to 411)		
TITLE	Tonnelle,C.		
JOURNAL	Direct Submission		
FEATURES	Submitted (26-JUN-1996) Cecile Tonnelle, Centre d'Immunologie Marseille Luminy, Marseille, 13288, France		
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Qy	64	GGTGGCTCCATCCGAGAGTGTGTATTATATGAGTTGGGTGGGTCCGCAAGCTCCAGAGAG	123
Db	133	GGTGGCTCCATCCGAGAGTGTGTATTACTACTGAGCTGTGATTCGGCTTCGACCCAGAGAG	192

QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGTGGCAACCTTCAACAAACCCGTCCTC 183  
DB 193 GGCTGGAGTGGATGGGTGATCATCTATTACGTGGAGACCTTCAACACCGTCCTC 252  
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LOCUS Synthetic construct clone 7-161VH rotavirus VP7-specific antibody  
DEFINITION heavy chain variable region mRNA, partial sequence.  
ACCESSION AF452917  
VERSION AF452917.1 GI:25988060  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
AUTHORS 1 (bases 1 to 403)  
Weitekamp,J.H., Kallewaard,N., Kusuhara,K., Bures,E., Williams,J.V.,  
Lapleur,B., Greenberg,H.B. and Crowe,J.E. Jr.  
Infant and adult human B cell responses to rotavirus share common  
immunodominant variable gene repertoires  
J. Immunol. 171 (9), 4680-4688 (2003)  
22930557  
14568943  
JOURNAL 2 (bases 1 to 403)  
MEDLINE Weitekamp,J.H. and Crowe,J.E. Jr.  
PUBMED Direct Submission  
REFERENCE Submitted (28-NOV-2001) Pediatrics, Vanderbilt University Medical  
AUTHORS Center, 1161 21st Avenue South, D-7235 Medical Center North,  
JOURNAL Nashville, TN 37232-2581, USA  
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QY 185 AGAGTGAATTACCATGTCTAGTAGACGCTTAAAGAACCACTTCTCCCTGAGACTGACCT 244

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 34239544 seqs, 19032134700 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_est4.\*  
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6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_est9.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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5	249.6	73.0	607	4	BM783015
6	248.2	72.6	490	6	CD689564
7	241.4	70.6	725	4	BG431274
8	241.2	70.5	643	1	AU134293
9	240	70.2	904	5	BQ710488
10	239.8	70.1	959	5	BQ899307
11	238.2	69.6	903	5	BQ706579
12	238.2	69.6	1108	5	BM920469
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14	237	69.3	939	5	BQ708070
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17	234.8	68.7	596	4	BM817833
18	234.8	68.7	813	5	BQ710364
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20	234.6	68.6	814	4	BG685325
21	233.6	68.3	508	7	CR747031
22	233.6	68.3	1019	5	BQ072420
23	233.6	68.3	1195	5	BQ707644
24	233.4	68.2	474	2	AM408410

25	233.4	68.2	915	5	BQ706358
26	233.2	68.2	658	5	BX505812
27	232.8	68.1	421	2	AM407630
28	232	67.8	363	2	AM403420
29	232	67.8	915	5	BQ711871
30	232	67.8	923	5	BQ707945
31	232	67.8	928	5	BQ707875
32	232	67.8	959	5	BQ709473
33	231.6	67.7	924	5	BQ708516
34	231.6	67.7	924	4	BG758027
35	231.6	67.7	987	5	BQ707970
36	231.4	67.7	650	4	BG684403
37	231.4	67.7	778	4	BF975836
38	231.4	67.7	929	4	BG341823
39	231	67.5	524	5	BQ429270
40	231	67.5	856	5	BQ421299
41	230.6	67.4	661	4	BG686421
42	230.6	67.4	921	5	BQ710000
43	230.6	67.4	959	4	BG757666
44	230	67.3	542	2	AM951834
45	229.8	67.2	435	2	BF871158

## ALIGNMENTS

RESULT 1	AU122174	832 bp	mRNA	linear	EST 01-AUG-2002
LOCUS	AU122174	MAMMA1	Homo sapiens	CDNA clone	MAMMA1001802 5', mRNA
DEFINITION	AU122174	sequence.			
ACCESSION	AU122174				
VERSION	AU122174.1	GI:10937409			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.				
AUTHORS	Unpublished (2000)				
TITLE	HRI human CDNA project				
JOURNAL	Genomics Laboratory				
COMMENT	Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human CDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.				
FEATURES	Location/Qualifiers				
source	1..832				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="MAMMA1001802"				
	/tissue_type="mammary gland"				
	/clone_lib="MAMMA1"				
	/note="Vector: pME18SF13"				
ORIGIN					
Query Match	77.1%; Score 263.8; DB 1; Length 832;				
Best Local Similarity	86.1%; Pred. No. 3.2e-67;				
Matches	292; Conservative 0; Mismatches 47; Indels 0; Gaps 0;				
QY	4 GAGTCTGCGCCAGCAGCTGAGACCTTCACAGCCCTGTCCTCAGCTGCTCTCT 63				
DB	110 GAGTCTGCGCCAGCAGCTGAGACCTTCACAGCCCTGTCCTCAGCTGCTCTCT 169				

QY	64	GGTGGCTCATCCCGACGGTGTATTATATGAGTTGGGTTCGCCAGCCTTCAGGGAG	123
Db	170	GGTGGCTCATCAGCAGTGTGAGGCCCTACTGGAGTTGGATTCGGCAGCCCCAGGGAG	229
QY	124	GGCTTGGAGTGGATTCGGCAATCTATCAGCTGGCAAACCTTACACACATCCGCTCTC	183
Db	230	GGCTTGAAGTGGATTGGCTACATCTATTATCAATGGGAACACTCTACACACCGTCCCTC	289
QY	184	AAGATGGAATTACATGTCTAGTAGACACGTCCTAAGAACCACTTCTCCCTGAGACTGACC	243
Db	290	AAGATGAGATTACATATCAATCAACGACATGTCCAGAGACGATTTCTCCCTGAAGCTAAAC	349
QY	244	TCTGTGACTGCTCGCGGACACGGCGCTCTATTACTGTGCGGCTCATGATGGGTATACITTTG	303
Db	350	TCTGTGACTGCTCGGACACCGCGCTGTATTACTGTGCCAATCATATTAAACAACAGAGGG	409
QY	304	GACAACTGGGGCGAGGGAAACCTGTGTCACGCTTCCTCTCA	342
Db	410	GACTTCTGGGGCGACGGAAACCTGTGACACCGCTTCATACA	448

RESULT 2	AM406349	LOCUS	DEFINITION
AM406349	509 bp	mRNA	linear
AM406349	UT-HF-B10-aco-h-03-0-UT.1	NIH_MGC_37	Homo sapiens cDNA clone
AM406349	IMAGE:3059933	5', mRNA sequence.	

ACCESSION	AW406349	GI:6925406
VERSION	AW406349.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homini; Hominidae; Homo. 1 (bases 1 to 509)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Straudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
cDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
[www-bio.llnl.gov/bdnp/image/image.html](http://www-bio.llnl.gov/bdnp/image/image.html)  
Seq primer: M13 Forward.

FEATURES	Location/Qualifiers
source	1. .509

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cd_name="IMAGE:3059933"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="MDH10B (LTR)"
/clone_lib="NH_MGC_37"
/note="Vector: pVT3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafide, Ph.D. and M. Bento Soares, Ph.D."

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ORIGIN

Query Match	73.3%	Score 250.8	DB 2	Length 509
Best Local Similarity	85.4%	Pred. No. 21e-63		
Matches 292	Conservative	0	Mismatches 47	Indels 3
			Gaps	1

  

QY	4	GAGTCGGCCAGAGCTGTGAAGCTTCACAGACCTGTCCCTCACTGACCTGTCTCT	63

Db	54	GAGTCGGGCCCAAGCACTGGTAAGCCTTCGGAGACCTGTGTCCTCACTTCACCTGCACGTCTCT	113
Qy	64	GGTGGCTTCATCCGAGATGGGTGTTATTAATTGAGATTGGGTCGGCCAGCCGCTCAGGGGAAG	123
Db	114	GGTGGCTTCATCAGCAGTAGTAGTTACTACTGGGGCTGGATCGCCAGCCCCCAGGGGAAG	173
Qy	124	GGCCTTGAGTGGATCGGCAACATCTATCAACAGTGGCAACACTTACACAACACCCGTCCCTC	183
Db	174	GGGCTGGAATGGATTGGGAGTATCTATTATGTGGGAGCACTTACTCAACCCGTCCCTC	233
Qy	184	AAGAGTCGAATTAACATGTCACTGATGACACGATCTTAAGAACCACTTCTCCGAGACTGACC	243
Db	234	AAGATCGAGTCAACCATATCACTAGTACACGTCACAGAACACAGTTCTCCCTGAAGCTGAGC	293
Qy	244	TCTGTACTGCGCCGCGACACCGGCCGTCTAATTACTGTGCG---CGGTGAGATGGGTATACT	300
Db	294	TCTGTACCGCGCGGACACACGGCCGCTCTAATTACTGTGCGAGAACCTCTCTTACGGACCTGG	353
Qy	301	TTTGACAACATGGGGGCCAGGGAAACCTGTGTACACGCTTCTCTCA	342
Db	354	TTTGACCCCTTGGGGCCAGGAAACCTGTGTACACGCTTCTCTCA	395

RESULT 3	369 bp	mRNA	linear	EST 16-FEB-2000
AM404242				
LOCUS	U1-HF-B10-abq-f-09-0-U1.r1	NIH_MGC_37	Homo sapiens	CDNA clone
DEFINITION	IMAGE:3057545	5',	mRNA sequence.	

ACCESSION	AW404242	
VERSION	AW404242.1	GI:6923299
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 369)  
NIH-MGC <http://mgc.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Email: [cgabds-rc@mail.nih.gov](mailto:cgabds-rc@mail.nih.gov)  
 Eco RI site shown at the beginning of the sequence.  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: M.B. Soares Lab  
 CDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
[www-bio.lnl.gov/bdbp/image/image.html](http://www-bio.lnl.gov/bdbp/image/image.html)  
 Seq primer: M13 forward.

FEATURES	Location/Qualifiers
source	1. .369

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3057545"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_1ib="NH MGC 37"
/note="Vector: pTZ19-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and W. Berto Soares, Ph.D."

```

## ORIGIN

Query Match	73.2%	Score	250.2	DB	2	Length	369
Best Local Similarity	86.5%	Pred.	No. 3e-63				
Matches	276	Conservative	0	Mismatches	43	Indels	0
				Gaps			0
OY	4	GAGTCGTGGCCAGAGCTGGTGAAGCCCTTCACAGACCTGTCCCTCACTGCACTGTCTCT	63				

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|||||
Db 34 GAGTCGGGCCAGAGACTGTGAACCTTCACAGACCCCTGTCCCTCACCCTGACGTCTCT 93
Qy 64 GGTGGCTCCATCCGACAGTGGTGTATTATTTAGATTGGGTGGCGGACGCTCCAGGGAG 123
Db 94 GGTGGCTCCATCCGACAGTGGTGTATTATTTAGATTGGGTGGCGGACGCTCCAGGGAG 153
Qy 124 GGCCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACTTAACAACCCGCTCC 183
Db 154 GGCCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACTTAACAACCCGCTCC 213
Qy 184 AAGAGTGAATTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTAGC 243
Db 214 AAGAGTGGCTTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAACTGAGC 273
Qy 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGCGCTGAGATGGTATACCTTG 303
Db 274 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGAGATCTTTGGCGTATTA 333
Qy 304 GACAACTGGGGCCAGGAA 322
Db 334 GATAGTAGTGTTACGGA 352

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RESULT 4  
 BG686767 677 bp mRNA linear EST 01-MAY-2001  
 LOCUS 602650737F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4763217 5',  
 DEFINITION mRNA sequence.

ACCESSION BG686767  
 VERSION BG686767.1 GI:13918164  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 677)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
 COMMENT Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: rgabers-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.llnl.gov  
 Plate: LICM618 row: 1 column: 10  
 High quality sequence stop: 675.  
 Location/Qualifiers

FEATURES  
 source

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1. 677
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:4763217"
  /tissue_type="Primary B-cells from tonsils (cell line)"
  /lab_host="DH10B (phage-resistant)"
  /clone_id="NIH_MGC_48"
  /note="Organ: B-cells; Vector: pORF7; Site 1: XhoI;
  Site 2: EcoRI. cDNA made by oligo-dT priming.
  Directionally cloned into EcoRI/XhoI sites using the
  following 5' adaptor: GGCACGAG(G). Size-selected >500bp
  for average insert size 1.8kb. Library constructed by Ling
  Hong in the laboratory of Gerald M. Rubin (University of
  California, Berkeley) using ZAP-cDNA synthesis kit
  (Stratagene) and Superscript II RT (Life Technologies).
  Note: this is a NIH_MGC Library."

```

ORIGIN  
 Query Match 73.2%; Score 250.2; DB 4; Length 677;  
 Best Local Similarity 87.0%; Pred. No. 3.4e-63;

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Matches 300; Conservative 0; Mismatches 38; Indels 7; Gaps 2;
Qy 4 GAGTCTGGCCAGAGACTGTGAAGCCCTTCAAGACCCCTGTCCCTCACCCTGACGTCTCT 63
Db 99 GAGTCTGGCCAGAGACTGTGAAGCCCTTCAAGACCCCTGTCCCTCACCCTGACGTCTCT 158
Qy 64 GGTGGCTCCATCCGACAGTGGTGTATTATTTAGATTGGGTGGCGGACGCTCCAGGGAG 123
Db 159 GGTGGCTCCATCCGACAGTGGTGTATTATTTAGATTGGGTGGCGGACGCTCCAGGGAG 217
Qy 124 GGCCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACTTAACAACCCGCTCC 183
Db 218 GGCCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACTTAACAACCCGCTCC 277
Qy 184 AAGAGTGAATTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTAGC 243
Db 278 AAGAGTGAATTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTAGC 337
Qy 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCG-----CGGTGAGTGGGTAT 297
Db 338 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGAGATCCGACAGAGAGAGAGGC 397
Qy 298 ACTTGGACAACCTGGGCGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db 398 GGGTTGACCCCTGGGCGCCAGGGAACCTGTGTCACCGTCTCTCA 442

```

RESULT 5  
 BM783015 607 bp mRNA linear EST 05-MAR-2002  
 LOCUS K-EST060735 S18N669761 Homo sapiens cDNA clone S18N669761-2-E06  
 DEFINITION 5', mRNA sequence.

ACCESSION BM783015  
 VERSION BM783015.1 GI:19131247  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 607)  
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.

JOURNAL 21C Frontier Korean EST Project 2001  
 COMMENT Unpublished (2002)  
 Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongseung@mail.krdb.re.kr

High quality sequence stop: 607.  
 Location/Qualifiers

FEATURES  
 source

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1. 607
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  /db_xref="taxon:9606"
  /clone="S18N669761-2-E06"
  /sex="F"
  /lab_host="Top10P"
  /clone_id="S18N669761"
  /note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
  Site 2: NotI; The poly (A) + RNA was dephosphorylated with
  bacterial alkaline phosphatase (BAP) and then deapped
  with tobacco acid pyrophosphatase (TAP). The deapped
  intact mRNA was ligated with DNA-RNA linker including EcoR
  I site by treatment of T4 RNA ligase and the first strand
  cDNA was synthesized from oligo dT-selected mRNA by
  priming with dT-tailed vector. The dT-tailed vector was
  adjusted to have about 60nt. The cDNA vector was
  circularized with E. coli DNA ligase after digestion of

```

ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells *E. coli* Top10<sup>®</sup> by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

## ORIGIN

Query Match 73.0%; Score 249.6; DB 4; Length 607;  
Best Local Similarity 84.8%; Pred. No. 5e-63;  
Matches 295; Conservative 0; Mismatches 44; Indels 9; Gaps 1;

QY 4 GAGTCTGCCCCAGGACCTGTTGAAAGCTTTCACAGACCTGTCTCCTGACCTGCTCTCT 63  
DB 112 GAGTCGGGCCCCAGGACCTGTTGAAAGCTTTCACAGACCTGTCTCCTGACCTGCTCTCT 171  
QY 64 GGTGGCTCCACCCAGTGGTGTATTATTGAGTTGGGTGGCCAGCCCTCCAGGGAG 123  
DB 172 GGTGGCTCCACCCAGTGGTGTATTATTGAGTTGGGTGGCCAGCCCTCCAGGGAG 231  
QY 124 GGCTGGAGTGGATGGGCAACATCTATCAGAGTGGCAACCTTACAAACACCCGCTCC 183  
DB 232 GGCTGGAGTGGATGGGCAACATCTATCAGAGTGGCAACCTTACAAACACCCGCTCC 291  
QY 184 AAGAGTGAATTACCATGTCAGTACAGACCTTAAAGAACCTTCTCCCTGAGACTGACC 243  
DB 292 AAGAGTGAATTACCATGTCAGTACAGACCTTAAAGAACCTTCTCCCTGAGACTGACC 351  
QY 244 TCTGTGACTGCGCGGACAGCGCCGTCTATTACTGTCGGG-----GTGATGGG 294  
DB 352 TCTGTGACTGCGCGGACAGCGCCGTCTATTACTGTCGGGAGATGGCAATTACGATATT 411  
QY 295 TATACTTTGACAACTGGGGCCAGGAAACCTGTGTCACCGTCTCTCA 342  
DB 412 TAGCGTATGACGCTGGGGCCAGGAAACCGTCTCAACCGTCTCTCA 459

RESULT 6  
CD689564 490 bp mRNA linear EST 25-JUN-2003  
LOCUS  
DEFINITION EST6087 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD689564  
VERSION CD689564.1 GI:32209443  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 490)  
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.  
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 DongFeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@sysu.edu.cn.

FEATURES  
source  
1. .490  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/issue\_type="normal nasopharynx"  
/clone\_id="human nasopharynx"  
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

## ORIGIN

Query Match 72.6%; Score 248.2; DB 6; Length 490;  
Best Local Similarity 85.0%; Pred. No. 1.2e-62;

Matches 290; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 5 AGTGTGCCCCAGGACCTGTTGAAAGCTTTCACAGACCTGTCTCCTGACCTGCTCTCTG 64  
DB 111 AGTCGGGCCCCAGGACCTGTTGAAAGCTTTCACAGACCTGTCTCCTGACCTGCTCTCTG 170  
QY 65 GTGGCTTCATCCGACGTGGTGTATTATTGAGTTGGGTGGCCAGCCCTCCAGGGAGG 124  
DB 171 GTGACTTCATCCACAGTGGTGTATTATTGAGTTGGGTGGCCAGCCCTCCAGGGAGG 230  
QY 125 GGCTGGAGTGGATGGGCAACATCTATCAGAGTGGCAACCTTACAAACACCCGCTCC 184  
DB 231 GGCTGGAGTGGATGGGCAACATCTATCAGAGTGGCAACCTTACAAACACCCGCTCC 290  
QY 185 AAGTGAATTACCATGTCAGTACAGACCTTAAAGAACCTTCTCCCTGAGACTGACC 244  
DB 291 AAGTGAATTACCATGTCAGTACAGACCTTAAAGAACCTTCTCCCTGAGACTGACC 350  
QY 245 CTGTGACTGCGCGGACAGCGCCGTCTATTACTGTGGCGGTACAT--GGTATATCTT 301  
DB 351 CTGTGACTGCGCGGACAGCGCCGTCTATTACTGTGGCGGTACAT--GGTATATCTT 410  
QY 302 TGAGCAACTGGGGCCAGGAAACCTGGTCAACCGTCTCTCA 342  
DB 411 TTGACTATGCGGGCCAGGAAATCTGTGACCGTCTCTCA 451

RESULT 7  
BG431274 725 bp mRNA linear EST 14-MAR-2001  
LOCUS  
DEFINITION BG431274 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:461345 5', mRNA sequence.  
ACCESSION BG431274  
VERSION BG431274.1 GI:13337780  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 725)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: gsaabs-r@mail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.jnl.gov  
Plate: LNCM363 row: h column: 12  
High quality sequence stop: 716.  
Location/Qualifiers

FEATURES  
source  
1. .725  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone\_id="IMAGE:461345"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1: 5' flil (ggcgctggcc); Site 2: 5' flil (ggcgatratggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAAGCATTATGACC-3' and 3' adaptor sequence: 5'-ATTCTAAGGCGCAGGCGGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 70.6%; Score 241.4; DB 4; Length 725;  
Best Local Similarity 82.0%; Pred. No. 1.4e-60;  
Matches 278; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 4 GAGTCTG3CCAGAGACTGTGAGAGCTTACAGACCCTGTCTCCCTGACCTGACTGTCTCT 63  
DB 109 GAGTGGG3CCAGAGACTGTGAGAGCTTCCGGGAGCCCTGTCTCCCTGACCTGACTGTCTCT 168  
QY 64 GGTGGCTCCATCCGAGTGGTGTATTATGAGTTGGTGGTCCCGGAGCTCCAGGGAG 123  
DB 169 GGTGGCTCCATCCGAGTGGTGTATTATGAGTTGGTGGTCCCGGAGCTCCAGGGAG 228  
QY 124 GGCTGGAGTGGATGGGCAACATCTATCAAGTGGGCAACACTTCCCTGAGACTGACC 183  
DB 229 GGCTGGAGTGGATGGGCAACATCTATCAAGTGGGCAACACTTCCCTGAGACTGACC 288  
QY 184 AAGAGTGAATTACCATGTCTAGTAGACAGCTCTAAGAACACTTCTCCCTGAGACTGACC 243  
DB 289 GAGAGTGAAGTCAACATATCCGTAGACAGCTCAAGAACAGCTTCTCCCTGAGACTGAGG 348  
QY 244 TCTGTACTGCGCGGAGACAGCGCGCTATTAATCTGTGGCGGTCAATGGGTATATCTTTG 303  
DB 349 CCTGTGACCGCGGAGACAGCTCTGTATATTAATGTTGAGAGATTACTGGGAGGAGTTT 408  
QY 304 GACAACCTGGGCGGAGAACCTGTCTACCGCTCTCTCA 342  
DB 409 GACTATTGGGCGGAGAACCTGTCTCTCTCTCA 447

RESULT 8  
AUI34293 643 bp mRNA linear EST 01-AUG-2002  
LOCUS AUI34293  
DEFINITION AUI34293 OVARC1 Homo sapiens cDNA clone OVARC1001672 5', mRNA  
SEQUENCE  
AUI34293.1 GI:10994832  
EST.  
Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 643)  
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.  
HRI human cDNA project  
Unpublished (2000)  
CONTACT: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: genomics@hri.co.jp  
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.  
LOCATION/Qualifiers  
1. 643  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="OVARC1001672"  
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/clone\_id="OVARC1"  
/note="Vector: pME18SFL3"

ORIGIN  
Query Match 70.5%; Score 241.2; DB 1; Length 643;  
Best Local Similarity 82.9%; Pred. No. 1.6e-60;  
Matches 295; Conservative 0; Mismatches 43; Indels 18; Gaps 1;

QY 5 AGTCTG3CCAGAGACTGTGAGAGCTTACAGACCCTGTCTCCCTGACCTGACTGTCTCTG 64  
DB 110 AGTCTG3CCAGAGACTGTGAGAGCTTACAGACCCTGTCTCCCTGACCTGACTGTCTCTG 169  
QY 65 GTGGCTCCATCCGAGTGGTGTATTATGAGTTGGTGGTCCCGGAGCTCCAGGGAGG 124  
DB 170 GTGGCTCCATCCGAGTGGTGTATTATGAGTTGGTGGTCCCGGAGCTCCAGGGAGG 229  
QY 125 GGCTGGAGTGGATGGGCAACATCTATCAAGTGGGCAACACTTCCCTGAGACTGACC 184  
DB 230 GGCTGGAGTGGATGGGCAACATCTATCAAGTGGGCAACACTTCCCTGAGACTGACC 289  
QY 185 AAGATGAATTACCATGTCTAGTAGACAGCTCTAAGAACACTTCTCCCTGAGACTGACC 244  
DB 290 AAGATGAATTACCATGTCTAGTAGACAGCTCTAAGAACACTTCTCCCTGAGACTGACC 349  
QY 245 CTGTGACTGCGCGGAGACAGCGCGCTATTAATCTGTGGCGGTCAATGGGTATATCT--- 300  
DB 350 CTGTGACTGCGCGGAGACAGCGCGCTATTAATCTGTGGCGGTCAATGGGTATATAGTG 409  
QY 301 -----TTGACACACTGGGCGGAGAACCTGTGTACCGCTCTCTCA 342  
DB 410 GGACCTACAGTAAATTGACACAGCTGGGCGGAGAACCTGTGTACCGCTCTCTCA 465

RESULT 9  
B0710488 904 bp mRNA linear EST 16-JUL-2002  
LOCUS B0710488  
DEFINITION AGENCOURT 8352970 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6278137  
5', mRNA sequence.  
B0710488  
B0710488.1 GI:21849387  
EST.  
Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 904)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
Email: sgabbs-remail.nih.gov  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM2465 row: k column: 02  
High quality sequence stop: 728.  
LOCATION/Qualifiers  
1. 904  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:6278137"  
/lab\_host="NIH MGC 113"  
/clone\_id="NIH MGC 113"  
/note="Organ: spleen; Vector: pORF7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 70.2%; Score 240; DB 5; Length 904;  
Best Local Similarity 83.0%; Pred. No. 3.9e-60;

Matches 289; Conservative 0; Mismatches 50; Indels 9; Gaps 1;

QY 4 GAGCTGGCCCAAGACTGTGTAAGCCCTTCACAGACCCCTGTCCCTACCTGCACTGTCTCT 63  
DB 86 GAGTCGGGCCCAAGACTGTGTAAGCCCTTCACAGACCCCTGTCCCTACCTGCACTGTCTCT 145  
QY 64 GGTGGCTCCATCCGCACTGGTGTATTTATTTGAGTTGGGTCCGCCAGCTCCAGGGAG 123  
DB 146 GGTGGCTCCATCCGCACTGGTGTATTTATTTGAGTTGGGTCCGCCAGCTCCAGGGAG 205  
QY 124 GGCTGGAGTGAATCCGCAATCTATCAAGTGGCAACCTTCAACAACCCGTCCCTC 183  
DB 206 GGCTGGAGTGAATCCGCAATCTATCAAGTGGCAACCTTCAACAACCCGTCCCTC 265  
QY 184 AAGAGTGAATTCATGATGATGAGACAGCTTAAAGACCACTTCTCCCTGAGACTGACC 243  
DB 266 AAGAGTGAATTCATGATGATGAGACAGCTTAAAGACCACTTCTCCCTGAGACTGACC 325  
QY 244 TCTGTGACTCCGCGGACACAGGCGCTGTATTTACTGTGCGGCTCAGA-----TGGG 294  
DB 326 TCTGTGACTCCGCGGACACAGGCGCTGTATTTACTGTGCGGCTCAGA-----TGGG 385  
QY 295 TATACCTTGGACAATGGGGCCAGAGAACCCCTGTGCAACCCGTCTCTCA 342  
DB 386 CATTAATTCCAGCACTGGGGCCAGAGAACCCCTGTGCAACCCGTCTCTCA 433

RESULT 10  
BU899307 959 bp mRNA linear EST 17-OCT-2002  
LOCUS BU899307  
DEFINITION ABEHCOURT\_8532130 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6280128  
5', mRNA sequence.  
ACCESSION BU899307  
VERSION BU899307.1 GI:24081220  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 959)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
[found through the I.M.A.G.E. Consortium/LLNL at:](http://image.llnl.gov)  
<http://image.llnl.gov>  
Plate: LCM2470 row: n column: 01  
High quality sequence stop: 605.  
Location/Qualifiers

FEATURES  
source  
1. .959  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6280128"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; CDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

Query Match

70.1%; Score 239.8; DB 5; Length 959;

Best Local Similarity 83.2%; Pred. No. 4.5e-60;  
Matches 287; Conservative 0; Mismatches 52; Indels 6; Gaps 1;

QY 4 GAGCTGGCCCAAGACTGTGTAAGCCCTTCACAGACCCCTGTCCCTACCTGCACTGTCTCT 63  
DB 86 GAGTCGGGCCCAAGACTGTGTAAGCCCTTCACAGACCCCTGTCCCTACCTGCACTGTCTCT 145  
QY 64 GGTGGCTCCATCCGCACTGGTGTATTTATTTGAGTTGGGTCCGCCAGCTCCAGGGAG 123  
DB 146 GGTGGCTCCATCCGCACTGGTGTATTTATTTGAGTTGGGTCCGCCAGCTCCAGGGAG 205  
QY 124 GGCTGGAGTGAATCCGCAATCTATCAAGTGGCAACCTTCAACAACCCGTCCCTC 183  
DB 206 GGCTGGAGTGAATCCGCAATCTATCAAGTGGCAACCTTCAACAACCCGTCCCTC 265  
QY 184 AAGAGTGAATTCATGATGATGAGACAGCTTAAAGACCACTTCTCCCTGAGACTGACC 243  
DB 266 AAGAGTGAATTCATGATGATGAGACAGCTTAAAGACCACTTCTCCCTGAGACTGACC 325  
QY 244 TCTGTGACTCCGCGGACACAGGCGCTGTATTTACTGTGCGGCTCAGA-----ATGGGTAT 297  
DB 326 TCTGTGACTCCGCGGACACAGGCGCTGTATTTACTGTGCGGCTCAGA-----ATGGGTAT 385  
QY 298 ACTTGGACAATGGGGCCAGAGAACCCCTGTGCAACCCGTCTCTCA 342  
DB 386 GCTTTGATATCTGGGGCCAGAGAACCCCTGTGCAACCCGTCTCTCA 430

RESULT 11  
B0706579 903 bp mRNA linear EST 16-JUL-2002  
LOCUS B0706579  
DEFINITION ABEHCOURT\_8487944 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6300935  
5', mRNA sequence.  
ACCESSION B0706579  
VERSION B0706579.1 GI:21845478  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 903)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
[found through the I.M.A.G.E. Consortium/LLNL at:](http://image.llnl.gov)  
<http://image.llnl.gov>  
Plate: LCM2515 row: p column: 24  
High quality sequence start: 4  
High quality sequence stop: 584.  
Location/Qualifiers

FEATURES  
source  
1. .903  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6300935"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; CDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

ORIGIN

Query Match 69.6%; Score 238.2; DB 5; Length 903;  
Best Local Similarity 82.9%; Pred. No. 1.3e-59;  
Matches 286; Conservative 0; Mismatches 53; Indels 6; Gaps 1;

QY 4 GAGTCTGCCCCAGAGCTGTGTAAGCCCTTCACAGACCCCTGTCCTCCTGACCTGCTCT 63  
DB 98 GAGTCGAGCCAGAGCTGTGTAAGCCCTTCGAGACCCCTGTCCTCCTGACCTGCTCT 157  
QY 64 GGTGGCTCCACATCCGAGTGTGTATTTATTTGAGTTGGGTCGCGCCAGCTCCAGGGAAG 123  
DB 158 GGTGGCTCCACATCCGAGTGTGTATTTATTTGAGTTGGGTCGCGCCAGCTCCAGGGAAG 217  
QY 124 GGCCTGAGTGTGATCGGCAACATCTATCAACAGTGGCAACCTTCAACACCCGCTCC 183  
DB 218 GGCCTGAGTGTGATCGGCAACATCTATCAACAGTGGCAACCTTCAACACCCGCTCC 277  
QY 184 AAGAGTCGAATTACCATGTGATGAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243  
DB 278 AAGAGTCGAATTACCATGTGATGAGACACGCTTAAGAACCACTTCTCCCTGAGACTGAG 337  
QY 244 TCTGTGACTGCGCGGAGACCGCCGTCTATTACTGTGCG-----GCGGTCAAGTGGTAT 297  
DB 338 TCTGTGACCGCGGAGACCGCCGTCTATTACTGTGCGAAAGGGGCGATGTTATGGGC 397  
QY 298 ACTTTGGCAACTGGGGCCAGGAAACCTGTGTCACCGTCTCTCA 342  
DB 398 TGGTTCAGACCTTGGGGCCAGGAAACCTGTGTCACCGTCTCTCA 442

RESULT 12

LOCUS BM920469 1108 bp mRNA linear EST 12-MAR-2002  
DEFINITION AGENCOURT\_6709612 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5750444  
5', mRNA sequence.  
ACCESSION BM920469  
VERSION BM920469.1 GI:19370848  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.lnl.gov  
Plate: LHAM12781 row: g column: 21  
High quality sequence stop: 626.

FEATURES

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Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:5750444"  
/lab\_host="DH10B"  
/clone\_id="NIH\_MGC\_122"  
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber

ORIGIN (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH\_MGC Library."

Query Match 69.6%; Score 238.2; DB 5; Length 1108;  
Best Local Similarity 82.9%; Pred. No. 1.4e-59;  
Matches 286; Conservative 0; Mismatches 53; Indels 6; Gaps 1;

QY 4 GAGTCTGCCCCAGAGCTGTGTAAGCCCTTCACAGACCCCTGTCCTCCTGACCTGCTCT 63  
DB 110 GAGTCGAGCCAGAGCTGTGTAAGCCCTTCGAGACCCCTGTCCTCCTGACCTGCTCT 169  
QY 64 GGTGGCTCCACATCCGAGTGTGTATTTATTTGAGTTGGGTCGCGCCAGCTCCAGGGAAG 123  
DB 170 GGTGGCTCCGTCAGCATGTGATGTTATCTACTGAGCTGTGATCCGCGACCCCGAGGGAAG 229  
QY 124 GGCCTGAGTGTGATCGGCAACATCTATCAACAGTGGCAACCTTCAACACCCGCTCC 183  
DB 230 GCACTGAGTGTGATGGGTATCTATTAACAGTGGGAGCAACCACTCAACCCCTCCCTC 289  
QY 184 AAGAGTCGAATTACCATGTGATGAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243  
DB 290 AAGAGTCGAATTACCATGTGATGAGACACGCTTAAGAACCACTTCTCCCTGAGACTGAGC 349  
QY 244 TCTGTGACTGCGCGGAGACCGCCGTCTATTACTGTGCGCGGTGAGTGGG-----TAT 297  
DB 350 TCTGTGACCGCTGGGAGACCGCCGTGTATTACTGTGCGAGCGGGGGGGGAGACTAC 409  
QY 298 ACTTTGGCAACTGGGGCCAGGAAACCTGTGTCACCGTCTCTCA 342  
DB 410 TACATGAGACGTCGTGGGCAAGGAGACCGGTCAACCGTCTCTCA 454

RESULT 13

LOCUS BG757054 914 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602710478P1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4850851 5', mRNA sequence.  
ACCESSION BG757054  
VERSION BG757054.1 GI:14067707  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.lnl.gov  
Plate: LNCM1692 row: 1 column: 20  
High quality sequence stop: 854.

FEATURES

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Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="IMAGE:4850851"  
/tissue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_48"  
/note="Organ: B-cells; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp



## ORIGIN

for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

Query Match 69.3%; Score 237; DB 4; Length 914;  
Best Local Similarity 84.4%; Pred. No. 3e-59;  
Matches 293; Conservative 0; Mismatches 45; Indels 9; Gaps 2;

4 GAGTCTGGCCAGGAGCTGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 63  
|||  
93 GAGTGGGCCCCAGAGCTGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 152  
|||  
64 GGTGGCTCCATCCGACGTGTGTTATTAATGAGTTGGTCCGCCAGCCTCCAGGAG 123  
|||  
153 GGTGGCTCCATCCGACGTGTGTTATTAATGAGTTGGTCCGCCAGCCTCCAGGAG 211  
|||  
124 GGCCTGAGTGAATCGGCAATCTATCAAGTGGCAACACTTAACAACCCGTCCTC 183  
|||  
212 GGCCTGAGTGAATCGGCAATCTATCAAGTGGCAACACTTAACAACCCGTCCTC 271  
|||  
184 AAGAGTGAATTAACATGTCAGTAGACACGCTTAAGAACACTTCTCCCTGAGACTGACC 243  
|||  
272 AAGAGTGAATTAACATGTCAGTAGACACGCTTAAGAACACTTCTCCCTGAGACTGACC 331  
|||  
244 TCTGTGACTGCGCGGACACGCGCTATTAATGAGTTGGTCCGCCAGCCTCCAGGAG 303  
|||  
332 TCTGTGACTGCGCGGACACGCGCTATTAATGAGTTGGTCCGCCAGCCTCCAGGAG 391  
|||  
304 GACAACT-----GGGGCCAGGAAACCTGTGACCGTCTCTCA 342  
|||  
392 CAGCACTTTGACTACTGCGGCGCAGGAACCTGTGACCGTCTCTCA 438  
|||

## RESULT 14

B0708070

LOCUS B0708070 939 bp mRNA linear EST 16-JUL-2002  
DEFINITION AGENCOURT 8495323 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6301745  
5', mRNA sequence.

ACCESSION B0708070  
VERSION B0708070.1 GI:21846969  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 939)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM2518 row: b column: 18  
High quality sequence start: 12  
High quality sequence stop: 587.  
Location/Qualifiers

## FEATURES

source

1. 939  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6301745"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_113"  
/note="Organ: spleen; Vector: pOTB7; Site\_1: XhoI; Site\_2:

## ORIGIN

ECORI, cDNA made by oligo-dT priming. Directionally cloned into EcorI/XhoI sites using the following 5' adaptor: GGACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

Query Match 69.3%; Score 237; DB 5; Length 939;  
Best Local Similarity 82.3%; Pred. No. 3e-59;  
Matches 289; Conservative 0; Mismatches 50; Indels 12; Gaps 1;

4 GAGTCTGGCCAGGAGCTGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 63  
|||  
95 GAGTGGGCCCCAGAGCTGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 154  
|||  
64 GGTGGCTCCATCCGACGTGTGTTATTAATGAGTTGGTCCGCCAGCCTCCAGGAG 123  
|||  
155 GGTGGCTCCATCCGACGTGTGTTATTAATGAGTTGGTCCGCCAGCCTCCAGGAG 214  
|||  
124 GGCCTGAGTGAATCGGCAATCTATCAAGTGGCAACACTTAACAACCCGTCCTC 183  
|||  
215 GGCCTGAGTGAATCGGCAATCTATCAAGTGGCAACACTTAACAACCCGTCCTC 274  
|||  
184 AAGAGTGAATTAACATGTCAGTAGACACGCTTAAGAACACTTCTCCCTGAGACTGACC 243  
|||  
275 AAGAGTGAATTAACATGTCAGTAGACACGCTTAAGAACACTTCTCCCTGAGACTGACC 334  
|||  
244 TCTGTGACTGCGCGGACACGCGCTATTAATGAGTTGGTCCGCCAGCCTCCAGGAG 291  
|||  
335 TCTGTGACTGCGCGGACACGCGCTATTAATGAGTTGGTCCGCCAGCCTCCAGGAG 394  
|||  
292 GGTATTAATTTGGAACAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 342  
|||  
395 AAGAGATTTTGAATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 445  
|||

## RESULT 15

BF974568

LOCUS BF974568 828 bp mRNA linear EST 22-JAN-2001  
DEFINITION 602243482F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4334541 5',  
mRNA sequence.

ACCESSION BF974568  
VERSION BF974568.1 GI:12341783  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 828)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM204 row: c column: 22  
High quality sequence stop: 800.  
Location/Qualifiers

## FEATURES

source

1. 828  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4334541"  
/tissue\_type="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"



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/clone_lib="NIH_MGC_48"
/notes="Organ: B-cells; Vector: pOTB; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCCGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

```

**ORIGIN**

	Query Match	Similarity	90.6%	Score	236.4	DB	4	Length	828
Best Local									
Matches	252	Conservative	0	Mismatches	26	Indels	0	Gaps	0
QY	4	GAGTGTGGCCAGAGACTGATGAAGCCTTACAGACCCCTGTCCCTCACTGCAGCTGTCTCT							63
Db	92	GAGTGTGGCCAGAGACTGATGAAGCCTTACAGACCCCTGTCCCTCACTGCAGCTGTCTCT							151
QY	64	GGTGGCTTCATCCGCAGTGTGTATTATTGAGATTGGATTCGCGCAGCCTTCAGGGAAG							123
Db	152	GGTGGCTTCATCGACAGTGTGTATTACTACTGGAATTTGGATTCGCGCAGCCTTCAGGGAAG							211
QY	124	GGCCTGAGTGGATCGCAACATCTATCAACAGTGGCAACACTTACACAACCCGTCCTC							183
Db	212	GGCCTGAGTGGATCGATGTGATATCATCTATTACAGTGGGACACCTATATACCCGTCCTC							271
QY	184	AAGAGTCGAATTACATGTCAGTAGACACGTCTAAGAACCACTTCTCCCTGAGATTGACC							243
Db	272	AAGAGTCGAATTACATGTCAGTAGACACGTCTAAGAACCACTTCTCCCTGAGATTGACC							331
QY	244	TCTGTGACTGCGCGGAGACACGGCCGTCTATTACTGTGC							281
Db	332	TCTGTGATTGCGCGAGACACGGCCGTGTATTACTGTGC							369

Search completed: July 27, 2005, 12:32:07  
Job time : 2107.58 secs

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```
XX PN WO200253595-A1.
XX PD 11-JUL-2002.
XX PF 27-DEC-2001; 2001WO-SE002908.
XX PR 29-DEC-2000; 2000SE-00004892.
XX PA (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX P-PSDB; ABG30446.
XX DR WPI; 2002-583604/62.
XX PT Group 2 allergen-specific immunoglobulins (Ig) E fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX PS Disclosure; Page 32; 45pp; English.
XX CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to Phi p 2. The present sequence represents the DNA
CC encoding the human IgG fab, clone 60 heavy chain protein of the invention
XX SQ Sequence 342 BP; 70 A; 105 C; 90 G; 77 T; 0 U; 0 Other;
XX
Query Match 99.5%; Score 340.4; DB 6; Length 342;
Best Local Similarity 99.7%; Pred. No. 5.3e-87;
Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 CTGAGTCTGAGCCGAGACTGCTGTAAGCTTACAGACAGACCCCTGCTCACCCTGACATGTC 60
Db 1 CTGAGTCTGAGCCGAGACTGCTGTAAGCTTACAGACAGACCCCTGCTCACCCTGACATGTC 60
XX QY 61 TCTGGTGGCTTCCATCCGAGTGGTGTATTATTGAGTTGGTCCGCGACGCTCCAGGG 120
Db 61 TCTGGTGGCTTCCATCCGAGTGGTGTATTATTGAGTTGGTCCGCGACGCTCCAGGG 120
XX QY 121 AAGGCGCTGAGTGGATCGGCAACATCTATACAGATGAGCAACACTCAACACCGCTCC 180
Db 121 AAGGCGCTGAGTGGATCGGCAACATCTATACAGATGAGCAACACTCAACACCGCTCC 180
XX QY 181 CTGAAGAGTGAATTATTCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTAGACTG 240
Db 181 CTGAAGAGTGAATTATTCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTAGACTG 240
XX QY 241 ACCTCTGTACTGCGCGGAGACACGCGCTTATTACTGTGCGCGCTGATGGGTATTA 300
Db 241 ACCTCTGTACTGCGCGGAGACACGCGCTTATTACTGTGCGCGCTGATGGGTATTA 300
XX QY 301 TTGGACAACATGGGGGCGAGGAACCGTGTACCGCTCCCTCA 342
Db 301 TTGGACAACATGGGGGCGAGGAACCGTGTACCGCTCCCTCA 342
XX
RESULT 2
ABK89639
ID ABK89639 standard; DNA, 342 BP.
```

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XX AC ABK89639;
XX XX 21-OCT-2002 (first entry)
XX DT DNA encoding human IgE Fab clone 100 heavy chain.
XX DE
XX XX
XX KM Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;
XX KM timothy grass pollen allergen; passive immunotherapy.
XX OS Homo sapiens.
XX
XX PH Key
XX PH CDS
XX FT Location/Qualifiers
XX FT 1..342
XX FT /*tag= a
XX FT /product= "Fab clone 100 heavy chain"
XX FT 7..78
XX FT /*tag= b
XX FT /note= "PR1 region"
XX FT 79..99
XX FT /*tag= c
XX FT /note= "CDR1 region"
XX FT 100..123
XX FT /*tag= d
XX FT /note= "PR2 region"
XX FT 134..141
XX FT /*tag= e
XX FT /note= "PR3 region"
XX FT 142..189
XX FT /*tag= f
XX FT /note= "CDR2 region"
XX FT 190..285
XX FT /*tag= g
XX FT /note= "PR3 region"
XX FT 286..309
XX FT /*tag= h
XX FT /note= "CDR3 region"
XX FT 310..342
XX FT /*tag= i
XX FT /note= "PR4 region"
XX
XX PN WO200253595-A1.
XX XX 11-JUL-2002.
XX XX 27-DEC-2001; 2001WO-SE002908.
XX PF 29-DEC-2000; 2000SE-00004892.
XX PR
XX XX (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX PA Flicker S, Steinberger P, Kraft D, Valenta R;
XX PI
XX P-PSDB; ABG30447.
XX DR WPI; 2002-583604/62.
XX DR P-PSDB; ABG30446.
XX XX
XX PT Group 2 allergen-specific immunoglobulins (Ig) E fabs or IgG comprising
XX PT variable region of group 2 allergen specific-human IgE fabs, useful for
XX PT diagnosing or passive immunotherapy of type I allergy, for environmental
XX PT allergen detection.
XX
XX PS Disclosure; Page 33; 45pp; English.
XX
XX CC This invention relates to the DNA and protein sequences of group 2
XX CC allergen-specific human IgE fabs and methods for their use. The proteins
XX CC of the invention may have antiallergic activities and may be used as a
XX CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
XX CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX CC 2 allergen-specific fabs of the invention may be useful for environmental
XX CC allergen detection and for standardisation of allergen extracts. The fabs
XX CC - or a vaccine against a type I allergy is useful for passive
XX CC immunotherapy of type I allergy, it is also useful for diagnosing a type
XX CC I allergy. The allergen-specific fabs of the invention are useful for
```



```
QY 301 TTGGACAACCTGGGCGAGGAACCTGTGTCACCGTCTCTCA 342
DB 301 TTGGACAATCTGGGCGAGGAACCTGTGTCACCGTCTCTCA 342

RESULT 4
ID ADC99786 standard; DNA, 352 BP.
XX
XX ADC99786;
AC
XX
XX 01-JAN-2004 (first entry)
DT
XX
XX Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 15.
DE
XX
XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
XX cytosarctic; melanoma; oesophageal; pancreatic; colorectal tumor;
XX cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
XX lung cancer; human; ds. gene.
XX
XX Homo sapiens.
OS
XX WO2003057838-A2.
XX
XX 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041581.
XX
XX 28-DEC-2001; 2001US-0346299P.
XX
XX (ABGE-) ABGENIX INC.
PA
XX
XX Gudas J;
PI
XX
XX WPI; 2003-587113/55.
XX
XX P-PSDB; ADC99784.
DR
XX
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
XX
XX Claim 8; SEQ ID NO 15; 78pp; English.
XX
XX
XX The invention relates to a novel isolated monoclonal antibody comprising
XX a heavy or light chain amino acid or a heavy or light chain variable
XX domain where the antibody binds to MUC18. The monoclonal antibody of the
XX invention demonstrates cytostatic activity and may be useful for treating
XX a disease or condition associated with the expression of MUC18 on the
XX cell surface such as tumors, specifically melanoma, oesophageal,
XX pancreatic or colorectal tumors, carcinomas, particularly cervical
XX carcinomas and cervical intraepithelial neoplasia and cancers including
XX colorectal, breast or lung cancer, as well as other malignancies. The
XX current sequence is that of the anti-human MUC18 monoclonal antibody
XX heavy chain variable domain DNA of the invention.
XX
XX
XX Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;
SQ

Query Match 79.5%; Score 271.8; DB 10; Length 352;
Best Local Similarity 89.7%; Pred. No. 1.9e-67;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

QY 4 GAGTCTGAGCCAGAGACTGTGAAGCCCTTACAGACCCCTGTCTCACTGTGACTGTCTCT 63
DB 16 GAGTCGGGCGCCAGAGACTGTGAAGCCCTTACAGACCCCTGTCTCACTGTGACTGTCTCT 75
QY 64 GGTGGCTCCATCCGCACTGCTGCTTATTTATTTAGATTGGGTCGCGCAGCCCTCCAGGAG 123
DB 76 GGTGGCTCCATCCGCACTGCTGCTTATTTATTTAGATTGGGTCGCGCAGCCCTCCAGGAG 135
QY 124 GGCTTGAGTGATGGCAACATCTATACAGTGGCAACCTCTCAACACCCGTCCTC 183
DB 136 GGCTTGAGTGATGGGTTTATCTATTTACAGTGGGAGCACTTCTACACCCGTCCTC 195
```

```
QY 184 AAGAGTCGAATTACATGTGATGAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTCGAATTACATGTGATGAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGAGC 255
QY 244 TCTGTGACTGCGCGGACAGCGCGTCTATTACTGTGCGGAGTCAGATGGGTATCTTGG 303
DB 256 TCTGTGACTGCGCGGACAGCGCGTCTATTACTGTGCGGAGTCAGATGGGTATCTTGG 312
QY 304 GACAACTGGGGCGAGGGAACCTGTGTCACCGTCTCTCA 342
DB 313 GACTACTGGGGCGAGGGAACCTGTGTCACCGTCTCTCA 351

RESULT 5
ADD05390
ID ADD05390 standard; DNA, 352 BP.
XX
XX ADD05390;
AC
XX
XX 01-JAN-2004 (first entry)
DT
XX
XX Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 15.
DE
XX
XX monoclonal antibody; tumor; MUC18; proliferation; cytostatic; vaccine;
XX antigen; tumor metastasis; melanoma; metastatic; human; heavy chain;
XX gene; ds.
XX
XX Homo sapiens.
OS
XX WO2003057006-A2.
XX
XX 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041582.
XX
XX 28-DEC-2001; 2001US-0346460P.
XX
XX (ABGE-) ABGENIX INC.
PA
XX
XX Gudas J, Bar-El M;
PI
XX
XX WPI; 2003-577496/54.
XX
XX P-PSDB; ADD05388.
DR
XX
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
XX
XX Disclosure; SEQ ID NO 15; 87pp; English.
XX
XX
XX The invention relates to a novel monoclonal antibody used for inhibiting
XX tumor growth in an animal. The tumor inhibition process comprises
XX selecting an animal in need of treatment for a tumor, providing a
XX monoclonal antibody comprising a heavy chain amino acid, where the
XX antibody consists of any one of 10 fully defined sequences of 117-123
XX amino acids given in the specification, and where the monoclonal antibody
XX binds MUC18, and contacting the tumor with the antibody resulting in
XX inhibited proliferation of the cells. The monoclonal antibody has
XX cytostatic and can be used in the production of a vaccine. The monoclonal
XX antibodies against the MUC18 antigen are useful for diagnosing and
XX treating tumors, inhibiting tumor growth (e.g. melanoma, lung tumor or
XX tumor metastasis), inhibiting cell invasion associated with melanoma, or
XX increasing survival of an animal having a metastatic tumor. This
XX polynucleotide sequence represents the DNA encoding an anti-MUC18
XX antibody heavy chain, variable region, protein of the invention.
XX
XX
XX Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;
SQ

Query Match 79.5%; Score 271.8; DB 10; Length 352;
Best Local Similarity 89.7%; Pred. No. 1.9e-67;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
```

QY 4 GAGTCTGGCCCAAGAGCTGTGAAAGCCTTTCACAGACCCCTGTCTCTACCTGCACTGTCTCT 63  
DB 16 GAGTCGGGGCCAGAGACTGTGAAAGCCTTTCACAGACCCCTGTCTCTACCTGCACTGTCTCT 75  
QY 64 GGTGGCTCCATCCCACTGTGTGTATTATTGAGTTGGGTCCGCCAGCCCTCCAGGGAAG 123  
DB 76 GGTGGCTCCATCCCACTGTGTGTATTATTGAGTTGGGTCCGCCAGCCCTCCAGGGAAG 135  
QY 124 GGCCTGAGTGAATCGGCAACATCTATCAAGTGGCAACCTTAAACAAACCCGTCCCTC 183  
DB 136 GGCCTGAGTGAATCGGCAACATCTATCAAGTGGCAACCTTAAACAAACCCGTCCCTC 195  
QY 184 AAGAGTGAATTACCATGTGAGTGAAGACAGTCTAAGAACCACTTCTCTGAGACTGAGC 243  
DB 196 AAGAGTGAATTACCATGTGAGTGAAGACAGTCTAAGAACCACTTCTCTGAGACTGAGC 255  
QY 244 TCTGTGACTGCGCGGACAGCGCGCTCTATTACTGTGCGCGGTCAAGTGGTATACCTTTG 303  
DB 256 TCTGTGACTGCGCGGACAGCGCGCTCTATTACTGTGCGAG--AGAGGAGATGGCTTT 312  
QY 304 GACAACCTGGGGCCAGGGAAACCTGTGACCGTCTCTCA 342  
DB 313 GACTACTGGGGCCAGGGAAACCTGTGACCGTCTCTCA 351

## RESULT 6

ADP09828 standard; DNA, 352 BP.

AC ADF09828;

DT 12-FEB-2004 (first entry)

DE Human anti-MUC18 monoclonal antibody heavy chain coding sequence #4.

XX cell proliferation inhibitor; MUC18 tumour antigen;  
KM anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KM carcinoma; cancer; malignancy; heavy chain; human; ds; gene.

OS Homo sapiens.

PN WO2003057837-A2.

PD 17-JUL-2003.

PF 26-DEC-2002; 2002WO-US041580.

PR 28-DEC-2001; 2001US-0346414P.

PA (ABGE-) ABGENIX INC.

PI Gudae J;

DR WPI; 2003-598367/56.

DR P-PSDB; ADF09826.

PT Inhibiting cell proliferation associated with expression of MUC18 tumor  
PT antigen, involves incubating and inhibiting cell by administering anti-  
PT MUC18 monoclonal antibody.

PS Disclosure; SEQ ID NO 15; 83bp; English.

XX The invention comprises a method for inhibiting cell proliferation  
CC associated with expression of MUC18 tumour antigen. The method involves  
CC administering anti-MUC18 monoclonal antibody. The method of the invention  
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
CC proliferation associated with the expression of MUC18 tumour antigen, the  
CC method is preferably useful for inhibiting tumour metastasis. The method  
CC is useful for inhibiting cell proliferation in patients with tumours,  
CC carcinomas, cancer and other malignancies. The present DNA sequence  
CC encodes a heavy chain from an MUC18 tumour antigen-specific monoclonal  
XX antibody.

SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;  
Query Match 79.5%; Score 271.8; DB 10; Length 352;  
Best Local Similarity 89.7%; Pred. No. 1,9e-67;  
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCAAGAGCTGTGAAAGCCTTTCACAGACCCCTGTCTCTACCTGCACTGTCTCT 63  
DB 16 GAGTCGGGGCCAGAGACTGTGAAAGCCTTTCACAGACCCCTGTCTCTACCTGCACTGTCTCT 75  
QY 64 GGTGGCTCCATCCCACTGTGTGTATTATTGAGTTGGGTCCGCCAGCCCTCCAGGGAAG 123  
DB 76 GGTGGCTCCATCCCACTGTGTGTATTATTGAGTTGGGTCCGCCAGCCCTCCAGGGAAG 135  
QY 124 GGCCTGAGTGAATCGGCAACATCTATCAAGTGGCAACCTTAAACAAACCCGTCCCTC 183  
DB 136 GGCCTGAGTGAATCGGCAACATCTATCAAGTGGCAACCTTAAACAAACCCGTCCCTC 195  
QY 184 AAGAGTGAATTACCATGTGAGTGAAGACAGTCTAAGAACCACTTCTCTGAGACTGAGC 243  
DB 196 AAGAGTGAATTACCATGTGAGTGAAGACAGTCTAAGAACCACTTCTCTGAGACTGAGC 255  
QY 244 TCTGTGACTGCGCGGACAGCGCGCTCTATTACTGTGCGCGGTCAAGTGGTATACCTTTG 303  
DB 256 TCTGTGACTGCGCGGACAGCGCGCTCTATTACTGTGCGAG--AGAGGAGATGGCTTT 312  
QY 304 GACAACCTGGGGCCAGGGAAACCTGTGACCGTCTCTCA 342  
DB 313 GACTACTGGGGCCAGGGAAACCTGTGACCGTCTCTCA 351

## RESULT 7

AAF29076 standard; DNA, 360 BP.

AC AAF29076;

DT 03-APR-2001 (first entry)

DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 32.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;

KM envelope glycoprotein; gp120; diagnosis; ds.

OS Homo sapiens.

PN WO200100678-A1.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-US017327.

PR 30-JUN-1999; 99US-0141701P.

PA (USSH) US DEPT HEALTH &amp; HUMAN SERVICES.

PI Watkins BA, Reitz MS;

DR WPI; 2001-112438/12.

DR P-PSDB; AAB62775.

PT Novel human monoclonal antibody immunoreactive with human  
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
PT in biological sample and providing passive immunotherapy to HIV-1  
PT infected mammal.

PS Claim 4; Page 45; 81bp; English.

XX The present invention provides the protein and coding sequences for the  
CC variable regions of human monoclonal antibodies which are immunoreactive  
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
CC These can be used in diagnosis and therapy of HIV-1 infection

Sequence 360 BP; 73 A; 104 C; 107 G; 76 T; 0 U; 0 Other;

Query Match 78.5%; Score 268.4; DB 4; Length 360;  
Best Local Similarity 88.6%; Pred. No. 1.8e-66;  
Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

4 GAGCTGCGCCAGAGACTGTGGAAGCCCTTCCACAGCCCTGCTCCCTGACCTGCTCTCT 63  
19 GAGTGGGGCCAGAGACTGTGGAAGCCCTTCCACAGCCCTGCTCCCTGACCTGCTCTCT 78  
64 GGTGCTCCATCCGACGTGGTGTATTATTGAGTTGGGCGCCAGCCTCCAGGGAG 123  
79 GGTGCTCCATCCGACGTGGTGTATTATTGAGTTGGGCGCCAGCCTCCAGGGAG 138  
124 GGCCTGAGTGTGATGGCAACATCTATCAGTGGCAACCTTCAACAAACCCGCTCC 183  
139 GGCCTGAGTGTGATGGTGTATCTATCTATCAGTGGGAGCACTTCAACAAACCCGCTCC 198  
184 AAGAGTGAATTTTCCATGTGATGAGACCGCTTAAAGAACCTTCTCCCTGAGCTGACC 243  
199 AAGAGTGAATTTTACATATCAGTGAACCGCTTAAAGAACCGTTCCTGAACTGAGC 258  
244 TCTGTGACTGCGCGGACACGCGCGCTTATTACTGTGG--CGGTGAGATGGTATACT 300  
259 TCTGTGACTGCGCGGACACGCGCGCTTATTACTGTGCGAGAGGGGTATGATGACTGG 318  
301 TTGAGACACTGGGGCCAGGGAACTGTGTCACCGCTCTCTCA 342  
319 TTGAGACCTGTGGGGCCAGGGAACTGTGTCACCGCTCTCTCA 360

RESULT 8  
ADS84403 standard; DNA; 354 BP.

ADS84403;  
18-NOV-2004 (first entry)

Human anti-EPO-R antibody heavy chain variable region DNA SEQ ID NO:42.

human; erythropoietin receptor; EPO receptor;  
erythropoietin receptor binding antibody; gene receptor binding antibody;  
antianemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;  
wound healing; neural cell damage protection;  
neural tissue damage protection; brain injury; spinal cord injury;  
stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;  
de.

OS Homo sapiens.  
PN WO2004035603-A2.  
PD 29-APR-2004.  
PF 14-OCT-2003; 2003WO-US032243.  
PR 14-OCT-2002; 2002US-00269711.  
PR 10-OCT-2003; 2003US-00684109.  
PA (ABBO ) ABBOTT LAB.  
PI Devices PJ, Green LL, Ostrow DH, Reilly EB, Wielek J;  
DR WPI; 2004-348433/32.  
DR P-PSDB; ADS84404.

New antibodies that bind to or activate an endogenous human  
erythropoietin receptor, useful for diagnosing, preventing or treating  
disorders associated with dysfunctional erythropoietin receptor, e.g.  
anemia.

Claim 47; SEQ ID NO 42; 192pp; English.

XX The present invention describes an antibody or its fragment that binds to  
CC or activates an endogenous activity of a human erythropoietin (EPO)  
CC receptor in a mammal, but does not interact with a peptide having a  
CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
CC methods of modulating or activating an endogenous activity of a human EPO  
CC receptor in a mammal, comprising administering to the mammal a  
CC therapeutic amount of the above antibody or its fragment to modulate or  
CC activate the receptor; (2) a method of treating a mammal suffering from  
CC aplasia, comprising administering to the mammal a therapeutic amount of  
CC the above antibody or its fragment to modulate or activate the receptor;  
CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
CC an isolated and purified polynucleotide sequence, and their fragments,  
CC complements and degenerate codon equivalents; and (5) an isolated and  
CC purified amino acid sequence, and their fragments. The EPO receptor  
CC binding antibody has antianemic, neuroprotective and vulnerary  
CC activities, and can be used in gene therapy. The compositions and methods  
CC from the present invention can be used for modulating an endogenous  
CC activity of a human EPO receptor or for treating mammals suffering from  
CC aplasia or anaemia. They may also be used for identifying mammals having  
CC a dysfunctional EPO receptor. The composition may also be used in  
CC promoting wound healing or in protecting against neural cell and/or  
CC tissue damage resulting from brain/spinal cord injury, stroke and the  
CC like. The present sequence encodes a human anti-EPO-R antibody heavy  
CC chain variable region, which is given in the exemplification of the  
CC present invention.

Sequence 354 BP; 76 A; 105 C; 97 G; 76 T; 0 U; 0 Other;

Query Match 78.1%; Score 267; DB 13; Length 354;  
Best Local Similarity 86.7%; Pred. No. 4.5e-66;  
Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

4 GAGCTGCGCCAGAGACTGTGGAAGCCCTTCCACAGCCCTGCTCCCTGACCTGCTCTCT 63  
16 GAGTGGGGCCAGAGACTGTGGAAGCCCTTCCACAGCCCTGCTCCCTGACCTGCTCTCT 75  
64 GGTGCTCCATCCGACGTGGTGTATTATTGAGTTGGGCGCCAGCCTCCAGGGAG 123  
76 GGTGCTCCATCCGACGTGGTGTATTATTGAGTTGGGCGCCAGCCTCCAGGGAG 135  
124 GGCCTGAGTGTGATGGCAACATCTATCAGTGGCAACCTTCAACAAACCCGCTCC 183  
136 GGCCTGAGTGTGATGGGTCATCTTAAAGTGAAGACCTTCAACAAACCCGCTCC 195  
184 AAGAGTGAATTTTCCATGTGATGAGACCGCTTAAAGAACCGTTCCTGAGACTGACC 243  
196 AAGAGTGAATTTTACATATCAGTGAACCGCTTAAAGAACCGTTCCTGAACTGAGC 255  
244 TCTGTGACTGCGCGGACACGCGCGCTTATTACTGTGCGCGGTCAATGAGTATCTTG 303  
256 TCTGTGACTGCGCGGACACGCGCGGTATTATTGTCGAGATAACTGGGATGCGG 315  
304 GACAACTGGGGCCAGGGAACTGTGTCACCGCTCTCTCA 342  
316 GACTACTGGGGCCAGGGAACTGTGTCACCGCTCTCTCA 354

RESULT 9  
ADR68545 standard; DNA; 354 BP.

ADR68545;  
02-DEC-2004 (first entry)

Anti-EPO-R-antibody heavy chain variable region DNA seqid 42.

antianemic; respiratory; vulnerary; gene therapy; vaccine;  
erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
wound healing; neural cell damage; tissue damage; brain injury;



KW spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;  
 XX variable region; ds.  
 OS Homo sapiens.  
 XX US2004175379-A1.  
 XX 09-SEP-2004.  
 XX 10-OCT-2003; 2003US-00684109.  
 XX 14-OCT-2002; 2002US-0418031P.  
 XX (DEVIR/) DEVIRIES P J.  
 XX (OSTR/) OSTROW D H.  
 XX (REIL/) REILLY E B.  
 XX (GREE/) GREEN L L.  
 XX (WIEL/) WIELER J.  
 XX Devires PJ, Ostrow DH, Reilly EB, Green LL, Wieler J,  
 XX WPI; 2004-661369/64.  
 XX P-PSDB; ADR68546.  
 XX  
 XX New antibody or its antibody fragment that activates an endogenous  
 PT activity or is capable of binding to a human erythropoietin receptor in a  
 PT mammal, useful for treating a mammal suffering aplasia or anemia.  
 XX  
 XX Claim 47; SEQ ID NO 42; 156pp; English.  
 XX  
 XX The invention describes an antibody or its fragment that activates an  
 CC endogenous activity or capable of binding to a human erythropoietin  
 CC receptor in a mammal, or that comprises at least one heavy or light chain  
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
 CC given in the specification. Also described are: a method of activating or  
 CC modulating an endogenous activity of a human erythropoietin receptor in a  
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
 CC isolated and purified polynucleotide sequence selected from 28 sequences  
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in  
 CC the specification; and their fragments, complements, and degenerate codon  
 CC equivalents; and an isolated and purified amino acid sequence selected  
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between  
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
 CC their fragments. The antibody or its antibody fragment that activates or  
 CC modulates the activity of the receptor is useful in a method of treating  
 CC a mammal suffering aplasia or anemia. The antibodies are also useful for  
 CC treating disorders characterised by decreased or subnormal levels of  
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
 CC hypoxia and/or diseases characterised by inadequate blood circulation or  
 CC reduced blood flow. They are also useful for promoting wound healing or  
 CC for protecting against neural cell and/or tissue damage, resulting from  
 CC brain/spinal cord injury, stroke and the like. The antibodies are also  
 CC useful for identifying or diagnosing mammals having dysfunctional  
 CC erythropoietin receptor. This sequence encodes an anti-EPO-R-antibody  
 CC heavy chain variable region.  
 XX  
 XX Sequence 354 BP; 76 A; 105 C; 97 G; 76 T; 0 U; 0 Other;  
 SQ  
 XX Query Match 78.1%; Score 267; DB 13; Length 354;  
 XX Best Local Similarity 86.7%; Pred. No. 4.5e-66;  
 XX Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;  
 XX  
 XX 4 GAGTCTGCGCCAGGAGCTGTGAAGCTTTCACAGACCTGTCTCCCTACCTGCACTGTCTCT 63  
 XX |||||  
 XX 16 GAGTCTGCGCCAGGAGCTGTGAAGCTTTCACAGACCTGTCTCCCTACCTGCACTGTCTCT 75  
 XX |||||  
 XX 64 GGTGCTTCATCCGAGTGTGTATTATTGAGTTGGGTCCGCGACCTCCAGGGAG 123  
 XX |||||  
 XX 76 GTGTCCCTCATCAGACAGTGTGTACTACTGAGTGTGATCCGCGACGCCAGGGAG 135  
 XX |||||

QY 124 GGCCTGAGTGTGATCGGCAACATCTATACAGTGGCAACACTTAACAACCCGCTCC 183  
 |||||  
 DB 136 GGCCTGAGTGTGATCGGCAACATCTATACAGTGGCAACACTTAACAACCCGCTCC 195  
 |||||  
 QY 184 AAGAGTGAATTATACATGTAGTACAGTCTTAAGAACCACTTCTCCCTGAGACTGACC 243  
 |||||  
 DB 196 AAGAGTGAATTATACATGTAGTACAGTCTTAAGAACCACTTCTCCCTGAGACTGACC 255  
 |||||  
 QY 244 TCTGTGACTGCGCGGACACAGGCGCTATTACGTGCGGGGTGAGATGGGTATACCTTGG 303  
 |||||  
 DB 256 TCTGTGACTGCGCGGACACAGGCGCTATTATTTATTTGTCGAGATTAACCTGGGGATCGCG 315  
 |||||  
 QY 304 GACAACCTGGGCGGACAGGACACCTGTGTCACCGCTCTCTCA 342  
 |||||  
 DB 316 GACTACTGGGCGGACAGGACACCTGTGTCACCGCTCTCTCA 354  
 |||||  
 XX  
 XX RESULT 10  
 XX ADS84454/c  
 XX ID ADS84454 standard; DNA; 1996 BP.  
 XX  
 XX ADS84454;  
 XX  
 XX 18-NOV-2004 (first entry)  
 XX  
 XX Human anti-EPO-R antibody Ab412 heavy chain complementary DNA SEQ ID:93.  
 DE  
 XX human; erythropoietin receptor; EPO receptor;  
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
 KW antianemic; neuroprotective; vulnery; gene therapy; aplasia; anaemia;  
 KW wound healing; neural cell damage protection;  
 KW neural tissue damage protection; brain injury; spinal cord injury;  
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;  
 KW ds.  
 XX  
 XX Homo sapiens.  
 XX  
 XX W02004035603-A2.  
 XX  
 XX 29-APR-2004.  
 XX  
 XX 14-OCT-2003; 2003WO-US032243.  
 XX  
 XX 14-OCT-2002; 2002US-00269711.  
 XX  
 XX 10-OCT-2003; 2003US-00684109.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX  
 XX Devires PJ, Green LL, Ostrow DH, Reilly EB, Wieler J,  
 XX WPI; 2004-348433/32.  
 XX P-PSDB; ADS84455.  
 XX  
 XX New antibodies that bind to or activate an endogenous human  
 PT erythropoietin receptor, useful for diagnosing, preventing or treating  
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
 PT anemia.  
 FT  
 XX  
 XX Disclosure; SEQ ID NO 93; 192pp; English.  
 XX  
 XX The present invention describes an antibody or its fragment that binds to  
 CC or activates an endogenous activity of a human erythropoietin (EPO)  
 CC receptor in a mammal, but does not interact with a peptide having a  
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
 CC methods of modulating or activating an endogenous activity of a human EPO  
 CC receptor in a mammal, comprising administering to the mammal a  
 CC therapeutic amount of the above antibody or its fragment to modulate or  
 CC activate the receptor; (2) a method of treating a mammal suffering from  
 CC aplasia, comprising administering to the mammal a therapeutic amount of  
 CC the above antibody or its fragment to modulate or activate the receptor;  
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
 CC an isolated and purified polynucleotide sequence, and their fragments,

CC complements and degenerate codon equivalents; and (5) an isolated and  
CC purified amino acid sequence, and their fragments. The EPO receptor  
CC binding antibody has antianaemic, neuroprotective and vlneryary  
CC activities, and can be used in gene therapy. The compositions and methods  
CC from the present invention can be used for modulating an endogenous  
CC activity of a human EPO receptor or for treating mammals suffering from  
CC aplasia or anaemia. They may also be used for identifying mammals having  
CC a dysfunctional EPO receptor. The composition may also be used in  
CC promoting wound healing or in protecting against neural cell and/or  
CC tissue damage resulting from brain/spinal cord injury, stroke and the  
CC like. The present sequence represents a human anti-EPO-R antibody heavy  
CC chain complementary DNA sequence, which is given in the exemplification  
CC of the present invention.

XX  
XX  
SQ Sequence 1996 BP; 351 A; 537 C; 686 G; 422 T; 0 U; 0 Other;

Query Match 78.1%; Score 267; DB 13; Length 1996;  
Best Local Similarity 86.7%; Pred. No. 7e-66;  
Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 4 GAGCTGGGCCAGAGACTGTGTGAACCTTCAACAGACCTGTCCCTGACCTGTCTCT 63  
DB 1924 GAGTCGGGGCCAGAGACTGTGTGAACCTTCAACAGACCTGTCCCTGACCTGTCTCT 1865

QY 64 GGTGGCTCCATCCGAGTGGTATTATTGAGTTGGGTGGCCAGCCCTCCAGGGAG 123  
DB 1864 GGTGGCTCCATCCGAGTGGTATTATTGAGTTGGGTGGCCAGCCCTCCAGGGAG 1805

QY 124 GGCCTGAGTGTATCGCAACATCTATACAGATGGCAACCTTCAACACCCGTCCTC 183  
DB 1804 GGCCTGAGTGTATCGCAACATCTATACAGATGGCAACCTTCAACACCCGTCCTC 1745

QY 184 AAGAGTGAATTACCATGTACATGATGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243  
DB 1744 AAGAGTGAATTACCATGTACATGATGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 1685

QY 244 TCTGTGACTCCCGGAGACAGGCGCGCTTATTAACGTGCGGGGTACAGATGGTAACTTTG 303  
DB 1684 TCTGTGACTCCCGGAGACAGGCGCGCTTATTAACGTGCGGGGTACAGATGGTAACTTTG 1625

QY 304 GACAACCTGGGGCCAGGAGAACCTTGTACCGTCTCTCA 342  
DB 1624 GACAACCTGGGGCCAGGAGAACCTTGTACCGTCTCTCA 1586

RESULT 11  
ADS84453  
ID ADS84453 standard; DNA; 1996 BP.  
XX  
XX ADS84453;  
XX  
XX 18-NOV-2004 (first entry)  
XX  
XX Human anti-EPO-R antibody Ab412 heavy chain DNA SEQ ID NO:92.  
XX  
XX human; erythropoietin receptor; EPO receptor;  
KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
KW antianaemic; neuroprotective; vulneryary; Gene therapy; aplasia; anaemia;  
KW wound healing; neural cell damage protection;  
KW neural tissue damage protection; brain injury; spinal cord injury;  
KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;  
KW de.

XX  
XX OS Homo sapiens.  
XX PN WO2004035603-A2.  
XX  
XX 29-APR-2004.  
XX  
XX 14-OCT-2003; 2003MO-US032243.  
XX  
XX 14-OCT-2002; 2002US-00269711.  
PR 10-OCT-2003; 2003US-00684109.

XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Devries PJ, Green JL, Ostrow DH, Reilly EB, Wieler J;  
XX  
DR WPI: 2004-348433/32.  
XX  
DR P-P-SDB: ADS84455.  
XX  
XX  
PS New antibodies that bind to or activate an endogenous human  
PS erythropoietin receptor, useful for diagnosing, preventing or treating  
PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
PT anemia.  
XX  
XX Disclosure; SEQ ID NO 92; 192pp; English.

XX  
XX  
XX The present invention describes an antibody or its fragment that binds to  
CC or activates an endogenous activity of a human erythropoietin (EPO)  
CC receptor in a mammal, but does not interact with a peptide having a  
CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
CC methods of modulating or activating an endogenous activity of a human EPO  
CC receptor in a mammal, comprising administering to the mammal a  
CC therapeutic amount of the above antibody or its fragment to modulate or  
CC activate the receptor; (2) a method of treating a mammal suffering from  
CC aplasia, comprising administering to the mammal a therapeutic amount of  
CC the above antibody or its fragment to modulate or activate the receptor;  
CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
CC an isolated and purified polynucleotide sequence; and (5) an isolated and  
CC complements and degenerate codon equivalents; and their fragments.  
CC purified amino acid sequence, and their fragments. The EPO receptor  
CC binding antibody has antianaemic, neuroprotective and vulneryary  
CC activities, and can be used in gene therapy. The compositions and methods  
CC from the present invention can be used for modulating an endogenous  
CC activity of a human EPO receptor or for treating mammals suffering from  
CC aplasia or anaemia. They may also be used for identifying mammals having  
CC a dysfunctional EPO receptor. The composition may also be used in  
CC promoting wound healing or in protecting against neural cell and/or  
CC tissue damage resulting from brain/spinal cord injury, stroke and the  
CC like. The present sequence encodes a human anti-EPO-R antibody heavy  
CC chain, which is given in the exemplification of the present invention.

XX  
SQ Sequence 1996 BP; 422 A; 686 C; 537 G; 351 T; 0 U; 0 Other;

Query Match 78.1%; Score 267; DB 13; Length 1996;  
Best Local Similarity 86.7%; Pred. No. 7e-66;  
Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 4 GAGCTGGGCCAGAGACTGTGTGAACCTTCAACAGACCTGTCCCTGACCTGTCTCT 63  
DB 73 GAGTCGGGGCCAGAGACTGTGTGAACCTTCAACAGACCTGTCCCTGACCTGTCTCT 132

QY 64 GGTGGCTCCATCCGAGTGGTATTATTGAGTTGGGTGGCCAGCCCTCCAGGGAG 123  
DB 133 GGTGGCTCCATCCGAGTGGTATTATTGAGTTGGGTGGCCAGCCCTCCAGGGAG 192

QY 124 GGCCTGAGTGTATCGCAACATCTATACAGATGGCAACCTTCAACACCCGTCCTC 183  
DB 193 GGCCTGAGTGTATCGCAACATCTATACAGATGGCAACCTTCAACACCCGTCCTC 252

QY 184 AAGAGTGAATTACCATGTACATGATGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243  
DB 253 AAGAGTGAATTACCATGTACATGATGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 312

QY 244 TCTGTGACTCCCGGAGACAGGCGCGCTTATTAACGTGCGGGGTACAGATGGTAACTTTG 303  
DB 313 TCTGTGACTCCCGGAGACAGGCGCGCTTATTAACGTGCGGGGTACAGATGGTAACTTTG 372

QY 304 GACAACCTGGGGCCAGGAGAACCTTGTACCGTCTCTCA 342  
DB 373 GACAACCTGGGGCCAGGAGAACCTTGTACCGTCTCTCA 411

RESULT 12

ID	ADR68595	ADR68595 standard; DNA; 1996 BP.
AC	AC	
XX	ADR68595;	
DT	02-DEC-2004	(first entry)
XX	XX	
DE	Human antibody Ab412 heavy chain polynucleotide seqid 92.	
KW	antianaemic; respiratory; vulnary; gene therapy; vaccine;	
KW	erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;	
KW	hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;	
KW	wound healing; neural cell damage; tissue damage; brain injury;	
KW	spinal cord injury; stroke; human; anti-EPO-R-antibody; heavy chain;	
KM	Ab412; ds.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	US2004175379-A1.	
PD	09-SEP-2004.	
XX	XX	
PF	10-OCT-2003; 2003US-00684109.	
XX	XX	
PR	14-OCT-2002; 2002US-0418031P.	
XX	XX	
PA	(DEVIR/) DEVRIES P J.	
PA	(OSTRO/) OSTROW D H.	
PA	(REIL/) REILLY E B.	
PA	(GREE/) GREEN L L.	
PA	(WIEL/) WIELER J.	
XX	XX	
PI	Devries PJ, Ostrow DH, Reilly EB, Green LL, WIELER J;	
XX	XX	
DR	WPI: 2004-661369/64.	
DR	P-PSDB; ADR68597, ADR68575, ADR68576, ADR68577.	
XX	XX	
PT	New antibody or its antibody fragment that activates an endogenous	
PT	activity or is capable of binding to a human erythropoietin receptor in a	
PT	mammal, useful for treating a mammal suffering aplasia or anemia.	
XX	XX	
PS	Disclosure; SEQ ID NO 92; 156bp; English.	
XX	XX	
CC	The invention describes an antibody or its fragment that activates an	
CC	endogenous activity or capable of binding to a human erythropoietin	
CC	receptor in a mammal, or that comprises at least one heavy or light chain	
CC	variable region having a sequence comprising 116 or 107 amino acids (SEQ	
CC	ID NO: 3 or 5) given in the specification or its fragment, but does not	
CC	interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also	
CC	given in the specification. Also described are: a method of activating or	
CC	modulating an endogenous activity of a human erythropoietin receptor in a	
CC	mammal; a pharmaceutical composition comprising a therapeutic amount of	
CC	an antibody or antibody fragment above and a pharmaceutical excipient; an	
CC	isolated and purified polynucleotide sequence selected from 28 sequences	
CC	comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in	
CC	the specification, and their fragments, complements, and degenerate codon	
CC	equivalents; and an isolated and purified amino acid sequence selected	
CC	from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between	
CC	SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or	
CC	their fragments. The antibody or its antibody fragment that activates or	
CC	modulates the activity of the receptor is useful in a method of treating	
CC	a mammal suffering aplasia or anaemia. The antibodies are also useful for	
CC	treating disorders characterised by decreased or subnormal levels of	
CC	oxygen in the blood or tissue such as hypoxaemia or chronic tissue	
CC	hypoxia and/or diseases characterised by inadequate blood circulation or	
CC	reduced blood flow. They are also useful for promoting wound healing or	
CC	for protecting against neural cell and/or tissue damage, resulting from	
CC	brain/spinal cord injury, stroke and the like. The antibodies are also	
CC	useful for identifying or diagnosing mammals having dysfunctional	
CC	erythropoietin receptor. This sequence represents a human Ab412 antibody	
XX	XX	
XX	heavy chain polynucleotide.	
XX	Sequence 1996 BP; 422 A; 686 C; 537 G; 351 T; 0 U; 0 Other;	

Query Match	Similarity	78.1%	Score 267	DB 13	Length 1996
Best Local	Similarity	86.7%	Pred. No. 7e-66		
Matches	294	Conservative	0	Mismatches	45
				Indels	0
				Gaps	0
QY	4	GAGTCTGGCCCGAGGAGCTGTGAAGCTTTCACAGACCCTGTCCCTCACTGCATGTCTCT	63		
DB	73	GAGTCTGGCCCGAGGAGCTGTGAAGCTTTCACAGACCCTGTCCCTCACTGCATGTCTCT	132		
QY	64	GCTGCTTCATCCGACGCTGTGTATTATTGTGAAGTTGGGCTCCGACCTTCAGGGAAG	123		
DB	133	GCTGCTTCATCCGACGCTGTGTATTATTGTGAAGTTGGGCTCCGACCTTCAGGGAAG	192		
QY	124	GGCCCTGAGTGAATCCGCAACATCTATACAGTGGCAACCTTACAAACAACCCGCTCC	183		
DB	193	GGCCCTGAGTGAATCCGCAACATCTATACAGTGGCAACCTTACAAACAACCCGCTCC	252		
QY	184	AAGAGTCGAATTAACATGTCTAGTAGACACGTCCTAAGAACCACTTCTCCGTGAGCTGAC	243		
DB	253	AAGAGTCGAATTAACATGTCTAGTAGACACGTCCTAAGAACCACTTCTCCGTGAGCTGAC	312		
QY	244	TCTGTGACTGCCGCGGAGACACGCGCTCTATTACTGTGCGCGTCAAGATGGTATCTTG	303		
DB	313	TCTGTGACTGCCGCGGAGACACGCGCTCTATTACTGTGCGCGTCAAGATGGTATCTTG	372		
QY	304	GACAACTGGGGGCAAGGAAACCTGGTCAACCGTCTCTCA	342		
DB	373	GACTACTGGGGGCAAGGAAACCTGGTCAACCGTCTCTCTCA	411		
RESULT 13					
ADR68596/C					
ID	ADR68596 standard; DNA; 1996 BP.				
XX	ADR68596;				
XX	02-DEC-2004 (first entry)				
DE	Human antibody Ab412 heavy chain polynucleotide seqid 93.				
XX					
KM	antihaemic; respiratory; vulnery; gene therapy; vaccine;				
KM	erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;				
KM	hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;				
KM	wound healing; neural cell damage; tissue damage; brain injury;				
KM	spinal cord injury; stroke; human; anti-EPO-R-antibody; heavy chain;				
XX	Ab412; ds.				
OS	Homo sapiens.				
XX					
PN	US2004175379-A1.				
XX					
PD	09-SEP-2004.				
XX					
PF	10-OCT-2003; 2003US-00684109.				
XX					
PR	14-OCT-2002; 2002US-0418031P.				
XX					
PA	(DEVYR/) DEVYRIS P J.				
PA	(OSTR/) OSTROW D H.				
PA	(REIL/) REILLY E B.				
PA	(GREEN/) GREEN L L.				
PA	(WIEL/) WIELER J.				
XX					
PI	Devries PJ, Ostrow DH, Reilly EB, Green LL, WIELER J;				
XX					
DR	WPI; 2004-661369/64.				
XX					
PT	New antibody or its antibody fragment that activates an endogenous				
PT	activity or is capable of binding to a human erythropoietin receptor in a				
XX	mammal, useful for treating a mammal suffering aplasia or anemia.				
PS	Disclosure: SEQ ID NO 93; 156pp; English.				
XX					



XX 01-JAN-2004 (first entry)  
 DT Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID NO 7.  
 XX  
 DE monoclonal antibody; tumour; MUC18; proliferation; cytotoxic; vaccine;  
 XX antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;  
 KW gene; de.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057006-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041582.  
 XX  
 PR 28-DEC-2001; 2001US-0346460P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudae J, Bar-Eli M;  
 XX  
 DR WPI; 2003-577496/54.  
 DR P-PSDB; ADD05380.  
 XX  
 XX  
 PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 PT treating tumore, inhibiting tumor growth, inhibiting cell invasion  
 PT associated with melanoma, or increasing survival of an animal having a  
 PT metastatic tumor.  
 XX  
 PS Disclosure; SEQ ID NO 7; 87pp; English.  
 XX  
 CC The invention relates to a novel monoclonal antibody used for inhibiting  
 CC tumour growth in an animal. The tumour inhibition process comprises  
 CC selecting an animal in need of treatment for a tumour, providing a  
 CC monoclonal antibody comprising a heavy chain amino acid, where the  
 CC antibody consists of any one of 10 fully defined sequences of 117-123  
 CC amino acids given in the specification, and where the monoclonal antibody  
 CC binds MUC18, and contacting the tumour with the antibody resulting in  
 CC inhibited proliferation of the cells. The monoclonal antibody has  
 CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 CC antibodies against the MUC18 antigen are useful for diagnosing and  
 CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 CC increasing survival of an animal having a metastatic tumour. This  
 CC polynucleotide sequence represents the DNA encoding an anti-MUC18  
 CC antibody heavy chain, variable region, protein of the invention.  
 XX  
 SO Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;

Query Match 76.7%; Score 262.2; DB 10; Length 352;  
 Best Local Similarity 87.9%; Pred. No. 1e-64;  
 Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTCGCGCCAGAGACGTGTAAGCTTCAAGACCCCTGCTCAGCTGCTCT 63  
 DB 16 GAGTCGCGCCAGAGACGTGTAAGCTTCAAGACCCCTGCTCAGCTGCTCT 75  
 QY 64 GGTGGCTCCATCCGACGTGTTATTAATGAGTTGGTCCGACGCTCCAGGGAAG 123  
 DB 76 GGTGGCTCCATCCGACGTGTTATTAATGAGTTGGTCCGACGCTCCAGGGAAG 135  
 QY 124 GGCCTGAGTGGATGGGCACTATATCAAGTGGCAACACTTAACACCCGCTCC 183  
 DB 136 GGCCTGAGTGGATGGGCACTATATCAAGTGGCAACACTTAACACCCGCTCC 195  
 QY 184 AAGAGTGAATTACATGTCAGTAGACACGCTAAGAACCACTTCCCTGAGACTGACC 243  
 DB 196 AAGAGTGAATTACATGTCAGTAGACACGCTAAGAACCACTTCCCTGAGACTGACC 255  
 QY 244 TCTGTGACTGCGCGGACACGCGCTTATTACTGTGCGCGGTGAGATGGGTATATCTTTG 303

DB 256 TCTGTGACTGCGCGGACACGCGCTTATTACTGTGCGGAG---AGGGGAGATGGCTAC 312  
 QY 304 GACAACTGGGGCCAGGGAACTTGTGTCACCGTCTCTCA 342  
 DB 313 AAGTACTGGGGCCAGGGAACTTGTGTCACCGTCTCTCTCA 351

Search completed: July 27, 2005, 05:59:44  
 Job time : 322.618 secs

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 09:08:49 ; Search time 512.827 Seconds  
(without alignments)  
4312.305 Million cell updates/sec

Title: US-10-027-725A-2

Perfect score: 342  
Sequence: 1 ctcgagctgtgcccagact.....ccctgtaccgtctctca 342

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 7277826 seqs, 3233139505 residues

Total number of hits satisfying chosen parameters: 1455652

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCRT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
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- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
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- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	342	100.0	342	14	US-10-027-725A-2
2	324.4	94.9	342	14	US-10-027-725A-1
3	298.8	87.4	342	14	US-10-027-725A-1
4	271.8	79.5	352	15	US-10-330-613-15
5	271.8	79.5	352	16	US-10-330-530-15
6	271.8	79.5	352	19	US-10-660-357-15
7	267	78.1	354	19	US-10-684-109-42

c	8	267	78.1	1996	19	US-10-684-109-92	Sequence 92, Appl
	9	267	78.1	1996	19	US-10-684-109-93	Sequence 93, Appl
	10	262.2	76.7	352	15	US-10-330-613-7	Sequence 7, Appl
	11	262.2	76.7	352	16	US-10-330-530-7	Sequence 7, Appl
	12	262.2	76.7	352	19	US-10-660-357-7	Sequence 7, Appl
	13	262.2	76.7	355	19	US-10-684-109-54	Sequence 54, Appl
	14	262.2	76.7	1996	19	US-10-684-109-110	Sequence 110, App
	15	262.2	76.7	1996	19	US-10-684-109-111	Sequence 111, App
c	16	261.4	76.4	560	21	US-10-644-277-9	Sequence 93, Appl
	17	261.4	76.4	663	10	US-09-972-656-79	Sequence 79, Appl
	18	260.4	76.1	358	15	US-10-330-613-27	Sequence 27, Appl
	19	260.4	76.1	358	16	US-10-330-530-27	Sequence 27, Appl
	20	260.4	76.1	358	19	US-10-660-357-27	Sequence 27, Appl
	21	260.4	76.1	1338	21	US-10-644-277-61	Sequence 61, Appl
	22	258.4	75.6	420	21	US-10-893-576-18	Sequence 18, Appl
	23	257.8	75.4	366	22	US-10-984-960A-19	Sequence 19, Appl
	24	256.4	75.0	370	17	US-10-309-762-186	Sequence 186, App
	25	255	74.6	429	17	US-10-309-762-110	Sequence 110, App
	26	254.8	74.5	352	15	US-10-330-613-35	Sequence 35, Appl
	27	254.8	74.5	352	16	US-10-330-530-35	Sequence 35, Appl
	28	254.8	74.5	352	19	US-10-660-357-35	Sequence 35, Appl
	29	254.6	74.4	366	22	US-10-984-960A-55	Sequence 55, Appl
	30	252.6	73.9	361	17	US-10-309-762-191	Sequence 191, App
	31	252.6	73.9	1392	21	US-10-910-901-9	Sequence 9, Appl
	32	251.6	73.6	370	17	US-10-309-762-189	Sequence 189, App
	33	251.2	73.5	516	20	US-10-612-497-33	Sequence 33, Appl
	34	251.2	73.5	516	20	US-10-776-649-33	Sequence 33, Appl
	35	250.6	73.3	370	17	US-10-309-762-185	Sequence 185, App
	36	250.4	73.2	376	17	US-10-309-762-187	Sequence 187, App
	37	249.4	72.9	352	17	US-10-309-762-203	Sequence 203, App
	38	248.8	72.7	376	17	US-10-309-762-184	Sequence 184, App
	39	248.8	72.7	376	17	US-10-309-762-197	Sequence 197, App
	40	248.8	72.7	376	17	US-10-309-762-199	Sequence 199, App
	41	248.4	72.6	519	17	US-10-309-762-174	Sequence 174, App
	42	248.2	72.6	367	17	US-10-309-762-195	Sequence 195, App
	43	247.8	71.9	467	20	US-10-478-056-16	Sequence 16, Appl
	44	245.8	71.9	384	21	US-10-727-155-1	Sequence 1, Appl
	45	245.8	71.9	384	21	US-10-727-155-9	Sequence 9, Appl

## ALIGNMENTS

RESULT 1  
US-10-027-725A-2  
; Sequence 2, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific Ige-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027, 725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259, 436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 342  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-027-725A-2

Query Match 100.0%; Score 342; DB 14; Length 342;  
Best Local Similarity 100.0%; Pred. No. 1,4e+02; Indels 0; Gaps 0;  
Matches 342; Conservative 0; Mismatches 0

Qy	1	CTCGAGCTGGCCAGGACTGTGTAAGCTTCACAGACCCGTCCTCACTGACGTC	60
Db	1	CTCGAGCTGGCCAGGACTGTGTAAGCTTCACAGACCCGTCCTCACTGACGTC	60
Qy	61	TCGTGGCTTCATCCGACGTGTGTTATTGAGTTGGTCCGCCACCTCCAGGG	120

```
Db      61 TCTGTGGCTCCATCCGAGTGGTATTATTGAGTTGGTCCGCCAGCTCCAGGG 120
Qy      121 AAGGGCTGGAGTGAATCGCAACATCTATCATCAGTGGCAACACCTAACAAACCCGTCC 180
Db      121 AAGGGCTGGAGTGAATCGCAACATCTATCATCAGTGGCAACACCTAACAAACCCGTCC 180
Qy      181 CTGAAGAGTGAATTACATGTCTGAGACACGCTTAAGAACCTTCTCCCTGAAGCTG 240
Db      181 CTGAAGAGTGAATTACATGTCTGAGACACGCTTAAGAACCTTCTCCCTGAAGCTG 240
Qy      241 ACCTCTGACTGCGCGGAGACACGCGCTTATTAATCTGCGCGGTGAGATGGGTATACT 300
Db      241 ACCTCTGACTGCGCGGAGACACGCGCTTATTAATCTGCGCGGTGAGATGGGTATACT 300
Qy      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342

RESULT 2
US-10-027-725a-3
; Sequence 3, Application US/10027725a
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725a
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725a-3

Query Match      94.9%; Score 324.4; DB 14; Length 342;
Best Local Similarity 96.8%; Pred. No. 9.2e-97;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy      1 CTGAGTCTGGCCCAAGACTGTTGAAGCTTTCACAGACCTGTCTCCATCGACTGTC 60
Db      1 CTGAGTCTGGCCCAAGACTGTTGAAGCTTTCACAGACCTGTCTCCATCGACTGTC 60
Qy      61 TCTGTGGCTCCATCCGAGTGGTATTATTGAGTTGGTCCGCCAGCTCCAGGG 120
Db      61 TCTGTGGCTCCATCCGAGTGGTATTATTGAGTTGGTCCGCCAGCTCCAGGG 120
Qy      121 AAGGGCTGGAGTGAATCGCAACATCTATCATCAGTGGCAACACCTAACAAACCCGTCC 180
Db      121 AAGGGCTGGAGTGAATCGCAACATCTATCATCAGTGGCAACACCTAACAAACCCGTCC 180
Qy      181 CTGAAGAGTGAATTACATGTCTGAGACACGCTTAAGAACCTTCTCCCTGAAGCTG 240
Db      181 CTGAAGAGTGAATTACATGTCTGAGACACGCTTAAGAACCTTCTCCCTGAAGCTG 240
Qy      241 ACCTCTGACTGCGCGGAGACACGCGCTTATTAATCTGCGCGGTGAGATGGGTATACT 300
Db      241 ACCTCTGACTGCGCGGAGACACGCGCTTATTAATCTGCGCGGTGAGATGGGTATACT 300
Qy      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342

RESULT 3
US-10-027-725a-1
; Sequence 1, Application US/10027725a
; Publication No. US20030082659A1
; GENERAL INFORMATION:
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```
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725a
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725a-1

Query Match      87.4%; Score 298.8; DB 14; Length 342;
Best Local Similarity 92.1%; Pred. No. 2.7e-88;
Matches 315; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy      1 CTGAGTCTGGCCCAAGACTGTTGAAGCTTTCACAGACCTGTCTCCATCGACTGTC 60
Db      1 CTGAGTCTGGCCCAAGACTGTTGAAGCTTTCACAGACCTGTCTCCATCGACTGTC 60
Qy      61 TCTGTGGCTCCATCCGAGTGGTATTATTGAGTTGGTCCGCCAGCTCCAGGG 120
Db      61 TCTGTGGCTCCATCCGAGTGGTATTATTGAGTTGGTCCGCCAGCTCCAGGG 120
Qy      121 AAGGGCTGGAGTGAATCGCAACATCTATCATCAGTGGCAACACCTAACAAACCCGTCC 180
Db      121 AAGGGCTGGAGTGAATCGCAACATCTATCATCAGTGGCAACACCTAACAAACCCGTCC 180
Qy      181 CTGAAGAGTGAATTACATGTCTGAGACACGCTTAAGAACCTTCTCCCTGAAGCTG 240
Db      181 CTGAAGAGTGAATTACATGTCTGAGACACGCTTAAGAACCTTCTCCCTGAAGCTG 240
Qy      241 ACCTCTGACTGCGCGGAGACACGCGCTTATTAATCTGCGCGGTGAGATGGGTATACT 300
Db      241 ACCTCTGACTGCGCGGAGACACGCGCTTATTAATCTGCGCGGTGAGATGGGTATACT 300
Qy      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db      301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342

RESULT 4
US-10-330-613-15
; Sequence 15, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Guigas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-15

Query Match      79.5%; Score 271.8; DB 15; Length 352;
Best Local Similarity 89.7%; Pred. No. 2.2e-79;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

Qy      4 GAGTCTGGCCCAAGACTGTTGAAGCTTTCACAGACCTGTCTCCATCGACTGTC 63
Db      16 GAGTGGGGCCCAAGACTGTTGAAGCTTTCACAGACCTGTCTCCATCGACTGTC 75
Qy      64 GTGTGCTCCATCCGAGTGGTATTATTGAGTTGGTCCGCCAGCTCCAGGGAG 123
```



Db	76	GGTGGCTCCATCAGCAGTGSTGGTTACTACTGGACTTGAGATTCGGCAGACCCAGGGAG	135
Qy	124	GGCTTGAGTGGATCCGCAACATCTTATCAAGTGGCAACCTTACAAACAAACCCGTCCCTC	183
Db	136	GGCTTGAGTGGATGGTGGTTTCACTATTAACAATGGAGACCTTACTAAACCCGTCCCTC	199
Qy	184	AAGAGTGAATTACCATGTCAGTAGACACGTCTAAGAACCACTTCTCCCTGAGACTGACC	243
Db	196	AAGAGTCAAGTTACCATATCAGTAGACAGTCTAAGAACCAAGTTCTCCCTGAACTAGC	255
Qy	244	TCTGTGACTGCGCCGAGACACGGCCGCTTTTACTGTCGCGGTGAGTGGTATATCTTTC	303
Db	256	TCTGTGACTGCGCGGAGACACGGCCGCTGTATTTCTGTGGAG---AGAGGAGATGGCTTT	312
Qy	304	GACAACTGGGGCCAGGGAACCTCTGGTCAACCGTCTCTCA	342
Db	313	GACTACTGGGGCCAGGGAACCTCTGGTCAACCGTCTCTCA	351

```

, RESULT 5
, US-10-330-530-15
, Sequence 15, Application US/10330530
, Publication No. US20030152514A1
, GENERAL INFORMATION:
, APPLICANT: Gudas, Jean
, TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
, FILE REFERENCE: ABGENIX.031A
, CURRENT APPLICATION NUMBER: US/10/330,530
, CURRENT FILING DATE: 2002-12-26
, PRIOR APPLICATION NUMBER: US 60/346414
, PRIOR FILING DATE: 2001-12-18
, NUMBER OF SEQ ID NOS: 40
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 15
, LENGTH: 352
, TYPE: DNA
, ORGANISM: Homo Sapiens
, US-10-330-530-15

```

Query Match	Similarity	Score	271.8:	DB 16:	Length 352:
Best Local	Similarity	89.7%:	Pred. No. 2.2e-79:		
Matches	304:	Conservative	0:	Mismatches 32:	Indels 3, Gaps 1
QY	4	GAGTGTGGCCCGAGACGTGTGAAGCCTTCACAGACCCTGTCCCTCAGCTGACTGTCT	63		
Db	16	GAGTGGGGCCAGAGACTGTGTGAAGCCTTCACAGACCCTGTCCCTCAGCTGACTGTCT	75		
QY	64	GATGGCTCCATCCGAGTGGTGTATTATTGAGTGGGTCCGCCAGCCTTCAGAGGAAG	123		
Db	76	GATGGCTCCATCAGCAGTGGTGTATTACTGACTGACTGGATCCGCCAGCACCAGAGGAAG	135		
QY	124	GGCTTGAAGTGGATGGCGAACATCTATCACAAGTGGCAACACTCAACAACACCCGTCCCTC	183		
Db	136	GGCTTGAAGTGGATGGGTGTTACTATTAACAAGTGGAGACCTTACTCAACACCCGTCCCTC	195		
QY	184	AAGAGTCGAATTACCATGTCAGTAGACACGCTAAGAACACACTTCTCCCTGAGACTGACC	243		
Db	196	AAGAGTCGAATTACCATGTCAGTAGACACGCTAAGAACACAGTTCTCCCTGAGACTGACC	255		
QY	244	TCTGTGACTGCCCGCGAACACGGCCGCTATTATCTGTGCGCGGTCAAGATGGATTAATTG	303		
Db	256	TCTGTGACTGCCCGCGGAACACGGCCGCTATTATCTGTGGGAG---AGAGGAATATGGCTTT	312		
QY	304	GACAACTGGGGCCAGAGAACCTTGTCACCCGTCTCTCA	342		
Db	313	GACTACTGGGGCCAGAGAACCTTGTCACCCGTCTCTCTCA	351		

RESULT 6  
US-10-660-357-15  
; Sequence 15, Application US/10660357  
; Publication No. US20040115205A1

```

1  GENERAL INFORMATION:
2  APPLICANT: Bar-Eli, Menashe
3  TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
4  TITLE OF INVENTION: ANTIGEN
5  FILE REFERENCE: ABGENIX .030C1
6  CURRENT APPLICATION NUMBER: US/10/660,357
7  CURRENT FILING DATE: 2003-09-10
8  PRIOR APPLICATION NUMBER: 10/330,560
9  PRIOR FILING DATE: 2002-12-26
10 NUMBER OF SEQ ID NOS: 40
11 SOFTWARE: FastSeq for Windows Version 4.0
12 SEQ ID NO 15
13 LENGTH: 352
14 TYPE: DNA
15 ORGANISM: Homo Sapiens
16 US-10-660-357-15

```

Query Match	79.5%	Score 271.8;	DB 19;	Length 352;
Best Local Similarity	89.7%	Pred. No. 2,28-79;		
Matches 304;	Conservative 0;	Mismatches 32;	Indels 3;	Gaps 1;
Qy	4	GAGCTTGCGCCACGAGACTGTGAAGCCCTTCA	CAGACCCTGTCCCTCACCTGACTGTCTCT	63
Db	16	GAGTCGGGGCCACGAGACTGTGAAGCTTTCA	CAGACCCTGTCCCTCACCTGACTGTCTCT	75
Qy	64	GGTGGCTTCATCCGCAATGCTGTTATTATTGA	GTGGGTCCGCCCACTTCAGGAAAG	123
Db	76	GGTGGCTTCATCAGCAATGCTGTTACTACG	ACTTGATCCCCACAGCAACCAAGGAAAG	135
Qy	124	GGCCTGAGAGGAATCGGCAACATTATAC	AGTGGCAACCTACCAACCCGTCCTC	183
Db	136	GGCCTGAGAGGAATGAGTTGATATATTAC	AGTGGAGACCTACCTACCAACCCGTCCTC	195
Qy	184	AAGAGTCGAATTACATATGATAGACACGCT	CTTAAGAACCACTTCTCCTGAGACTGACC	243
Db	196	AAGAGTCGAATTACATATGATAGACACGCT	CTTAAGAACCACTTCTCCTGAGACTGAGC	255
Qy	244	TCCTGTGACTGCGCGGACACGGCCGCTAT	TATTACTGTGCGCGGTAGATGGTATACCTTTG	303
Db	256	TCCTGTGACTGCGCGGACACGGCCGCTAT	TACTGTGCGGAG--AGAGGAGATGGCTTTT	312
Qy	304	GACAACTGGGGCCAGGAAACCTGGTACCG	CTCCCTCA	342
Db	313	GACTACTGGGGCCAGGAAACCTGGTACCG	CTCCCTCA	351

```

RESULT 7
US-10-684-109-42
; Sequence 42, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wielez, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989_US_02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/265,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-42
Query Match
78.1%; Score 267; DB 19; Length 354

```

Best Local Similarity 86.7%; Pred. No. 8.7e-78;  
Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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QY 4 GAGTCTGCCCCAGAGCTGGTGAACCTTTCACAGACCTGTGCTCACTGACGTGTCT 63
Db 16 GAGTCGGGCCCAAGAGCTGTGAACCTTTCACAGACCTGTGCTCACTGACGTGTCT 75
QY 64 GGTGGCTCCATCCGCACTGGTGTGTATTATTGAGTTGGGTCCGCGCACTCCAGGGAG 123
Db 76 GGTGCTTCATCAGACAGTGGTGTGTATTATTGAGTTGGGTCCGCGCACTCCAGGGAG 135
QY 124 GGCCTGAGTGAATGATCGGCAACATCTATCAAGTGGCAACCTTCAACACCTGCTCC 183
Db 136 GGCCTGAGTGAATGATCGGCAACATCTATCAAGTGGCAACCTTCAACACCTGCTCC 195
QY 184 AAGAGTGAATTAATCATGTCAAGTGAACCGTCTAAGAACCACTTCTGCTGAGACTGAC 243
Db 196 AAGAGTGAATTAATCATGTCAAGTGAACCGTCTAAGAACCACTTCTGCTGAGACTGAC 255
QY 244 TCTGTGACTGCGCGGAGACGCGCGCTCTATTACTGTGCGCGGTCAAGATGGTATATTG 303
Db 256 TCTGTGACTGCGCGGAGACGCGCGCTCTATTACTGTGCGCGGTCAAGATGGTATATTG 315
QY 304 GACAACCTGGGGCCAGGGAACCTGTGATCAACCTGCTCTCA 342
Db 316 GACTACTGGGGCCAGGGAACCTGTGATCAACCTGCTCTCA 354
```

## RESULT 8

US-10-684-109-92  
; Sequence 92, Application US/10684109  
; Publication No. US20040175379A1  
; GENERAL INFORMATION:  
; APPLICANT: Deviles, Peter J.  
; APPLICANT: Green, Larry L.  
; APPLICANT: Ostrow, David H.  
; APPLICANT: Reilly, Edward B.  
; APPLICANT: Wielez, James  
; TITLE OF INVENTION: Erythropoietin Receptor Binding  
; TITLE OF INVENTION: Antibodies  
; FILE REFERENCE: 6989, US. 02  
; CURRENT APPLICATION NUMBER: US/10/684,109  
; PRIOR FILING DATE: 2003-10-10  
; PRIOR APPLICATION NUMBER: 10/269,711  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 92  
; LENGTH: 1996  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-684-109-92

Query Match 78.1%; Score 267; DB 19; Length 1996;  
Best Local Similarity 86.7%; Pred. No. 1.4e-77;

Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

```
QY 4 GAGTCTGCCCCAGAGCTGGTGAACCTTTCACAGACCTGTGCTCACTGACGTGTCT 63
Db 73 GAGTCGGGCCCAAGAGCTGTGAACCTTTCACAGACCTGTGCTCACTGACGTGTCT 132
QY 64 GGTGGCTCCATCCGCACTGGTGTGTATTATTGAGTTGGGTCCGCGCACTCCAGGGAG 123
Db 133 GGTGCTTCATCAGACAGTGGTGTGTATTATTGAGTTGGGTCCGCGCACTCCAGGGAG 192
QY 124 GGCCTGAGTGAATGATCGGCAACATCTATCAAGTGGCAACCTTCAACACCTGCTCC 183
Db 193 GGCCTGAGTGAATGATCGGCAACATCTATCAAGTGGCAACCTTCAACACCTGCTCC 252
QY 184 AAGAGTGAATTAATCATGTCAAGTGAACCGTCTAAGAACCACTTCTGCTGAGACTGAC 243
Db 253 AAGAGTGAATTAATCATGTCAAGTGAACCGTCTAAGAACCACTTCTGCTGAGACTGAC 312
```

```
QY 244 TCTGTGACTGCGCGGAGACGCGCGTCTATTACTGTGCGCGGTCAAGTGGTATATTG 303
Db 313 TCTGTGACTGCGCGGAGACGCGCGTCTATTACTGTGCGCGGTCAAGTGGTATATTG 372
QY 304 GACAACCTGGGGCCAGGGAACCTGTGATCAACCTGCTCTCA 342
Db 373 GACTACTGGGGCCAGGGAACCTGTGATCAACCTGCTCTCA 411
```

## RESULT 9

US-10-684-109-93/c  
; Sequence 93, Application US/10684109  
; Publication No. US20040175379A1  
; GENERAL INFORMATION:  
; APPLICANT: Deviles, Peter J.  
; APPLICANT: Green, Larry L.  
; APPLICANT: Ostrow, David H.  
; APPLICANT: Reilly, Edward B.  
; APPLICANT: Wielez, James  
; TITLE OF INVENTION: Erythropoietin Receptor Binding  
; TITLE OF INVENTION: Antibodies  
; FILE REFERENCE: 6989, US. 02  
; CURRENT APPLICATION NUMBER: US/10/684,109  
; PRIOR FILING DATE: 2003-10-10  
; PRIOR APPLICATION NUMBER: 10/269,711  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 93  
; LENGTH: 1996  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-684-109-93

Query Match 78.1%; Score 267; DB 19; Length 1996;  
Best Local Similarity 86.7%; Pred. No. 1.4e-77;  
Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

```
QY 4 GAGTCTGCCCCAGAGCTGGTGAACCTTTCACAGACCTGTGCTCACTGACGTGTCT 63
Db 1924 GAGTCGGGCCCAAGAGCTGTGAACCTTTCACAGACCTGTGCTCACTGACGTGTCT 1865
QY 64 GGTGGCTCCATCCGCACTGGTGTGTATTATTGAGTTGGGTCCGCGCACTCCAGGGAG 123
Db 1864 GGTGCTTCATCAGACAGTGGTGTGTATTATTGAGTTGGGTCCGCGCACTCCAGGGAG 1805
QY 124 GGCCTGAGTGAATGATCGGCAACATCTATCAAGTGGCAACCTTCAACACCTGCTCC 183
Db 1804 GGCCTGAGTGAATGATCGGCAACATCTATCAAGTGGCAACCTTCAACACCTGCTCC 1745
QY 184 AAGAGTGAATTAATCATGTCAAGTGAACCGTCTAAGAACCACTTCTGCTGAGACTGAC 243
Db 1744 AAGAGTGAATTAATCATGTCAAGTGAACCGTCTAAGAACCACTTCTGCTGAGACTGAC 1685
QY 244 TCTGTGACTGCGCGGAGACGCGCGTCTATTACTGTGCGCGGTCAAGATGGTATATTG 303
Db 1684 TCTGTGACTGCGCGGAGACGCGCGTCTATTACTGTGCGCGGTCAAGATGGTATATTG 1625
QY 304 GACAACCTGGGGCCAGGGAACCTGTGATCAACCTGCTCTCA 342
Db 1624 GACTACTGGGGCCAGGGAACCTGTGATCAACCTGCTCTCA 1586
```

## RESULT 10

US-10-330-613-7  
; Sequence 7, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX 022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; PRIOR FILING DATE: 2002-12-26

; PRIOR APPLICATION NUMBER: 60/346299  
 ; PRIOR FILING DATE: 2001-12-18  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 352  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; US-10-330-613-7

Query Match 76.7%; Score 262.2; DB 15; Length 352;  
 Best Local Similarity 87.9%; Pred. No. 3.3e-76;  
 Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTCTGAGCCCAAGAGCTGTGAGACCTTTACAGACCTCTGTCTTCACTGACCTGTCTCT 63  
 DB 16 GAGTCGAGCCCAAGAGCTGTGAGACCTTTACAGACCTCTGTCTTCACTGACCTGTCTCT 75  
 QY 64 GGTGGCTCCATCCCACTGCTGTGTTATTATTGAGTTGGTCCGCGACCTCCAGGGAG 123  
 DB 76 GGTGGCTCCATCCCACTGCTGTGTTATTATTGAGTTGGTCCGCGACCTCCAGGGAG 135  
 QY 124 GGCCTGAGTGATCGGCAACATCTATCAAGTGGCAACCTTCAACCAACCCGTCCTC 183  
 DB 136 GGCCTGAGTGATCGGCAACATCTATCAAGTGGCAACCTTCAACCAACCCGTCCTC 195  
 QY 184 AAGAGTGAATTACCATGTCAAGTGAACAGCTCTAAGAACCACTTCTCTGAGACTGACC 243  
 DB 196 AAGAGTGAATTACCATGTCAAGTGAACAGCTCTAAGAACCACTTCTCTGAGACTGACC 255  
 QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGCGGTGAGATGGTATCTTTG 303  
 DB 256 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGAG---AGGGGAGATGGCTTAC 312  
 QY 304 GACAACTGGGGCCAGGAGACCTGTGACACCTGTCTCTCA 342  
 DB 313 AAGTACTGGGGCCAGGAGACCTGTGACACCTGTCTCTCA 351

RESULT 11

US-10-330-530-7  
 ; Sequence 7, Application US/10330530  
 ; Publication No. US20030152514A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gudas, Jean  
 ; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
 ; FILE REFERENCE: ABGENIX.031A  
 ; CURRENT APPLICATION NUMBER: US/10/330,530  
 ; PRIOR FILING DATE: 2002-12-26  
 ; PRIOR APPLICATION NUMBER: US 60/346414  
 ; PRIOR FILING DATE: 2001-12-18  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 352  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; US-10-330-530-7

Query Match 76.7%; Score 262.2; DB 16; Length 352;  
 Best Local Similarity 87.9%; Pred. No. 3.3e-76;  
 Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTCTGAGCCCAAGAGCTGTGAGACCTTTACAGACCTCTGTCTTCACTGACCTGTCTCT 63  
 DB 16 GAGTCGAGCCCAAGAGCTGTGAGACCTTTACAGACCTCTGTCTTCACTGACCTGTCTCT 75  
 QY 64 GGTGGCTCCATCCCACTGCTGTGTTATTATTGAGTTGGTCCGCGACCTCCAGGGAG 123  
 DB 76 GGTGGCTCCATCCCACTGCTGTGTTATTATTGAGTTGGTCCGCGACCTCCAGGGAG 135  
 QY 124 GGCCTGAGTGATCGGCAACATCTATCAAGTGGCAACCTTCAACCAACCCGTCCTC 183

DB 136 GGCCTGAGTGATGGGTAATCTATTAGAGTGGAGACCTTACCAACCCGTCCTC 195  
 QY 184 AAGAGTGAATTACCATGTCAAGTGAACAGCTCTAAGAACCACTTCTCTGAGACTGACC 243  
 DB 196 AAGAGTGAATTACCATGTCAAGTGAACAGCTCTAAGAACCACTTCTCTGAGACTGACC 255  
 QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGCGGTGAGATGGTATCTTTG 303  
 DB 256 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGAG---AGGGGAGATGGCTTAC 312  
 QY 304 GACAACTGGGGCCAGGAGACCTGTGACACCTGTCTCTCA 342  
 DB 313 AAGTACTGGGGCCAGGAGACCTGTGACACCTGTCTCTCA 351

RESULT 12

US-10-660-357-7  
 ; Sequence 7, Application US/10660357  
 ; Publication No. US20040115205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bar-Eli, Menashe  
 ; APPLICANT: Green, Larry L.  
 ; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
 ; FILE REFERENCE: ABGENIX.030C1  
 ; CURRENT APPLICATION NUMBER: US/10/660,357  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 10/330,580  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 352  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; US-10-660-357-7

Query Match 76.7%; Score 262.2; DB 19; Length 352;  
 Best Local Similarity 87.9%; Pred. No. 3.3e-76;  
 Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTCTGAGCCCAAGAGCTGTGAGACCTTTACAGACCTCTGTCTTCACTGACCTGTCTCT 63  
 DB 16 GAGTCGAGCCCAAGAGCTGTGAGACCTTTACAGACCTCTGTCTTCACTGACCTGTCTCT 75  
 QY 64 GGTGGCTCCATCCCACTGCTGTGTTATTATTGAGTTGGTCCGCGACCTCCAGGGAG 123  
 DB 76 GGTGGCTCCATCCCACTGCTGTGTTATTATTGAGTTGGTCCGCGACCTCCAGGGAG 135  
 QY 124 GGCCTGAGTGATCGGCAACATCTATCAAGTGGCAACCTTCAACCAACCCGTCCTC 183  
 DB 136 GGCCTGAGTGATCGGCAACATCTATCAAGTGGCAACCTTCAACCAACCCGTCCTC 195  
 QY 184 AAGAGTGAATTACCATGTCAAGTGAACAGCTCTAAGAACCACTTCTCTGAGACTGACC 243  
 DB 196 AAGAGTGAATTACCATGTCAAGTGAACAGCTCTAAGAACCACTTCTCTGAGACTGACC 255  
 QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGCGGTGAGATGGTATCTTTG 303  
 DB 256 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGAG---AGGGGAGATGGCTTAC 312  
 QY 304 GACAACTGGGGCCAGGAGACCTGTGACACCTGTCTCTCA 342  
 DB 313 AAGTACTGGGGCCAGGAGACCTGTGACACCTGTCTCTCA 351

RESULT 13

US-10-684-109-54  
 ; Sequence 54, Application US/10684109  
 ; Publication No. US20040175379A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Devries, Peter J.  
 ; APPLICANT: Green, Larry L.

```

; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989 US 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 355
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-54

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Best Local Similarity 85.8%; Pred. No. 3.4e-76;
Matches 291; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 4 GAGCTGAGCCAGAGCTGTGTAAGCTTCAACAGACCCGTCCTCACTGCTCTCT 63
Db 16 GAGTCGGGCCCAAGACTGTGTGAAGCCCTTACAGACCTGTCTCTCACTGCTCTCT 75
QY 64 GGTGGCTCCATCCGCACTGTGTGTTATTATTGAGTTGGTCCGCAAGCTCCAGAG 123
Db 76 GGTGGCTCCATCCGCACTGTGTGTTATTATTGAGTTGGTCCGCAAGCTCCAGAG 135
QY 124 GGCCTGAGTGTGATCCGCAACATTTATCAAGTGGCAACCTTCAACAAACCCGTCCTC 183
Db 136 GGCCTGAGTGTGATTTGGTATCTATCAAGTGAAGACCTTCTATTATATCCGTCCTC 195
QY 184 AAGAGTGAATTTACCATGTAGTACAGACCGTTAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTGAATTTACCATGTAGTACAGACCGTTAGAACCACTTCTCCCTGAGACTGACC 255
QY 244 TCTGTGACTGCGCGGACACAGCGCCGTATATTACTGTGCGCGGTGAGATGGTATACCTTTG 303
Db 256 TCTGTGACTGCGCGGACACAGCGCCGTATATTACTGTGCGAGATTAATTGGGATGCGG 315
QY 304 GACAACTGGGGCCAGGGAACCTGTGTACCGTCTCTCTCA 342
Db 316 GACTACTGGGGCCAGGGAACCTGTGTACCGTCTCTCTCA 354

RESULT 14
US-10-684-109-110
; Sequence 110, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989 US 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-110

Query Match          76.7%; Score 262.2; DB 19; Length 1996;
Best Local Similarity 85.8%; Pred. No. 3.4e-76;
Matches 291; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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```

Best Local Similarity 85.8%; Pred. No. 5.4e-76;
Matches 291; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 4 GAGCTGAGCCAGAGCTGTGTAAGCTTCAACAGACCCGTCCTCACTGCTCTCT 63
Db 73 GAGTCGGGCCCAAGACTGTGTGAAGCCCTTACAGACCTGTCTCTCACTGCTCTCT 132
QY 64 GGTGGCTCCATCCGCACTGTGTGTTATTATTGAGTTGGTCCGCAAGCTCCAGAG 123
Db 133 GGTGGCTCCATCCGCACTGTGTGTTATTATTGAGTTGGTCCGCAAGCTCCAGAG 192
QY 124 GGCCTGAGTGTGATCCGCAACATTTATCAAGTGGCAACCTTCAACAAACCCGTCCTC 183
Db 193 GGCCTGAGTGTGATTTGGTATCTATTAACAGTAAGACCTTCTATTATATCCGTCCTC 252
QY 184 AAGAGTGAATTTACCATGTAGTACAGACCGTTAGAACCACTTCTCCCTGAGACTGACC 243
Db 253 AAGAGTGAATTTACCATGTAGTACAGACCGTTAGAACCACTTCTCCCTGAGACTGACC 312
QY 244 TCTGTGACTGCGCGGACACAGCGCCGTATATTACTGTGCGCGGTGAGATGGTATACCTTTG 303
Db 313 TCTGTGACTGCGCGGACACAGCGCCGTATATTACTGTGCGAGATTAATTGGGATGCGG 372
QY 304 GACAACTGGGGCCAGGGAACCTGTGTACCGTCTCTCTCA 342
Db 373 GACTACTGGGGCCAGGGAACCTGTGTACCGTCTCTCTCA 411

RESULT 15
US-10-684-109-111/c
; Sequence 111, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989 US 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-111

Query Match          76.7%; Score 262.2; DB 19; Length 1996;
Best Local Similarity 85.8%; Pred. No. 5.4e-76;
Matches 291; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 4 GAGCTGAGCCAGAGCTGTGTAAGCTTCAACAGACCCGTCCTCACTGCTCTCT 63
Db 1924 GAGTCGGGCCCAAGACTGTGTGAAGCCCTTACAGACCTGTCTCTCACTGCTCTCT 1865
QY 64 GGTGGCTCCATCCGCACTGTGTGTTATTATTGAGTTGGTCCGCAAGCTCCAGAG 123
Db 1864 GGTGGCTCCATCCGCACTGTGTGTTATTATTGAGTTGGTCCGCAAGCTCCAGAG 1805
QY 124 GGCCTGAGTGTGATCCGCAACATTTATCAAGTGGCAACCTTCAACAAACCCGTCCTC 183
Db 1804 GGCCTGAGTGTGATTTGGTATCTATTAACAGTAAGACCTTCTATTATATCCGTCCTC 1745
QY 184 AAGAGTGAATTTACCATGTAGTACAGACCGTTAGAACCACTTCTCCCTGAGACTGACC 243
Db 1744 AAGAGTGAATTTACCATGTAGTACAGACCGTTAGAACCACTTCTCCCTGAGACTGACC 1685
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Qy	244	TCTGTGACTGCGCGGACACGCGCGCTATTACTGTGCGCGGTCAAGTGGTACTTTG	303
Db	1684	TCTGTGACTGCGCGGACACGCGCGCTATTACTGTGCGCGGTCAAGTGGTACTTTG	1625
Qy	304	GACAACTGGGGCCGAGGGAACCGTGTCAACGCTCTCTCA	342
Db	1624	GACTACTGGGGCCGAGGGAACCGTGTCAACGCTCTCTCA	1586

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:09:06 ; Search time 1956.83 Seconds  
(without alignments)  
8468.649 Million cell updates/sec

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Perfect score: 342  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hhg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
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12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	340.4	99.5	342	9	HSAA58382 Homo sapi
2	308.4	90.2	342	9	HSAA58384 Homo sapi
3	297.2	86.9	342	9	HSAA58383 Homo sapi
4	291	85.1	355	9	AY640579 Homo sapi
5	287.8	84.2	355	9	AY640487 Homo sapi
6	286.2	83.7	355	9	AY640580 Homo sapi
7	283	82.7	355	9	AY640509 Homo sapi
8	281.4	82.3	355	9	AY640564 Homo sapi
9	278.2	81.3	355	9	AY640507 Homo sapi
10	278.2	81.3	432	9	HSAA491911 Homo sapi
11	277.2	81.1	411	9	HSAT22X1 Homo sapi
12	276.6	80.9	432	9	HSAA491912 Homo sapi
13	276.4	80.8	351	9	HSAA244930 Homo sapi
14	276.4	80.8	360	6	AX061463 Sequence
15	275	80.4	414	9	AP062112 Homo sapi
16	273.8	80.1	414	9	HSAT14X13 Homo sapi
17	273.8	80.1	414	9	HSAT14X4 Homo sapi
18	272	79.5	357	9	HSAA244949 Homo sapi
19	271.8	79.5	354	9	HSAA245064 Homo sapi

20	271.8	79.5	360	9	HSU80129 Human immun
21	271.8	79.5	360	9	HSU80130 Human immun
22	271.6	79.4	358	9	AF021954 Homo sapi
23	270.6	79.1	341	9	AY607380 Homo sapi
24	270.4	79.1	403	12	AF452917 Synthetic
25	270.4	79.1	363	9	HSU80131 Human immun
26	269.2	78.7	354	9	HSAA244955 Homo sapi
27	269.2	78.7	417	9	HSAT14X9 Homo sapi
28	268.8	78.6	366	9	HSAA233698 Homo sapi
29	268.6	78.5	351	9	HSAA245020 Homo sapi
30	268.4	78.5	357	9	HSAA279523 Homo sapi
31	267.4	78.2	400	12	AF452909 Synthetic
32	267	78.1	354	9	HSAA579125 Homo sapi
33	266.8	78.0	357	9	HSAA279541 Homo sapi
34	266.8	78.0	357	9	HSU80168 Homo sapi
35	266.2	77.8	412	12	AF452912 Synthetic
36	265.8	77.7	366	9	HSAA244928 Homo sapi
37	265.8	77.7	369	6	AX061433 Homo sapi
38	265.6	77.7	363	9	HSU80128 Homo sapi
39	265.4	77.6	339	9	AY607360 Homo sapi
40	265.4	77.6	351	9	HSAA244958 Homo sapi
41	265	77.5	362	9	HSU80169 Homo sapi
42	264.6	77.4	351	9	AY607364 Homo sapi
43	264.4	77.3	355	9	AY640551 Homo sapi
44	264	77.2	328	9	AY607437 Homo sapi
45	264	77.2	362	9	AF126269 Homo sapi

#### ALIGNMENTS

RESULT 1  
HSAA58382  
LOCUS Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 94.  
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 94.  
ACCESSION AJ58382.1 GI:20387063  
VERSION AJ58382.1  
KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Flicker, S., Steinberger, P., Norderhaug, L., Sperry, W.R., Majlesi, Y., Valent, P., Kraft, D. and Valenta, R.  
TITLE Conversion of grass allergen-specific human IGB into a protective IgG1 antibody  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 342)  
AUTHORS Flicker, S.  
TITLE Direct Submission  
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA

FEATURES  
source  
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Best Local Similarity 99.7%; Pred. No. 1.3e-84;  
Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCGAGTCTGGCCAGAGACTGTGAAGCCTGCACAGACCTTCCTCCAGCTGGCGTTC 60  
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Qy 61 TCTGAGCTGCGCTTCATCCGAGTGTGTGTTACTACTGAGATTGGATCCGCCAACACCCAGG 120  
Db 61 TCTGAGCTGCGCTTCATCCGAGTGTGTGTTACTACTGAGATTGGATCCGCCAACACCCAGG 120

Qy 121 AAGGGCCCTGGAGTGGATTGGGTATCATCTACAGTGGGAACCTTACAAACCCGCTCC 180  
Db 121 AAGGGCCCTGGAGTGGATTGGGTATCATCTACAGTGGGAACCTTACAAACCCGCTCC 180

Qy 181 CTCGAAGTGCAGATTGCGATGCGTAGACAGCTCTGAGAACAGATTCTCCCTGAGGCTG 240  
Db 181 CTCGAAGTGCAGATTGCGATGCGTAGACAGCTCTGAGAACAGATTCTCCCTGAGGCTG 240

Qy 241 AACTCTGTACTGCCCGCGGACACGCGCGTGTATTACTGTGCGAGTTAGATGGCTACACT 300  
Db 241 AACTCTGTACTGCCCGCGGACACGCGCGTGTATTACTGTGCGAGTTAGATGGCTACACT 300

Qy 301 TTGGACATCTGGGGCCAGGGAACCTGTGCACCGCTCTCTCA 342  
Db 301 TTGGACATCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA 342

RESULT 2  
HSA458384 342 bp mRNA linear PRI 30-APR-2002  
LOCUS Homo sapiens partial mRNA for immunoglobulin heavy chain variable  
DEFINITION region (IGHV gene), clone 100.  
ACCESSION AJ458384  
VERSION AJ458384.1 GI:20387067  
KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Flicker S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y.,  
Valent, P., Kraft, D. and Valenta, R.  
Conversion of grass allergen-specific human IGE into a protective  
IgG1 antibody  
Unpublished  
2 (bases 1 to 342)  
Flicker S.  
Direct Submission  
Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,  
General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090  
Vienna, AUSTRIA

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Query Match 90.2%; Score 308.4; DB 9; Length 342;  
Best Local Similarity 93.9%; Pred. No. 1.3e-75;  
Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CTCGAGTCTGGCCAGAGACTGTGAAGCCTGCACAGACCTTCCTCCAGCTGGCGTTC 60  
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Qy 61 TCTGAGCTGCGCTTCATCCGAGTGTGTGTTACTACTGAGATTGGATCCGCCAACACCCAGG 120  
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Qy 121 AAGGGCCCTGGAGTGGATTGGGTATCATCTACAGTGGGAACCTTACAAACCCGCTCC 180  
Db 121 AAGGGCCCTGGAGTGGATTGGGTATCATCTACAGTGGGAACCTTACAAACCCGCTCC 180

Qy 181 CTCGAAGTGCAGATTGCGATGCGTAGACAGCTCTGAGAACAGATTCTCCCTGAGGCTG 240  
Db 181 CTCGAAGTGCAGATTGCGATGCGTAGACAGCTCTGAGAACAGATTCTCCCTGAGGCTG 240

Qy 241 AACTCTGTACTGCCCGCGGACACGCGCGTGTATTACTGTGCGAGTTAGATGGCTACACT 300  
Db 241 AACTCTGTACTGCCCGCGGACACGCGCGTGTATTACTGTGCGAGTTAGATGGCTACACT 300

Qy 301 TTGGACATCTGGGGCCAGGGAACCTGTGCACCGCTCTCTCA 342  
Db 301 TTGGACATCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA 342

RESULT 3  
HSA458383 342 bp mRNA linear PRI 30-APR-2002  
LOCUS Homo sapiens partial mRNA for immunoglobulin heavy chain variable  
DEFINITION region (IGHV gene), clone 60.  
ACCESSION AJ458383  
VERSION AJ458383.1 GI:20387065  
KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Flicker S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y.,  
Valent, P., Kraft, D. and Valenta, R.  
Conversion of grass allergen-specific human IGE into a protective  
IgG1 antibody  
Unpublished  
2 (bases 1 to 342)  
Flicker S.  
Direct Submission  
Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,  
General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090  
Vienna, AUSTRIA

FEATURES  
source location/Qualifiers  
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CDS



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Query Match 86.9%; Score 297.2; DB 9; Length 342;  
Best Local Similarity 91.8%; Pred. No. 1.8e-72;  
Matches 314; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCCAAGACTGTTGAAGCTTCACAGACCTTCCTTCAGCTGGCTGTC 60  
Db 1 CTCGAGTCTGGCCCAAGACTGTTGAAGCTTCACAGACCTTCCTTCAGCTGGCTGTC 60  
QY 61 TCTGGCGGCTCCATCCGAGTGTGTACTACTAGATTGGATCCGCGCAACCCAGGG 120  
Db 61 TCTGGTGTCTCCATCCGAGTGTGTATTATTTGAGATTGGTGGTCCGCGCAAGCTTCAGGG 120  
QY 121 AAGGCGCTGAGTGGATTGGTATCATCTATCAAGTGGGAACCTCAACAACCCGTC 180  
Db 121 AAGGCGCTGAGTGGATTGGTATCATCTATCAAGTGGGAACCTCAACAACCCGTC 180  
QY 181 CTCAGAGTCAATTTCCATGTCTGTAGACAGCTGTGAAACAGTTCTCCCTGAGGCTG 240  
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QY 241 AACCTGTGATGCGCGGAGACAGCGCCGTATTACTGTGGAGATTGATGGCTACACT 300  
Db 241 AACCTGTGATGCGCGGAGACAGCGCCGTATTACTGTGGAGATTGATGGCTACACT 300  
QY 241 ACCCTGTGATGCGCGGAGACAGCGCCGTATTACTGTGGAGATTGATGGCTACACT 300  
Db 241 ACCCTGTGATGCGCGGAGACAGCGCCGTATTACTGTGGAGATTGATGGCTACACT 300  
QY 301 TTGGACATCTGGGGCCAGGAACCTGTGACCGTCTCTCA 342  
Db 301 TTGGACATCTGGGGCCAGGAACCTGTGACCGTCTCTCA 342

RESULT 4 355 bp mRNA linear PRI 03-JUL-2004  
LOCUS AY640579  
DEFINITION Homo sapiens clone RT immunoglobulin E variable region mRNA,  
partial cds.  
ACCESSION AY640579  
VERSION AY640579.1 GI:49354899  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 355)  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VHS Igb+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 355)  
Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK  
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YTDYDYGQGLTVTVSS"

ORIGIN

Query Match 85.1%; Score 291; DB 9; Length 355;  
Best Local Similarity 91.2%; Pred. No. 9.7e-71;  
Matches 309; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCCAAGACTGTTGAAGCTTCACAGACCTTCCTTCAGCTGGCTGTC 63  
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QY 64 GCGCGCTCCATCCGAGTGTGTACTACTAGATTGGATCCGCGCAACCCAGGAAG 123  
Db 76 GGTGGCTCCATCCGAGTGTGTACTACTAGATTGGATCCGCGCAACCCAGGAAG 135  
QY 124 GCGCTGAGTGGATTGGTATCATCTATCAAGTGGGAACCTCAACAACCCGCTC 183  
Db 136 GCGCTGAGTGGATTGGTATCATCTATCAAGTGGGAACCTCAACAACCCGCTC 195  
QY 184 AAGAGTCAATTTCCATGTCTGTAGACAGCTGTGAAACAGTTCTCCCTGAGGCTG 243  
Db 196 AAGAGTCAATTTCCATGTCTGTAGACAGCTGTGAAACAGTTCTCCCTGAGGCTG 255  
QY 244 TCTGTGATGCGCGGAGACAGCGCCGTATTACTGTGAGATTGATGGCTACACTTTG 303  
Db 256 TCTGTGATGCGCGGAGACAGCGCCGTATTACTGTGAGATTGATGGCTACACTTTT 315  
QY 304 GACATCTGGGGCCAGGAACCTGTGACCGTCTCTCA 342  
Db 316 GACATCTGGGGCCAGGAACCTGTGACCGTCTCTCA 354

RESULT 5 355 bp mRNA linear PRI 03-JUL-2004  
LOCUS AY640487  
DEFINITION Homo sapiens clone AP immunoglobulin E variable region mRNA,  
partial cds.  
ACCESSION AY640487  
VERSION AY640487.1 GI:49354726  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 355)  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VHS Igb+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 355)  
Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK  
FEATURES  
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CDS

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YTDYDYGQGLTVTVSS"

ORIGIN YDPDWGGGTLVTVSS"

Query Match 84.2%; Score 287.8; DB 9; Length 355;  
Best Local Similarity 90.6%; Pred. No. 7.7e-70;  
Matches 307; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGACTGTGTGAGACCTGACAGACCCCTGTCTCTGAGCTGCTGTCT 63  
DB 16 GAGTCTGGCCAGAGACTGTGTGAGACCTGACAGACCCCTGTCTCTGAGCTGCTGTCT 75  
QY 64 GGGCGCTCCATCCGACAGTGTGTACTACTGAGATTGCGCAACCCAGGGAG 123  
DB 76 GGTGGCTCCATCCGACAGTGTGTACTACTGAGATTGCGCAACCCAGGGAG 135  
QY 124 GGCCTGAGTGTGATTGGGTATCATCTATCAGTGGGAACCTTCAACACCCGTCTC 183  
DB 136 GGCCTGAGTGTGATTGGGTATCATCTATCAGTGGGAACCTTCAACACCCGTCTC 195  
QY 184 AAGAGTGAATTGGCATGTCCGTAGACACGTCTGAGAACATTTCTCCCTGAGGCTGAA 243  
DB 196 AAGAGTGAATTGGCATGTCCGTAGACACGTCTGAGAACATTTCTCCCTGAGGCTGAA 255  
QY 244 TCTGTGACTCCGCGGACACCGCCGTGTATTACTGTGCGAGGTTAGATGCTACACTTTG 303  
DB 256 TCTGTGACTCCGCGGACACCGCCGTGTATTACTGTGCGAGGTTAGATGCTACACTTT 315  
QY 304 GACATCTGGGGCCAGGGAACCTGTGACCGTCTCTCA 342  
DB 316 GACTACTGGGGCCAGGGAACCTGTGACCGTCTCTCA 354

RESULT 6 355 bp mRNA linear PRI 03-JUL-2004  
LOCUS AY640580  
DEFINITION Homo sapiens clone RU immunoglobulin E variable region mRNA,  
partial cds.  
ACCESSION AY640580  
VERSION AY640580.1 GI:49354901  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VHS IGB+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK  
FEATURES  
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ORIGIN  
Query Match 83.7%; Score 286.2; DB 9; Length 355;

Best Local Similarity 90.3%; Pred. No. 2.2e-69;  
Matches 306; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGACTGTGTGAGACCTGACAGACCCCTGTCTCTGAGCTGCTGTCT 63  
DB 16 GAGTCTGGCCAGAGACTGTGTGAGACCTGACAGACCCCTGTCTCTGAGCTGCTGTCT 75  
QY 64 GGGCGCTCCATCCGACAGTGTGTACTACTGAGATTGCGCAACCCAGGGAG 123  
DB 76 GGTGGCTCCATCCGACAGTGTGTACTACTGAGATTGCGCAACCCAGGGAG 135  
QY 124 GGCCTGAGTGTGATTGGGTATCATCTATCAGTGGGAACCTTCAACACCCGTCTC 183  
DB 136 GGCCTGAGTGTGATTGGGTATCATCTATCAGTGGGAACCTTCAACACCCGTCTC 195  
QY 184 AAGAGTGAATTGGCATGTCCGTAGACACGTCTGAGAACATTTCTCCCTGAGGCTGAA 243  
DB 196 AAGAGTGAATTGGCATGTCCGTAGACACGTCTGAGAACATTTCTCCCTGAGGCTGAA 255  
QY 244 TCTGTGACTCCGCGGACACCGCCGTGTATTACTGTGCGAGGTTAGATGCTACACTTTG 303  
DB 256 TCTGTGACTCCGCGGACACCGCCGTGTATTACTGTGCGAGGTTAGATGCTACACTTT 315  
QY 304 GACATCTGGGGCCAGGGAACCTGTGACCGTCTCTCA 342  
DB 316 GACTACTGGGGCCAGGGAACCTGTGACCGTCTCTCA 354

RESULT 7 355 bp mRNA linear PRI 03-JUL-2004  
LOCUS AY640509  
DEFINITION Homo sapiens clone BM immunoglobulin E variable region mRNA,  
partial cds.  
ACCESSION AY640509  
VERSION AY640509.1 GI:49354765  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VHS IGB+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK  
FEATURES  
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ORIGIN  
Query Match 82.7%; Score 283; DB 9; Length 355;  
Best Local Similarity 89.7%; Pred. No. 1.7e-68;  
Matches 304; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGACTGTGTGAGACCTGACAGACCCCTGTCTCTGAGCTGCTGTCT 63

Db 16 GAGTGGGGCCAGAGACTGTGAAGCCTTCTCAGACCCCTGTCCCTCACTGACGTCTCT 75

Qy 64 GCGCGCTTCATCCGAGTGGTGTACTACTGAGATTGGATCCGCCAACCCAGGAG 123

Db 76 GGTGGCTCCATCAGACAGTGTGTACTACTGAGATTGGATCCGCCAACCCAGGAG 135

Qy 124 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 183

Db 136 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 195

Qy 184 AAGAGTCGAATTGGCATTCGGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTGAC 243

Db 196 AAGAGTCGGGTATACACATCAGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTGAC 255

Qy 244 TCTGTACTGCGCGGACACAGCGCGGTATATTACTGTGCGAGATTAGATGCTTCACTTTG 303

Db 256 TCTGTACTGCGCGGACACAGCGCGGTATATTACTGTGCGAGATTAGATGCTTCACTTTG 315

Qy 304 GACATCTGGGGCCAGGAAACCTGTGACCGCTCTCCCTCA 342

Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGCTCTCCCTCA 354

RESULT 8  
AY640564 355 bp mRNA linear PRI 03-JUL-2004  
LOCUS Homo sapiens clone RE immunoglobulin E variable region mRNA,  
partial cds.  
AY640564  
VERSION AY640564.1 GI:49354872  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 355)  
Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VHS IGE+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
Coker,H.A., Durham,S.R. and Gould,H.J.  
AUTHORS Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK  
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CDS  
Query Match 82.3%; Score 281.4; DB 9; Length 355;  
Best Local Similarity 89.4%; Pred. No. 4.8e-68;  
Matches 303; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 4 GAGTCTGGCCAGAGACTGTGAAGCCTTCTCAGACCTGTCCCTCAGTGGGCTGTCTCT 63

Db 16 GAGTGGGGCCAGAGACTGTGAAGCCTTCTCAGACCTGTCCCTCAGTGGGCTGTCTCT 75

Qy 64 GCGCGCTTCATCCGAGTGGTGTACTACTGAGATTGGATCCGCCAACCCAGGAG 123

Db 76 GGTGGCTCCATCAGACAGTGTGTACTACTGAGATTGGATCCGCCAACCCAGGAG 135

Qy 124 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 183

Db 136 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 195

Qy 184 AAGAGTCGAATTGGCATTCGGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTGAC 243

Db 196 AAGAGTCGGGTATACACATCAGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTGAC 255

Qy 244 TCTGTACTGCGCGGACACAGCGCGGTATATTACTGTGCGAGATTAGATGCTTCACTTTG 303

Db 256 TCTGTACTGCGCGGACACAGCGCGGTATATTACTGTGCGAGATTAGATGCTTCACTTTG 315

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Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGCTCTCCCTCA 354

RESULT 8  
AY640564 355 bp mRNA linear PRI 03-JUL-2004  
LOCUS Homo sapiens clone RE immunoglobulin E variable region mRNA,  
partial cds.  
AY640564  
VERSION AY640564.1 GI:49354872  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 355)  
Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VHS IGE+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
Coker,H.A., Durham,S.R. and Gould,H.J.  
AUTHORS Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK  
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CDS  
Query Match 81.3%; Score 278.2; DB 9; Length 355;  
Best Local Similarity 88.8%; Pred. No. 3.8e-67;  
Matches 301; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 4 GAGTCTGGCCAGAGACTGTGAAGCCTTCTCAGACCTGTCCCTCAGTGGGCTGTCTCT 63

Db 16 GAGTGGGGCCAGAGACTGTGAAGCCTTCTCAGACCTGTCCCTCAGTGGGCTGTCTCT 75

Qy 64 GCGCGCTTCATCCGAGTGGTGTACTACTGAGATTGGATCCGCCAACCCAGGAG 123

Db 76 GGTGGCTCCATCAGACAGTGTGTACTACTGAGATTGGATCCGCCAACCCAGGAG 135

Qy 124 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 183

Db 136 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 195

Qy 184 AAGAGTCGAATTGGCATTCGGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTGAC 243

Db 196 AAGAGTCGGGTATACACATCAGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTGAC 255

Qy 244 TCTGTACTGCGCGGACACAGCGCGGTATATTACTGTGCGAGATTAGATGCTTCACTTTG 303

Db 256 TCTGTACTGCGCGGACACAGCGCGGTATATTACTGTGCGAGATTAGATGCTTCACTTTG 315

Qy 304 GACATCTGGGGCCAGGAAACCTGTGACCGCTCTCCCTCA 342

Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGCTCTCCCTCA 354

RESULT 9  
AY640507 355 bp mRNA linear PRI 03-JUL-2004  
LOCUS Homo sapiens clone BK immunoglobulin E variable region mRNA,  
partial cds.  
AY640507  
VERSION AY640507.1 GI:49354762  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 355)  
Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VHS IGE+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
Coker,H.A., Durham,S.R. and Gould,H.J.  
AUTHORS Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK  
FEATURES  
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WTFPDYWGQGLTVTSVS"

CDS  
Query Match 81.3%; Score 278.2; DB 9; Length 355;  
Best Local Similarity 88.8%; Pred. No. 3.8e-67;  
Matches 301; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 4 GAGTCTGGCCAGAGACTGTGAAGCCTTCTCAGACCTGTCCCTCAGTGGGCTGTCTCT 63

Db 16 GAGTGGGGCCAGAGACTGTGAAGCCTTCTCAGACCTGTCCCTCAGTGGGCTGTCTCT 75

Qy 64 GCGCGCTTCATCCGAGTGGTGTACTACTGAGATTGGATCCGCCAACCCAGGAG 123

Db 76 GGTGGCTCCATCAGACAGTGTGTACTACTGAGATTGGATCCGCCAACCCAGGAG 135

Qy 124 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 183

Db 136 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 195

Qy 184 AAGAGTCGAATTGGCATTCGGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTGAC 243

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Qy 124 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 183

Db 136 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 195

Qy 184 AAGAGTCGAATTGGCATTCGGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTGAC 243

Db 196 AAGAGTCGGGTATACACATCAGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTGAC 255

Qy 244 TCTGTACTGCGCGGACACAGCGCGGTATATTACTGTGCGAGATTAGATGCTTCACTTTG 303

Db 256 TCTGTACTGCGCGGACACAGCGCGGTATATTACTGTGCGAGATTAGATGCTTCACTTTG 315

Qy 304 GACATCTGGGGCCAGGAAACCTGTGACCGCTCTCCCTCA 342

Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGCTCTCCCTCA 354

RESULT 9  
AY640507 355 bp mRNA linear PRI 03-JUL-2004  
LOCUS Homo sapiens clone BK immunoglobulin E variable region mRNA,  
partial cds.  
AY640507  
VERSION AY640507.1 GI:49354762  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 355)  
Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VHS IGE+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
Coker,H.A., Durham,S.R. and Gould,H.J.  
AUTHORS Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK  
FEATURES  
source  
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CDS  
Query Match 81.3%; Score 278.2; DB 9; Length 355;  
Best Local Similarity 88.8%; Pred. No. 3.8e-67;  
Matches 301; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 4 GAGTCTGGCCAGAGACTGTGAAGCCTTCTCAGACCTGTCCCTCAGTGGGCTGTCTCT 63

Db 16 GAGTGGGGCCAGAGACTGTGAAGCCTTCTCAGACCTGTCCCTCAGTGGGCTGTCTCT 75

Qy 64 GCGCGCTTCATCCGAGTGGTGTACTACTGAGATTGGATCCGCCAACCCAGGAG 123

Db 76 GGTGGCTCCATCAGACAGTGTGTACTACTGAGATTGGATCCGCCAACCCAGGAG 135

Qy 124 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 183

Db 136 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 195

Qy 184 AAGAGTCGAATTGGCATTCGGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTGAC 243

Db 196 AAGAGTCGGGTATACACATCAGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTGAC 255

Qy 244 TCTGTACTGCGCGGACACAGCGCGGTATATTACTGTGCGAGATTAGATGCTTCACTTTG 303

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Qy 304 GACATCTGGGGCCAGGAAACCTGTGACCGCTCTCCCTCA 342

Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGCTCTCCCTCA 354

RESULT 9  
AY640507 355 bp mRNA linear PRI 03-JUL-2004  
LOCUS Homo sapiens clone BK immunoglobulin E variable region mRNA,  
partial cds.  
AY640507  
VERSION AY640507.1 GI:49354762  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 355)  
Coker,H.A., Durham,S.R. and Gould,H.J.  
TITLE Biased use of VHS IGE+ B cells in the nasal mucosa of allergic  
rhinitis patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 355)  
Coker,H.A., Durham,S.R. and Gould,H.J.  
AUTHORS Direct Submission  
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St  
Thomas Street, London SE1 1UL, UK  
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/db\_xref="GI:49354762"  
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WTFPDYWGQGLTVTSVS"

CDS  
Query Match 81.3%; Score 278.2; DB 9; Length 355;  
Best Local Similarity 88.8%; Pred. No. 3.8e-67;  
Matches 301; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 4 GAGTCTGGCCAGAGACTGTGAAGCCTTCTCAGACCTGTCCCTCAGTGGGCTGTCTCT 63

Db 16 GAGTGGGGCCAGAGACTGTGAAGCCTTCTCAGACCTGTCCCTCAGTGGGCTGTCTCT 75

Qy 64 GCGCGCTTCATCCGAGTGGTGTACTACTGAGATTGGATCCGCCAACCCAGGAG 123

Db 76 GGTGGCTCCATCAGACAGTGTGTACTACTGAGATTGGATCCGCCAACCCAGGAG 135

Qy 124 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 183

Db 136 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGAACAACCTCAACAACCCGCTCC 195

Qy 184 AAGAGTCGAATTGGCATTCGGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTGAC 243

Db 196 AAGAGTCGGGTATACACATCAGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTGAC 255

Qy 244 TCTGTACTGCGCGGACACAGCGCGGTATATTACTGTGCGAGATTAGATGCTTCACTTTG 303

Db 256 TCTGTACTGCGCGGACACAGCGCGGTATATTACTGTGCGAGATTAGATGCTTCACTTTG 315

Qy 304 GACATCTGGGGCCAGGAAACCTGTGACCGCTCTCCCTCA 342

Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGCTCTCCCTCA 354

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Db 136 GGCCTGGAGTGATGTGATCATCTATTAACGGGGGACACCTACTACAAACCCGCTCC 195
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Db 196 AGAGTGGAAATATCATGTCTCAATTGACACGCTGCAAAATGCTTCTCCCTGAGGCTGACC 255
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Db 256 TCTCTGACTGCGGACACGCGCGGTATTCTGTGTGGCGCTGTAGATGAGTACAGTTTG 315
Qy 304 GACATCTGGGGCCAGGAAACCTGTGACCCGCTTCCTCA 342
Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGCTTCCTCA 354

RESULT 10
LOCUS HSA491911 432 bp mRNA linear PRI 20-NOV-2003
DEFINITION Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region
(IGV4-HD17 C9) .
ACCESSION AJ491911
VERSION AJ491911.1 GI:24415808
KEYWORDS constant region; epsilon chain; IGH gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Local somatic hypermutation and class switch recombination in the nasal mucosa of allergic rhinitis patients
JOURNAL J. Immunol. 171 (10), 5602-5610 (2003)
MEDLINE 22970235
PUBMED 14607969
REFERENCE 2 (bases 1 to 432)
AUTHORS Coker,H.A.
TITLE Direct Submision
JOURNAL Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall1 Centre, King's College London, Guy's Campus, London, SE1 1UL, UNITED KINGDOM
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/db_xref="taxon:9606"
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/sex="female"
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/tissue_type="nasal mucosa"
/dev_stage="adult"
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/country="United Kingdom"
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/db_xref="GI:24415809"
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316..355
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356..432
/gene="IGHB"
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C_region

D_segment
J_segment
gene
C_region

ORIGIN

Query Match 81.3%; Score 278.2; DB 9; Length 432;
Best Local Similarity 88.8%; Pred. No.3.ee-67;
Matches 301; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 4 GAGTCTGGCCAGAGTGTGTAAGCCGTGCACAGACCCGTCTCCCTGAGCTGCGTCTCT 63
Db 16 GAGTCGGGCCAGAGTGTGTAAGCCGTGCACAGACCCGTCTCCCTGAGCTGCGTCTCT 75
Qy 64 GCGCGCTCCATCCGCACTGTGTGTTACTGATGATTGGATCCGCCAACCCAGGAG 123
Db 76 GGTGGCCCATCATGATGTGTGTTACTGATGAGCTGTGATCCGCCAACCCAGGAG 135
Qy 124 GGCCTGGAGTGGATTTGGGTATCATCTATCAAGTGGGAGACCTTACAAACCCGCTCC 183
Db 136 GGCCTGGAGTGGATTTGGGTATCATCTATTAACAGGGAGACCTTACAAACCCGCTCC 195
Qy 184 AAGAGTCGAATTTGCGATGTCGGTAGACACGCTGTAGAAACAAGTTCTCCCTGAGGCTGAC 243
Db 196 AGAGTGGAAATATCATGTCTCAATTGACACGCTGCAAAATGAGTTCTCCCTGAGGCTGACC 255
Qy 244 TCTGTACTGCGCGGACACGCGCGGTATTACTGTGCGAGGTTAGATGCTTACACTTTG 303
Db 256 TCTCTGACTGCGGACACGCGCGGTATTCTGTGCGGCTGTAGATGGATACAGTTTG 315
Qy 304 GACATCTGGGGCCAGGAAACCTGTGACCGCTTCCTCA 342
Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGCTTCCTCA 354

RESULT 11
HST22X1 411 bp mRNA linear PRI 09-SEP-2004
LOCUS H.sapiens mRNA for Ig heavy chain variable region (VH4D) (clone T22.1).
DEFINITION
ACCESSION 275385
VERSION 275385.1 GI:2062048
KEYWORDS immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 411)
AUTHORS Tonnelie,C., D'Ercole,C., Depraetere,V., Metras,D., Boudli,L. and Fougereau,M.
TITLE Human thymic B cells largely overexpress the VH4 Ig gene family. A possible role in the control of tolerance in situ?
JOURNAL Int. Immunol. 9 (3), 407-414 (1997)
MEDLINE 97244170
PUBMED 9088979
REFERENCE 2 (bases 1 to 411)
AUTHORS Tonnelie,C.
TITLE Direct Submision
JOURNAL Submitted (26-JUN-1996) Cecile Tonnelie, Centre d'Immunologie Marseille Luminy, Marseille, 13288, France
FEATURES
SOURCE Location/Qualifiers
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V_segment
58..354
D_segment
355..377
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378..411
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Best Local Similarity 88.8%; Pred. No. 7.3e-67;
Matches 300; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 4 GAGTCTGCCCCAGAGCTGTGAACCTGCACAGACCCCTGTCCTCAGCTGCTCTCT 63
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Db 73 GAGTCGGGCCAGAGCTGTGAACCTTTCACAGACCCCTGTCCTCAGCTGCTCTCT 132

Qy 64 GCGGCTCCATCCGCACTGCTGTACTACTCTGAGTTGATCCGCCAACCCAGGAG 123
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Db 133 GGTGGCTCCATCAGACAGTGTGTACTACTCTGAGTGTGATCCGCCAACCCAGGAG 192

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Db 193 GGCCTGAGTGGATTGGTATCATCTATCAGATGGGAAACCTTCAACAACCCGTCCTC 252

Qy 184 AAGAGTCGAATTGCAATGCTGCTGAGACAGCTGTGAGAACAGTTCTCCCTGAGGCTGAA 243
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Qy 244 TCTGTGACTGCGCGGACAGCGCCGTGTATTACTGTGCGAGGTTAGATGGCTACACTTTG 303
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Db 313 TCTGTGACTGCGCGGACAGCGCCGTGTATTACTGTGCGAGGTTAGATGGCTACACTTTG 372

Qy 304 GACATCTGGGGCCAGGGAACCCGTGTACACCGTCTCCTC 341
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Db 373 TCCAGCTGGGGCCAGGGAACCCGTGTACACCGTCTCCTC 410

RESULT 12
HSA491912      432 bp      mRNA      linear      PRI 20-NOV-2003
LOCUS          Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region
                (clone HD17 C37).
ACCESSION      AJ491912
VERSION        AJ491912.1 GI:24415810
KEYWORDS       constant region; epsilon chain; IGH gene; immunoglobulin heavy
SOURCE         chain; variable region.
ORGANISM       Homo sapiens (human)
REFERENCE      1
AUTHORS        Coker H.A., Durham S.R. and Gould H.J.
TITLE          Local somatic hypermutation and class switch recombination in the
                nasal mucosa of allergic rhinitis patients
JOURNAL        J. Immunol. 171 (10), 5602-5610 (2003)
MEDLINE        22970235
PUBMED         14607969
REFERENCE      2 (bases 1 to 432)
AUTHORS        Coker H.A.
TITLE          Direct Submission
JOURNAL        Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall
                Centre, King's College London, Guy's Campus, London, SE1 1UL,
                UNITED KINGDOM
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356..432
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region"
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Query Match      80.9%; Score 276.6; DB 9; Length 432;
Best Local Similarity 88.5%; Pred. No. 1.1e-66;
Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 4 GAGTCTGCCCCAGAGCTGTGAACCTGCACAGACCCCTGTCCTCAGCTGCTCTCT 63
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Db 16 GAGTCGGGCCAGAGCTGTGAAGCCTTTCACAGAACCTGTCTCCCTGCACTGCTCT 75

Qy 64 GCGGCTCCATCCGCACTGCTGTACTACTCTGAGTTGATCCGCCAACCCAGGAG 123
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Db 76 GGTGGCTCCATCAGATGTGTGTACTACTCTGAGTGTGATCCGCCAACCCAGGAG 135

Qy 124 GGCCTGAGTGGATTGGTATCATCTATCAGATGGGAAACCTTCAACAACCCGTCCTC 183
    |||
Db 136 GGCCTGAGTGGATTGGTATCATCTATCAGATGGGAAACCTTCAACAACCCGTCCTC 195

Qy 184 AAGAGTCGAATTGCAATGCTGCTGAGACAGCTGTGAGAACAGTTCTCCCTGAGGCTGAA 243
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Qy 244 TCTGTGACTGCGCGGACAGCGCCGTGTATTACTGTGCGAGGTTAGATGGCTACACTTTG 303
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Db 256 TCTGTGACTGCGCGGACAGCGCCGTGTATTACTGTGCGAGGTTAGATGGCTACACTTTG 315

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Db 316 GACTACTGGGGCCAGGGAACCTTGTCACCGTCTCTCA 354

RESULT 13  
LOCUS HSA244930 351 bp mRNA linear PRI 01-JUN-2000  
DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone I-A34.  
ACCESSION AJ244930  
VERSION AJ244930.1 GI:4995319  
KEYWORDS IGM; IGM heavy chain; immunoglobulin mu heavy chain; variable region.

SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
AUTHORS Chiorazzi, N., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents  
JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)  
MEDLINE 20281644  
PUBMED 10820234  
REFERENCE 2 (bases 1 to 351)  
AUTHORS Dono, M.  
TITLE Direct Submission  
JOURNAL Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova, ITALY

FEATURES  
SOURCE Location/Qualifiers  
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Query Match 80.8%; Score 276.4; DB 9; Length 351;  
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Db 4 GAGTCTGGCCAGAGACTGTGAAGCTTGACACACCTCTGACGTGGCTGTCT 63  
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10 GAGTCGGGCCAGAGACTGTGAAGCTTGACACACCTCTGACGTGGCTGTCT 69  
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64 GCGGCTCCATCCGAGAGTGTGTTACTGAGTGGATCCGCAACCCAGGGAG 123  
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124 GCGCTGAGTGTGTTGTTACTGATCATCAAGTGGGACACCTCAACACCCGTCCTC 183  
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130 GCGCTGAGTGTGTTGTTACTGATCATCAAGTGGGACACCTCAACACCCGTCCTC 189  
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184 AAGAGTGAATTGCTATGCTGCTGAGACACGTCGTAGAACAAAGTTCTCCCTGAGGCTGAC 243

Db 190 AAGAGTGAATTGCTATGCTGCTGAGACACGTCGTAGAACAAAGTTCTCCCTGAGGCTGAC 249  
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244 TCTGTGACTGCGCGGAGACAGCGCGTGTATTACTGTGCGA---GGTTAGATGCTACT 300  
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250 TCTGTGACTGCGCGGAGACAGCGCGTGTATTACTGTGCGAGAGCAAAAGGACTTCTAC 309  
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301 TTGGACATCTGGGGCCAGGGAACCTTGTCACCGTCTCTCA 342  
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310 TTGACTACTGGGGCCAGGGAACCTTGTCACCGTCTCTCA 351  
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RESULT 14  
LOCUS AX061463 360 bp DNA linear PAT 22-JAN-2001  
DEFINITION Sequence 32 from Patent WO0100678.  
ACCESSION AX061463  
VERSION AX061463.1 GI:12406598  
KEYWORDS Human immunodeficiency virus 1 (HIV-1)  
SOURCE Human immunodeficiency virus 1  
ORGANISM Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.

REFERENCE  
AUTHORS Watkins, B.A. and Reitz, M.S.  
TITLE Human monoclonal antibodies to hiv-1 envelope glycoprotein gp120  
JOURNAL Patent: WO 0100678-A 32 04-JAN-2001;  
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)

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SOURCE Location/Qualifiers  
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ORIGIN

Query Match 80.8%; Score 276.4; DB 6; Length 360;  
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Matches 308; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

Db 4 GAGTCTGGCCAGAGACTGTGAAGCTTGACACACCTGTCCTGAGTGGCTGTCT 63  
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19 GAGTCGGGCCAGAGACTGTGAAGCTTGACACACCTGTCCTGAGTGGCTGTCT 78  
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64 GCGGCTCCATCCGAGAGTGTGTTACTGAGTGGATCCGCAACCCAGGGAG 123  
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79 GGTGGCTTCATCAGAGTGTGTTACTGAGTGGATCCGCAACCCAGGGAG 138  
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124 GCGCTGAGTGTGTTGTTACTGATCATCAAGTGGGACACCTCAACACCCGTCCTC 183  
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139 GCGCTGAGTGTGTTGTTACTGATCATCAAGTGGGACACCTCAACACCCGTCCTC 198  
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259 TCTGTGACTGCGCGGAGACAGCGCGTGTATTACTGTGCGAGAGGAGTGTAGTGGACTGG 318  
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RESULT 15  
LOCUS AF062112 414 bp mRNA linear PRI 08-MAY-2001  
DEFINITION Homo sapiens clone 21u-26 immunoglobulin heavy chain variable region (IGH) mRNA, partial cds.  
ACCESSION AF062112  
VERSION AF062112.1 GI:3170686  
KEYWORDS

## SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

## REFERENCE

1 (bases 1 to 414)

## AUTHORS

Wang, X. and Stollar, B.D.

## TITLE

Immunoglobulin VH gene expression in human aging

## JOURNAL

Clin. Immunol. 93 (2), 132-142 (1999)

## MEDLINE

99459182

## PubMed

10527689

## REFERENCE

2 (bases 1 to 414)

## AUTHORS

Wang, X. and Stollar, B.D.

## TITLE

Direct Submision

## JOURNAL

Submitted (22-APR-1998) Biochemistry Department, Tufts University School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA

## FEATURES

Location/Qualifiers

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58..&gt;414

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## ORIGIN

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## V\_region

Query Match 80.4%; Score 275; DB 9; Length 414;  
Best Local Similarity 88.2%; Pred. No. 3e-66;  
Matches 299; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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OY 64 GCGCGCTCCATCCGAGTGTGGTACTACTGAGTTGGATCCGCCAACACCCAGGGAAG 123
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OY 124 GCGCTGAGTGGATGGGTACATCTATCAAGTGGGAAACCTTACACAAACCCGTCCTC 183
   |||||
Db 193 GGCCTGAGTGGATGGGTATCATCTATTAAGTGGAGCACTTACAAACCCGTCCTC 252
   |||||
OY 184 AAGAGTCGAATGCGATGCGGTAGACAGTGTGAACAAGTCTCCCTGAGGCTGAAC 243
   |||||
Db 253 AAGAGTCGAATGCGATGCGGTAGACAGTGTGAACAAGTCTCCCTGAGGCTGAAC 312
   |||||
OY 244 TCTGTACTGCGCGAGACAGCGCCGTGATTAAGTGTGAGAGGTAGATGGCTACACTT 303
   |||||
Db 313 TCTGTACTGCGCGAGACAGCGCCGTGATTAAGTGTGAGAGGTAGATGGCTACACTT 372
   |||||
OY 304 GACATCTGGGGCCAGGGAACCTGTCAACCGTCTCTCTCA 342
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Db 373 GACTACTGGGGCCAGGGAACCTGTCAACCGTCTCTCTCA 411
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Search completed: July 27, 2005, 09:08:38

Job time : 1958.83 secs

**THIS PAGE BLANK (user)**



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:15:56 ; Search time 2106.58 Seconds  
(without alignments)  
6179.670 Million cell updates/sec

Title: US-10-027-725A-1

Perfect score: 342  
Sequence: 1 ctgcagctgcgcacaggaact.....ccctgcacccctctctca 342

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: gb\_esc1: \*  
2: gb\_esc2: \*  
3: gb\_hic: \*  
4: gb\_esc3: \*  
5: gb\_esc4: \*  
6: gb\_esc5: \*  
7: gb\_esc6: \*  
8: gb\_gse1: \*  
9: gb\_gse2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	270.2	79.0	832	1	AU122174 AU122174
2	260.8	76.3	607	4	BM783015 K-EST0060
3	256.6	75.0	677	4	BG686767 602650737
4	253	74.0	490	6	CD689564 EST6087 h
5	250.8	73.3	643	1	AU134293 AU134293
6	247	72.2	369	2	AM404242 UI-HF-BK0
7	246	71.9	509	2	AM406349 UI-HF-BK0
8	245.8	71.9	582	2	AM401348 UI-HF-BK0
9	244.6	71.5	1108	5	BM920469 AGENCOURT
10	241.8	70.7	914	4	BG757054 602710478
11	240	70.2	363	2	AM403420 UI-HF-BK0
12	239.4	70.0	813	5	BO710364 AGENCOURT
13	238.2	69.6	903	5	BO706579 AGENCOURT
14	237.8	69.5	924	4	BF974568 602243482
15	236.8	69.2	808	4	BO710488 AGENCOURT
16	236.2	69.1	814	4	BG685325 602637756
17	235.2	68.8	447	2	AM402200 UI-HF-BK0
18	235.2	68.8	508	7	CR747031 CR747031
19	235.2	68.8	1019	5	BO072420 AGENCOURT
20	235	68.7	474	2	AM408410 UI-HF-BK0
21	234.8	68.7	596	4	BM617833 K-EST0084
22	234.6	68.6	942	5	BO706244 AGENCOURT
23	233.8	68.4	661	4	BG686421 602638356
24	233.6	68.3	542	2	AM951834 EST363904

25	233.4	68.2	725	4	BG431274	BG431274 602499844
26	233.4	68.2	915	5	BO706358	BO706358 AGENCOURT
27	233.4	68.2	959	5	BO899307	BO899307 AGENCOURT
28	233.2	68.2	856	5	BO421299	BO421299 AGENCOURT
29	233	68.1	435	2	BF871158	BF871158 MRL-ET014
30	233	68.1	924	4	BG758027	BG758027 602715076
31	232.6	68.0	368	2	AM403989	AM403989 UI-HF-BK0
32	232.2	67.9	357	5	BP432480	BP432480 BP432480
33	232.2	67.9	921	5	BO710000	BO710000 AGENCOURT
34	232.2	67.9	925	5	BO710876	BO710876 AGENCOURT
35	231.8	67.8	367	2	AM403544	AM403544 UI-HF-BK0
36	231.8	67.8	924	5	BO708516	BO708516 AGENCOURT
37	231.2	67.6	421	2	AM407630	AM407630 UI-HF-BK0
38	230.8	67.5	454	7	CO774069	CO774069 ILLUMIN
39	230.4	67.4	1195	5	BO707644	BO707644 AGENCOURT
40	230	67.3	658	5	BX505812	BX505812 DKFZP686D
41	230	67.3	987	5	BO707970	BO707970 AGENCOURT
42	229.8	67.2	856	4	BG757400	BG757400 602711031
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45	229	67.0	959	4	BG757666	BG757666 602711256

#### ALIGNMENTS

RESULT 1  
AU122174  
LOCUS AU122174 832 bp mRNA linear EST 01-AUG-2002  
DEFINITION AU122174 MAMMAL Homo sapiens cDNA clone MAMMAL001802 5', mRNA  
SEQUENCE AU122174  
ACCESSION AU122174  
VERSION AU122174.1 GI:10937409  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

#### REFERENCE

1 (bases 1 to 832)  
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.  
HRI human cDNA project  
Unpublished (2000)  
Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: genom@hri.co.jp  
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

#### TITLE

JOURNAL  
COMMENT  
Helix Research Institute  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: genom@hri.co.jp  
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

#### FEATURES

source  
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Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="MAMMAL001802"  
/tissue\_type="mammary gland"  
/clone\_id="MAMMAL"  
/note="Vector: pMT18SFL3"

#### ORIGIN

Query Match 79.0%; Score 270.2; DB 1; Length 832;  
Best Local Similarity 87.3%; Pred. No. 4.1e-69;  
Matches 296; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

4 GAGTGTGCCCCAGAGAGCTGTGAAGCTTGACAGACCTGTCCCTCAGCTGAGCTGTCTCT 63  
DB 110 GAGTGTGCCCCAGAGAGCTGTGAAGCTTGACAGACCTGTCCCTCAGCTGAGCTGTCTCT 169

OY	64	GACCGCTCATCCGACAGTGGGTAACTACATCGAATGGGATATCCGGCAACACCCAGGGAAG	123
Db	170	GATGGCTCATACAGACAGTGTGACCCCTACATGGATGGATCCGCAACCCCAAGGANG	229
OY	124	GACCTGAGAGTGGATTGGGTACATCTATACACAGTGGGAACACCTTACAAACACCCTCTC	183
Db	230	GACCTGAGAGTGGATTGGGTACATCTATTAACAATGGGAACACTTACTAACACCCTCTCTC	289
OY	184	AAGAGTCAAATTGGCATGTGCGGTAGACACGTGGAACAATTCCTCCCTGAGGCTGAAC	243
Db	280	AAGAGTCGAATTACCATATCAACACAGCATGTCCAAAGAAAGAAATTCCTCCTGAAAGCTAAAC	349
OY	244	TCTGTGACTGCGCGGACACACGGCCGTGTATTTACTGTGCGAGGTATGATGGCTACATTTTG	303
Db	350	TCTGTGACTGCGCGGACACACGGCCGTGTATTTACTGTGCGAGATCATATTAACAACAGAGGG	409
OY	304	GACATCTGGGGCCAGGAAACCTGTATCACCCGTCTCTCA	342
Db	410	GACTTCTGTGGGCCAGGAAACCTGTGTACCCGTCTATCA	448

RESULT 2	LOCUS	DEFINITION
BM783015	BM783015	607 bp mRNA linear EST 05-MAR-2002
K-ST0060735	K-ST0060735	Sl8N669761 Homo sapiens cDNA clone Sl8N669761-2-E06
5', mRNA sequence.		

ACCESSION	BM783015
VERSION	BM783015.1
KEYWORDS	GI:19131247
SOURCE	EST.
	Homo sapiens (human)

SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 607)

Kim, N.-S., Hahn, Y., Oh, J.-H., Lee, J.-Y., Ahn, H.-Y., Chu, M.-Y., Kim, M.-B.

**AUTHORS**  
Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R., Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and Kim, Y. S.

TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished (2002)
COMMENT	Contact: Kim YS

Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel : +82-42-860-4470  
Fax : +82-42-860-4409  
Email : yongsung@mail.kribb.re.kr  
Plate: 2 row: E column: 06  
High quality sequence stop: 607.

**FEATURES**  
**Source**

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="S18N669761-2-E06"  
 /sex="F"  
 /lab\_host="Top10F"  
 /clone\_1fb="S18N669761"  
 /note="Organ: Stomach; Vector: PCNS; Site\_1: EcoRI;  
 Site\_2: NotI; The poly (A)+ RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then deacapped  
 with tobacco acid pyrophosphatase (TAP). The deacapped  
 intact mRNA was ligated with DNA-RNA linker including EcoRI  
 I site by treatment of T4 RNA ligase and the first strand  
 cDNA was synthesized from oligo dt-selected mRNA by  
 priming with dt-tailed vector. The dt-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10F by electroporation method.  
 The cDNA libraries constructed by this method are

ORIGIN	
Query Match	76.3%; Score 260.8; DB 4; Length 607;
Best Local Similarity	86.8%; Pred.No. 2.4e-66;
Matches 302; Conservative	0; Mismatches 37; Indels 9; Gaps 1;

full-length enriched cDNA library."

OY	4	GAGTCTGGCCCCAGGACCTGGTGAACCTCGCAACAGACCCGTGCTCCCTCAGCTGGCGTCTCT	63
Db	112	GAGTGGGGCCCAAGACCTGGTGAAGCTTTCACAGAACCTGTCTCCCTCACTGGACGTGTCTCT	171
OY	64	GACGCGTTCATCCGACAGTGTGGTTACTACTGAGTTGGATCGGCAACACCCAGGGAAG	123
Db	172	GGTGGCTTCATAGAAACAGTGTAGTTACTACGTGAGCTGGATCCGCCAACACCCAGGGGAAG	231
OY	124	GAGCGTGAAGTGGATTTGGGTACATCTATCACAGTGGGAAACCTTCAACAAACCCGTCCTC	183
Db	232	GGCTCGAGTGGATTTGGGTACATCTATCACACTGGAGACCTTACTACAAACCCGTCCCTC	291
OY	184	AAGAGTCGAATTGCCATGTCCGTAGACACGTCCTGAAACAAAGTTCTCCCTGAGCGTGAAC	243
Db	292	AAGAGTCCAGTTACCATATCTACTAGACACGTCCTAAGAACCAAGTCTCCCTCAAGGTGAGC	351
OY	244	TCTGAGACTGCGCGGACACAGCGCGTGTAACTACGTGGAG-----GTTAGATGGC	294
Db	352	TCTGTGACTGCGCGGACACAGCGCGCTTTATTAATCTGTGGAGAAAGATGGCAATTAGATATT	411
OY	295	TACACTTTGGAACATCTGTGGGCGCAGGGAACCCGTGTCACCGTCTCTCTCA	342
Db	412	TACGGTAAAGACGTCTGTGGGCGCAAGGGACACAGGTCAACCGTCTCTCTCA	459

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BG686767	BG686767	
LOCUS	677 bp	mRNA linear EST_01-MAY-2001
DEFINITION	602650737671 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4763217 5' ,	
	mRNA sequence.	

ACCESSION BG686767  
VERSION BG686767.1 GI:13918164

KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE  
1 (bases 1 to 677)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE	1 (bases 1 to 677)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .

TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

**COMMENT**  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Louis M. Straud, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MSC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LDCM618 row: 1 column: 10  
 High quality sequence stop: 675.

FEATURES  
SOURCE

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/organism="Homo sapiens"
/mol_type="mrna"
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/clone="TM6B:476317"
/issue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/notes="Organ: B-cells; Vector: pOT8; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACTGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by ligation

```

ORIGIN  
Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

Query Match 75.0%; Score 256.6; DB 4; Length 677;  
Best Local Similarity 88.1%; Pred. No. 4.3e-65;  
Matches 304; Conservative 0; Mismatches 34; Indels 7; Gaps 2;

QY 4 GAGTGGCCAGGAGCTGTGAGAGCTGACAGACCTGTCCCTGAGCTGCTCT 63  
DB 99 GAGTGGCCAGGAGCTGTGAGAGCTGACAGACCTGTCCCTGAGCTGCTCT 158  
QY 64 GCGGCTCCATCCGAGAGTGTGTTACTACTGAGTTGGATCCGCAACCCAGGAG 123  
DB 159 GGTGCTCATCAGAGAGTGTGTTACTACTGAGTTGGATCCGCAACCCAGGAG 217  
QY 124 GCGGCTCCATCCGAGAGTGTGTTACTACTGAGTTGGATCCGCAACCCAGGAG 183  
DB 218 GCGGCTCCATCCGAGAGTGTGTTACTACTGAGTTGGATCCGCAACCCAGGAG 277  
QY 184 AAGAGTCGATTCGATGCTGAGACAGCTGTGAGAACAAATTCTCCCTGAGCTGAG 243  
DB 278 AAGAGTCGATTCGATGCTGAGACAGCTGTGAGAACAAATTCTCCCTGAGCTGAG 337  
QY 244 TCTGTGACTGCGCGGAGACAGGCGCTGTATTACTGTGGA-----GTTAGATGCTAC 297  
DB 338 TCTGTGACTGCGCGGAGACAGGCGCTGTATTACTGTGAGAACAAATTCTCCCTGAGCTGAG 397  
QY 298 ACTTGGACATCTGGGGCCAGGGAACCTGTGACCGTCTCTCTCA 342  
DB 398 GAGTTCGACCCCTGGGGCCAGGGAACCTGTGACCGTCTCTCTCA 442

RESULT 4  
LOCUS CD689564 490 bp mRNA linear EST 25-JUN-2003  
DEFINITION EST6081 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD689564  
VERSION CD689564.1 GI:32209443  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 490)  
Zeng, Y.-X., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and  
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gszsums.edu.cn.

FEATURES  
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/tissue\_type="normal nasopharynx"  
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Query Match 74.0%; Score 253; DB 6; Length 490;  
Best Local Similarity 85.9%; Pred. No. 4.7e-64;  
Matches 293; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

QY 5 AGTGGCCAGGAGCTGTGAGAGCTGACAGACCTGTCCCTGAGCTGCTCTCTG 64  
DB 111 AGTGGCCAGGAGCTGTGAGAGCTGACAGACCTGTCCCTGAGCTGCTCTCTG 170  
QY 65 GCGGCTCCATCCGAGAGTGTGTTACTACTGAGTTGGATCCGCAACCCAGGAG 124  
DB 171 GTGACTCCATCAGAGAGTGTGTTACTACTGAGTTGGATCCGCAACCCAGGAG 230  
QY 125 GCGGAGTGTGAGTGTGTTACTACTGAGTTGGATCCGCAACCCAGGAG 184  
DB 231 GCGGAGTGTGAGTGTGTTACTACTGAGTTGGATCCGCAACCCAGGAG 290  
QY 185 AAGAGTCGATTCGATGCTGAGACAGCTGTGAGAACAAATTCTCCCTGAGCTGAG 244  
DB 291 AAGAGTCGATTCGATGCTGAGACAGCTGTGAGAACAAATTCTCCCTGAGCTGAG 350  
QY 245 CTGTGATGCGCGGAGACAGGCGCTGTATTACTGTGAGAGTTAGAT---GGTACACTT 301  
DB 351 CTGTGAGGCGCGGAGACAGGCGCTGTATTACTGTGAGAGTTAGAT---GGTACACTT 410  
QY 302 TGGACATCTGGGGCCAGGGAACCTGTGACCGTCTCTCA 342  
DB 411 TTGACTACTGCGGCGAGGAGATCTGTGTCAACCGTCTCTCA 451

RESULT 5  
LOCUS AU134293 643 bp mRNA linear EST 01-AUG-2002  
DEFINITION AU134293 OVARC1 Homo sapiens cDNA clone OVARC1001672 5', mRNA sequence.  
ACCESSION AU134293  
VERSION AU134293.1 GI:10994832  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 643)  
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and  
TITLE HRI human cDNA project  
JOURNAL Unpublished (2000)  
COMMENT Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: genom@hri.co.jp  
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.

FEATURES  
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/clone="OVARC1001672"  
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/note="Vector: pME18SFLJ"

ORIGIN  
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Best Local Similarity 84.6%; Pred. No. 2.2e-63;  
Matches 301; Conservative 0; Mismatches 37; Indels 18; Gaps 1;  
QY 5 AGTGGCCAGGAGCTGTGAGAGCTGACAGACCTGTCCCTGAGCTGCTCTCTG 64  
DB 110 AGTGGCCAGGAGCTGTGAGAGCTGACAGACCTGTCCCTGAGCTGCTCTCTG 169



Db 54 GAGTCGGGCGCAGAGCTGTGAAGCCTTCGAGAACCTTCCTCCCTACCTGACGTCTCT 113  
 Qy 64 GCGGCTTCATCCGAGTGTGTACTACTAGAGTTGGATCCGCCAACACCCAGGGAG 123  
 Db 114 GGTGCTTCATCCAGAGTGTGTACTACTAGAGTTGGATCCGCCAACACCCAGGGAG 173  
 Qy 124 GCGGCTTCATCCGAGTGTGTACTACTAGAGTTGGATCCGCCAACACCCAGGGAG 183  
 Db 174 GGTGCTTCATCCAGAGTGTGTACTACTAGAGTTGGATCCGCCAACACCCAGGGAG 233  
 Qy 184 AAGAGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 243  
 Db 234 AAGAGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 293  
 Qy 244 TCTGTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 300  
 Db 294 TCTGTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 353  
 Qy 301 TTGGCATCTGGGGCGAGGAAACCTGGTCAACCGTCTCTCA 342  
 Db 354 TTGGCATCTGGGGCGAGGAAACCTGGTCAACCGTCTCTCA 395

RESULT 8  
 AM401348 582 bp mRNA linear EST 16-FEB-2000  
 LOCUS UI-HF-BK0-aau-d-08-0-UT.r1 NIH\_MGC\_36 Homo sapiens cDNA clone  
 DEFINITION IMAGE:3055142 5', mRNA sequence.

ACCESSION AM401348  
 VERSION AM401348.1 GI:6920130  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 582)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Eco RI site shown at the beginning of the sequence.  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/bbrp/image/image.html  
 Seq primer: M13 Forward

FEATURES  
 source Location/Qualifiers

1..582  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3055142"  
 /tissue\_type="lymph"  
 /cell\_line="germinal center B cells"  
 /cell\_line="MGC85"  
 /lab\_host="DH10B (LTI)"  
 /clone\_id="NIH\_MGC\_36"  
 /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN  
 Query Match 71.9%; Score 245.8; DB 2; Length 582;  
 Best Local Similarity 86.1%; Pred. No. 6.7e-62;  
 Matches 297; Conservative 0; Mismatches 42; Indels 6; Gaps 2;  
 4 GAGTCGGGCGCAGAGCTGTGAAGCCTTCGAGAACCTTCCTCCCTACCTGACGTCTCT 63

Db 34 GAGTCGGGCGCAGAGCTGTGAAGCCTTCGAGAACCTTCCTCCCTACCTGACGTCTCT 93  
 Qy 64 GCGGCTTCATCCGAGTGTGTACTACTAGAGTTGGATCCGCCAACACCCAGGGAG 120  
 Db 94 GGTGCTTCATCCAGAGTGTGTACTACTAGAGTTGGATCCGCCAACACCCAGGGAG 153  
 Qy 121 GCGGCTTCATCCGAGTGTGTACTACTAGAGTTGGATCCGCCAACACCCAGGGAG 180  
 Db 154 GGTGCTTCATCCAGAGTGTGTACTACTAGAGTTGGATCCGCCAACACCCAGGGAG 213  
 Qy 181 AAGAGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 240  
 Db 214 AAGAGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 273  
 Qy 241 AACTGTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 297  
 Db 274 AACTGTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 333  
 Qy 298 ACTTGGCATCTGGGGCGAGGAAACCTGGTCAACCGTCTCTCA 342  
 Db 334 ACTTGGCATCTGGGGCGAGGAAACCTGGTCAACCGTCTCTCA 378

RESULT 9  
 BM920469 1108 bp mRNA linear EST 12-MAR-2002  
 LOCUS AGENCOURT 6709612 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5750444  
 DEFINITION 5', mRNA sequence.

ACCESSION BM920469  
 VERSION BM920469.1 GI:19370848  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1108)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov  
 Plate: LAM12781 row: g column: 21  
 High quality sequence stop: 626.

FEATURES  
 source Location/Qualifiers

1..1108  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5750444"  
 /lab\_host="DH10B"  
 /clone\_id="NIH\_MGC\_122"  
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source: anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 71.5%; Score 244.6; DB 5; Length 1108;  
 Best Local Similarity 84.1%; Pred. No. 1.8e-61;  
 4 GAGTCGGGCGCAGAGCTGTGAAGCCTTCGAGAACCTTCCTCCCTACCTGACGTCTCT 63

Matches 290; Conservative 0; Mismatches 49; Indels 6; Gaps 1;

QY 4 GAGTCTGGCCCAAGAGCTGTGAAGCTTGACAGACCCCTGCTCCCTGAGCTGGCTCTCT 63  
 |||||  
 Db 110 GAGTGGGGCCCAAGAGCTGTGAAGCTTGACAGACCCCTGCTCCCTGAGCTGTCTCT 169  
 |||||

QY 64 GGGGGCTTCATCCGAGTGTGTGTTACTACTGAGATTGGATCCGCAACACCCAGGGAG 123  
 |||||  
 Db 170 GGTGGCTCCCTCAGAGTGTGTGTTACTACTGAGATTGGATCCGCAACCCCAAGGAG 229  
 |||||

QY 124 GGGCGGAGTGGATTGGGTAGTATCATCTATGACAGTGGGAAACACTTCAAAACCCGCTC 183  
 |||||  
 Db 230 GGAAGTGAAGTGAATTGGGTATATCTATTATCAAGTGGGACCACTTAAACCCCTCCTC 289  
 |||||

QY 184 AAGAGTCGAATTGGCATGTCCGTAGACACGTCGTGAGAACAAATTCTCCCTGAGCTGAAC 243  
 |||||  
 Db 290 AAGAGTCGAATCACCATATCAGTAGACACGTCGAAGAACAGTTCTCCCTGAGCTGAGC 349  
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QY 244 TCTGTGACTGCCCGGAGACAGCGCGCTGTATTACTGTGCGA-----GGTTAGATGGCTAC 297  
 |||||  
 Db 350 TCTGTGACCGCTGGGAGACACGCGCTGTATTACTGTGCGAGCGGGGGGGGGAGCTAC 409  
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QY 298 ACTTGGACATCTGGGGGACAGGAAACCTGGTCAACCGTCTCTCA 342  
 |||||  
 Db 410 TACATGACGTCGTGGGCAAGGACACGCTACCGTCTCTCA 454  
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RESULT 10  
 BG757054 914 bp mRNA linear EST 15-MAY-2001  
 LOCUS 602710478F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4850851 5',  
 DEFINITION mRNA sequence.

ACCESSION BG757054  
 VERSION BG757054.1 GI:14067707  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 914)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaabs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLN at:

http://image.llnl.gov

Plate: ILGM1692 row: 1 column: 20

High quality sequence stop: 854.

Location/Qualifiers

FEATURES

SOURCE

1..914

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4850851"

/tissue\_type="Primary B-cells from tonsils (cell line)"

/lab\_host="DH10B (phage-resistant)"

/clone\_id="NIH MGC 48"

/note="Organ: B-cells; Vector: pOT7; Site 1: XhoI;

Site 2: EcoRI; cDNA made by oligo-CDT priming;

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGGACAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 70.7%; Score 241.8; DB 4; Length 914;  
 Best Local Similarity 85.3%; Pred. No. 1.1e-60;  
 Matches 296; Conservative 0; Mismatches 42; Indels 9; Gaps 2;

QY 4 GAGTCTGGCCCAAGAGCTGTGAAGCTTGACAGACCCCTGCTCCCTGAGCTGGCTCTCT 63  
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 Db 93 GAGTGGGGCCCAAGAGCTGTGAAGCTTGACAGACCCCTGCTCCCTGAGCTGTCTCT 152  
 |||||

QY 64 GGGGGCTTCATCCGAGTGTGTGTTACTACTGAGATTGGATCCGCAACCCAGGGAG 123  
 |||||  
 Db 153 GGTGGCTCCCTCAGAGTGTGTGTTACTACTGAGATTGGATCCGCAACCCAGGGAG 211  
 |||||

QY 124 GGGCGGAGTGGATTGGGTAGTATCATCTATGACAGTGGGAAACACTTCAAAACCCGCTC 183  
 |||||  
 Db 212 GGAAGTGAAGTGAATTGGGTATATCTATTATCAAGTGGGACCACTTAAACCCCTCCTC 271  
 |||||

QY 184 AAGAGTCGAATTGGCATGTCCGTAGACACGTCGTGAGAACAAATTCTCCCTGAGCTGAAC 243  
 |||||  
 Db 272 AAGAGTCGAATCACCATATCAGTAGACACGTCGAAGAACAGTTCTCCCTGAGCTGAGC 331  
 |||||

QY 244 TCTGTGACTGCCCGGAGACAGCGCGCTGTATTACTGTGCGAGGTTAGATGCTACTTTG 303  
 |||||  
 Db 332 TCTGTGACTGCCCGGAGACAGCGCGCTGTATTACTGTGCGAGGTTAGATGCTACTTTG 391  
 |||||

QY 304 GACATCT-----GGGGCCAGGAAACCTGTGACCGTCTCTCA 342  
 |||||  
 Db 392 CACGACTTTGACTACTGGGGCCAGGAAACCTGTGACCGTCTCTCA 438  
 |||||

RESULT 11  
 AM403420 363 bp mRNA linear EST 16-FEB-2000  
 LOCUS UI-HF-BKO-abe-g-03-0-UI.r1 NIH\_MGC\_36 Homo sapiens cDNA clone  
 DEFINITION IMAGE:3056068 5', mRNA sequence.

ACCESSION AM403420

VERSION AM403420.1 GI:6922356

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 363)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaabs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLN at:

www-bio.llnl.gov/bdrip/image/image.html

Seq primer: M13 Forward.

Location/Qualifiers

FEATURES

SOURCE

1..363

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3056068"

/tissue\_type="lymph"

/cell\_type="germinal center B cells"

/cell\_line="MGC85"

/lab\_host="DH10B (LTI)"

/clone\_id="NIH MGC 36"

/note="Vector: pUT73-Pac; Site 1: NotI; Site 2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

(0.5-1.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima

Bonafide, Ph.D. and M. Bento Soares, Ph.D."

## ORIGIN

Query Match 70.2%; Score 240; DB 2; Length 363;

Best Local Similarity 90.7%; Pred. No. 3.2e-60; Matches 255; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY 4 GAGTGTGACCCAGAGCTGTGAAGCTGCACAGACCCCTGTCCCTAGCTGGCTGTCT 63  
DB 34 GAGTGTGACCCAGAGCTGTGAAGCTGCACAGACCCCTGTCCCTAGCTGGCTGTCT 93  
OY 64 GCGCGCTCCATCCGAGTGTGTGTACTACTGAGTGGATCCGCCAACCAGAGGAG 123  
DB 94 GGTGGCTCCATCAGAGTGTGTGTACTACTGAGTGGATCCGCCAACCAGAGGAG 153  
OY 124 GGCCTGAGTGGATTGGGTACTTATCAACAGTGGGAAACCTTACAAACCCGCTCC 183  
DB 154 GGCCTGAGTGGATTGGGTACTTATCAACAGTGGGAAACCCCTTACAAACCCGCTCC 213  
OY 184 AAGAGTGAATTGCGATGTCCGTAGACACGCTGAGAACAAAGTTCTCCCTGAGGCTGAG 243  
DB 214 AAGAGTGAATTGCGATGTCCGTAGACACGCTGAGAACAAAGTTCTCCCTGAGGCTGAG 273  
OY 244 TCTGTGACTGCGCGCGAGACACGCGCGGTATTAATCTGTGCGAG 284  
DB 274 TCTGTGACTGCGCGCGAGACACGCGCGGTATTAATCTGTGCGAG 314

RESULT 12 813 bp mRNA linear EST 16-JUL-2002

LOCUS B0710364

DEFINITION AGENCOURT\_8351485 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6282412

5', mRNA sequence.

ACCESSION B0710364.1 GI:21849263

VERSION B0710364.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: LUCM2476 row: m column: 05

High quality sequence stop: 529.

Location/Qualifiers

1. 813

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6282412"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_113"

/note="Organ: spleen; Vector: pOT7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH\_MGC Library."

ORIGIN

Query Match 70.0%; Score 239.4; DB 5; Length 813;

Best Local Similarity 90.7%; Pred. No. 5.8e-60; Matches 255; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY 4 GAGTGTGACCCAGAGCTGTGAAGCTGCACAGACCCCTGTCCCTAGCTGGCTGTCT 63  
DB 82 GAGTGTGACCCAGAGCTGTGAAGCTGCACAGACCCCTGTCCCTAGCTGGCTGTCT 141  
OY 64 GCGCGCTCCATCCGAGTGTGTGTACTACTGAGTGGATCCGCCAACCAGAGGAG 123  
DB 142 GGTGGCTCCATCAGAGTGTGTGTACTACTGAGTGGATCCGCCAACCAGAGGAG 201  
OY 124 GGCCTGAGTGGATTGGGTACTTATCAACAGTGGGAAACCTTACAAACCCGCTCC 183  
DB 202 GGCCTGAGTGGATTGGGTACTTATCAACAGTGGGAAACCTTACAAACCCGCTCC 261  
OY 184 AAGAGTGAATTGCGATGTCCGTAGACACGCTGAGAACAAAGTTCTCCCTGAGGCTGAG 243  
DB 262 AAGAGTGAATTGCGATGTCCGTAGACACGCTGAGAACAAAGTTCTCCCTGAGGCTGAG 321  
OY 244 TCTGTGACTGCGCGCGAGACACGCGCGGTATTAATCTGTGCGAG 284  
DB 322 TCTGTGACTGCGCGCGAGACACGCGCGGTATTAATCTGTGCGAG 362

RESULT 13 903 bp mRNA linear EST 16-JUL-2002

LOCUS B0706579

DEFINITION AGENCOURT\_8487944 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6300935

5', mRNA sequence.

ACCESSION B0706579.1 GI:21845478

VERSION B0706579.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: LUCM2515 row: p column: 24

High quality sequence start: 4

High quality sequence stop: 584.

Location/Qualifiers

1. 903

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6300935"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_113"

/note="Organ: spleen; Vector: pOT7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH\_MGC Library."

ORIGIN

Query Match 69.6%; Score 238.2; DB 5; Length 903;

Best Local Similarity 82.9%; Pred. No. 1.3e-59; Matches 286; Conservative 0; Mismatches 53; Indels 6; Gaps 1;



Qy	4	GAGTCTGGCCAGGACTGCTGAAGCGCTGCACAGACCCTGCTCCCTCAGCGTGGCGTCTCT	63
Db	98	GAGTCTGGCCAGGACTGCTGAAGCGCTGCACAGACCCTGCTCCCTCAGCGTGGCGTCTCT	157
Qy	64	GGCGGCTTCATCCGAGTGTGTGTTACTACTGGAAGTGGATTCGCGCAACATCCAGGGAAG	123
Db	158	GGTGGCTTCATCAGAGTAGTAATTACTAGGGGCTGGATTCGCGCAATCCCGCAGGGAAG	217
Qy	124	GGCGGAGTGGATTGGGTACATCTATCAAGTGGGAACACTTAACAAACCCGCTCTC	183
Db	218	GGGCTGGAGTGGATTGGGAATATTCATTATAGTGGAGCATCTACTACAAACCCGCTCTC	277
Qy	184	AAGAGTCGAATTGGCATGTCCGTAGACAGTCTGGAACAATGTTCTCCCTGAGCTGAAC	243
Db	278	AAGAGTGAATCAACCATATCCGTAAACAGTCCAAAGACAGTTCTCCCTGAAGCTGAAG	337
Qy	244	TCTGTGACTGCCCGGCGACAAGCCCGTGAATTACTGTGGCA-----GGTTAGATGGCTAC	297
Db	338	TCTGTGACCGGCGCGACAGACGGCTGTCTTAATTACTGTGGAAAGGGGAGATGATTATGGGC	397
Qy	298	ACTTTGACATCTGGGGCCAGGGAACCTGGGCAACGATCTCTCA	342
Db	398	TGATTCGACCCCTGTGGGCGCAGGGAACTCTTGATCAACGATCTCTCA	442

RESULT	14
LOCUS	BF974568
DEFINITION	BP974568 828 bp mRNA EST 22-JAN-2001
ACCESSION	6022344821 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4334541 5,
VERSION	BF974568
KEYWORDS	BF974568.1 GI:12341783
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eumalyota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL	1 (bases 1 to 828)
COMMENT	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cga@bs-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: IlcM1204 row: C column: 22 High quality sequence stop: 800. Location/Qualifiers 1..828
FEATURES	
SOURCE	

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FEATURES
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                /clone_image="3334541"
                /tissue_type="Primary B-cells from consils (cell line)"
                /lab_host="DH10B (phage-resistant)"
                /clone_1ib="NIH_MGC_48"
                /note="Organ: B-cells; Vector: pORF7; Site:1: XhoI;
                Site 2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                for average insert size 1.8kb. library constructed by Ling
                Hong in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC library."

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Query Match	69.5%	Score 237.8	DB 4	Length 828
Best Local Similarity	90.4%	Pred. No. 1.7e-59		
Matches	254	Conservative	0	Mismatches 27
				Indels 0
				Gaps 0
QY	4	GAGTCTGGCCACGAGACTGTGTGAAGCTCTGCACAGACCTCTGTCCCTCAAGTCGGCTGTCTCT	63	
Db	92	GAGTCGGGGCCACGAGACTGTGTGAAGCCTTCTCAGACCTGTCCCTCAAGTCTGTCTCT	151	
QY	64	GGCGGCTTCATCCGACAGTGGTGTTACTCACTCGAGTTGGATTCGGCGCAACCCAGGGGAAG	123	
Db	152	GGTGGCTTCATCGACAGTGGTGTTACTACTGGAGTTGGATTCGGCGAGCCCCAGGGGAAG	211	
QY	124	GGCCTGAGTGGATTGGGTATCATCTATCACAGTGGGAACCTTCAACAAACCCGTCCTC	183	
Db	212	GGCCTGAGTGGATTGGATATCATCTATTAACAGTGGAGCACTACTATTAACCCGTCCTC	271	
QY	184	AAAGATCGAATTGGCATCTCGGTGACACGCTGTGAGAAACAAATTCCTCCCTGAGGCTGAAC	243	
Db	272	AAAGATCGAGTATTCATATCATGTGAGAACGCTCCAAAGAACCAAGTTCCTCCCTGAATCTGAAC	331	
QY	244	TCTGTGACTGCGCGGAGACAGCGCCGTGATTTACTGTGCGAG	284	
Db	332	TCTGTGATTGCCGACAGACAGCGCCGTGATTTACTGTGCGAG	372	

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RESULT 15
LOCUS      B0710488
DEFINITION B0710488      904 bp      mRNA      linear      EST 16-JUL-2002
AGENCOURT 8352970 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278137
5', mRNA sequence.
ACCESSION  B0710488
VERSION    B0710488.1  GI:21849387
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
REFERENCE  1 (bases 1 to 904)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA library Preparation: Rubin Laboratory
            cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNLN at:
            http://image.lnl.gov
            Plate: L10CM2465 row: k column: 02
            High quality sequence stop: 728.
            Location/Qualifiers
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                /organism="Homo sapiens"

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source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6278137"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_113"
/notes="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

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Job time : 2112.58 secs

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XX  11-JUL-2002.
XX  27-DEC-2001; 2001WO-SE002908.
XX  29-DEC-2000; 2000SF-00004892.
XX  (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX  Flicker S, Steinberger P, Kraft D, Valenta R;
XX  WPI; 2002-583604/62.
XX  P-PSDB; ABG30445.
XX  Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX  variable region of group 2 allergen specific-human IgE Fabs, useful for
XX  diagnosing or passive immunotherapy of type I allergy, for environmental
XX  allergen detection.
XX  Disclosure; Page 31-32; 45pp; English.
XX  This invention relates to the DNA and protein sequences of group 2
XX  allergen-specific human IgE Fabs and methods for their use. The proteins
XX  of the invention may have antiallergic activities and may be used as a
XX  vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
XX  antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX  2 allergen-specific fabs of the invention may be useful for environmental
XX  allergen detection and for standardisation of allergen extracts. The fabs
XX  - or a vaccine againsts a type I allergy is useful for diagnosing a type
XX  I allergy. The allergen-specific fabs of the invention are useful for
XX  inter alia, diagnosis, therapy and prevention of type I allergy. They are
XX  also useful for identification of group 2 allergen-containing pollen and
XX  may be used for blocking the binding of grass pollen allergic patients
XX  IgE antibodies to Phi p 2. The present sequence represents the DNA
XX  encoding the human IgG fab, clone 94 heavy chain protein of the invention
XX  Sequence 342 BP; 69 A; 100 C; 98 G; 75 T; 0 U; 0 Other;
XX
XX  Query Match          99.5%; Score 340.4; DB 6; Length 342;
XX  Best Local Similarity 99.7%; Pred. No. 1.2e-87;
XX  Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX  QY  1 CTCGAGTCTGGCCCGAGACTGCTGTAAGCCTGCACAGACCTGTCCCTCAGCTGCCTGTC 60
XX  DB  1 CTCGAGTCTGGCCCGAGACTGCTGTAAGCCTGCACAGACCTGTCCCTCAGCTGCCTGTC 60
XX
XX  QY  61 TCTGGCGGCTCTCCATCCGAGTGTGTGTTACTACTGAGTTGAGTCCGCGCAACCCAGGG 120
XX  DB  61 TCTGGCGGCTCTCCATCCGAGTGTGTGTTACTACTGAGTTGAGTCCGCGCAACCCAGGG 120
XX
XX  QY  121 AAGGGCCGTGGAGTGGATTGGTACATCTATCAAGTGGGAACCTATAAACCCTGCC 180
XX  DB  121 AAGGGCCGTGGAGTGGATTGGTACATCTATCAAGTGGGAACCTATAAACCCTGCC 180
XX
XX  QY  181 CTCAAGAGTCGATTTGCATGCGTAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240
XX  DB  181 CTCAAGAGTCGATTTGCATGCGTAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240
XX
XX  QY  241 AACTCTGTGACTGCGCGGAGACACGCGCGTGTATTACTGTGCGAGGTAGATGGCTACACT 300
XX  DB  241 AACTCTGTGACTGCGCGGAGACACGCGCGTGTATTACTGTGCGAGGTAGATGGCTACACT 300
XX
XX  QY  301 TTGACATCTGGGGCGAGGAAACCTGTGTCAACCCGCTCCTCA 342
XX  DB  301 TTGACATCTGGGGCGAGGAAACCTGTGTCAACCCGCTCCTCA 342
XX
XX  RESULT 2
XX  ABR89639
XX  ID ABR89639 standard; DNA; 342 BP.

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XX  ABR89639;
XX  21-OCT-2002 (first entry)
XX  DNA encoding human IgE Fab clone 100 heavy chain.
XX  Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;
XX  timothy grass pollen allergen; passive immunotherapy.
XX  Homo sapiens.
XX
XX  Key Location/Qualifiers
XX  CDS 1..342
XX  FT /*tag= a
XX  FT /product= "Fab clone 100 heavy chain"
XX  FT /*tag= b
XX  FT /note= "FR1 region"
XX  FT /*tag= c
XX  FT /note= "CDR1 region"
XX  FT /*tag= d
XX  FT /note= "FR2 region"
XX  FT /*tag= e
XX  FT /note= "FR3 region"
XX  FT /*tag= f
XX  FT /note= "CDR2 region"
XX  FT /*tag= g
XX  FT /note= "FR3 region"
XX  FT /*tag= h
XX  FT /note= "CDR3 region"
XX  FT /*tag= i
XX  FT /note= "FR4 region"
XX
XX  WO200253595-A1.
XX  11-JUL-2002.
XX  27-DEC-2001; 2001WO-SE002908.
XX  29-DEC-2000; 2000SF-00004892.
XX  (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX  Flicker S, Steinberger P, Kraft D, Valenta R;
XX  WPI; 2002-583604/62.
XX  P-PSDB; ABG30447.
XX
XX  Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX  variable region of group 2 allergen specific-human IgE Fabs, useful for
XX  diagnosing or passive immunotherapy of type I allergy, for environmental
XX  allergen detection.
XX  Disclosure; Page 33; 45pp; English.
XX
XX  This invention relates to the DNA and protein sequences of group 2
XX  allergen-specific human IgE Fabs and methods for their use. The proteins
XX  of the invention may have antiallergic activities and may be used as a
XX  vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
XX  antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX  2 allergen-specific fabs of the invention may be useful for environmental
XX  allergen detection and for standardisation of allergen extracts. The fabs
XX  - or a vaccine againsts a type I allergy is useful for diagnosing a type
XX  I allergy. The allergen-specific fabs of the invention are useful for

```

CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergenic patients  
 CC IGE antibodies to Phi P 2. The present sequence represents the DNA  
 CC encoding the human Ige fab, clone 100 heavy chain protein of the  
 CC invention

XX Sequence 342 BP; 69 A; 103 C; 94 G; 76 T; 0 U; 0 Other;

Query Match 90.2%; Score 308.4; DB 6; Length 342;  
 Best Local Similarity 93.9%; Pred. No. 1.9e-78;  
 Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCGAGAGCTGTTGAAGCTGACAGACCCCTGCTCCAGCTGGCTGTC 60  
 Db 1 CTCGAGTCTGGCCGAGAGCTGTTGAAGCTGACAGACCCCTGCTCCAGCTGTC 60  
 QY 61 TCTGGCGGCTTCATCCGAGTGTGTACTACTGAGTTGGATCCGCCAACCCAGGG 120  
 Db 61 TCTGGTGGCTTCATCCGAGTGTGTATTACTGAGTTGGATCCGCCAACCCAGGG 120  
 QY 121 AAGGCGCTGAGTGATGGTGGTACATCTATACAGTGGAAACCTTACACACCCGCTC 180  
 Db 121 AAGGCGCTGAGTGATGGTGGTACATCTATACAGTGGCAACCTTACACACCCGCTC 180  
 QY 181 CTCGAAGTGAATTCGATGCTGTGACAGCTGTGAGAACAGTTCCTCCAGAGCTG 240  
 Db 181 CTCGAAGTGAATTCGATGCTGTGACAGCTGTGAGAACAGTTCCTCCAGAGCTG 240  
 QY 241 AACTCTGTGACTGCGCGGAGACACGCGCTGTATTACTGTGCGAGTTAGATGGTACACT 300  
 Db 241 AGCTCTGTGACTGCGCGGAGACACGCGCTGTATTACTGTGCGAGTTAGATGGTACACT 300  
 QY 301 TTGACATCTGGGCGCAGGGAACCTTGCTACCCGTCCTCA 342  
 Db 301 TTGACATCTGGGCGCAGGGAACCTTGCTACCCGTCCTCA 342

RESULT 3

ABK89638  
 ID ABR89638 standard; DNA; 342 BP.

XX ABR89638;

XX 21-OCT-2002 (first entry)

XX DNA encoding human Ige Fab clone 60 heavy chain.

XX Human; fab; ds; gene; anti-allergic; vaccine; grass pollen; Phi p 2;

KW timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..342  
 /tag= a  
 /product= "Fab clone 60 heavy chain"

XX misc\_feature 7..78  
 /tag= b  
 /note= "FRI region"

XX misc\_feature 79..99  
 /tag= c  
 /note= "CDR1 region"

XX misc\_feature 100..123  
 /tag= d  
 /note= "FR2 region"

XX misc\_feature 134..141  
 /tag= e  
 /note= "FR3 region"

XX misc\_feature 142..189  
 /tag= f  
 /note= "CDR2 region"

XX misc\_feature 190..285

FT /\*tag= g  
 FT /note= "FR3 region"  
 FT misc\_feature 285..309  
 FT /\*tag= h  
 FT /note= "CDR3 region"  
 FT misc\_feature 310..342  
 FT /\*tag= i  
 FT /note= "FR4 region"

XX W0200253595-A1.

XX 11-JUL-2002.

XX 27-DEC-2001; 2001WO-SE002908.

XX 29-DEC-2000; 2000SE-00004892.

XX (PHAA ) PHARMACIA DIAGNOSTICS AB.

XX Flicker S, Steinberger P, Kraft D, Valenta R;

XX WPI; 2002-583604/62.

XX P-PSDB; ABG30446.

PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human Ige Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.

XX Disclosure; Page 32; 45pp; English.

CC This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human Ige Fabs and methods for their use. The proteins  
 CC of the invention may have anti-allergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergenic patient's Ige  
 CC antibodies to Phi P 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC Ige antibodies to Phi P 2. The present sequence represents the DNA  
 CC encoding the human Ige fab, clone 60 heavy chain protein of the invention  
 CC XX

XX Sequence 342 BP; 70 A; 105 C; 90 G; 77 T; 0 U; 0 Other;

Query Match 86.9%; Score 297.2; DB 6; Length 342;  
 Best Local Similarity 91.8%; Pred. No. 3e-75;  
 Matches 314; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCGAGAGCTGTTGAAGCTGACAGACCCCTGCTCCAGCTGGCTGTC 60

Db 1 CTCGAGTCTGGCCGAGAGCTGTTGAAGCTGACAGACCCCTGCTCCAGCTGTC 60

QY 61 TCTGGCGGCTTCATCCGAGTGTGTACTACTGAGTTGGATCCGCCAACCCAGGG 120

Db 61 TCTGGTGGCTTCATCCGAGTGTGTATTACTGAGTTGGATCCGCCAACCCAGGG 120

QY 121 AAGGCGCTGAGTGATGGTGGTACATCTATACAGTGGAAACCTTACACACCCGCTC 180

Db 121 AAGGCGCTGAGTGATGGTGGTACATCTATACAGTGGCAACCTTACACACCCGCTC 180

QY 181 CTCGAAGTGAATTCGATGCTGTGACAGCTGTGAGAACAGTTCCTCCAGAGCTG 240

Db 181 CTCGAAGTGAATTCGATGCTGTGACAGCTGTGAGAACAGTTCCTCCAGAGCTG 240

QY 241 AACTCTGTGACTGCGCGGAGACACGCGCTGTATTACTGTGAGAGTTAGATGGTACACT 300

Db 241 AACTCTGTGACTGCGCGGAGACACGCGCTGTATTACTGTGAGAGTTAGATGGTACACT 300

QY 301 TTGGACATCTGGGGCCAGGGAACCCCTGTGTCACCGTCTCTCA 342  
 Db 301 TTGGACATCTGGGGCCAGGGAACCCCTGTGTCACCGTCTCTCA 342

## RESULT 4

AAAF29076 ID AAF29076 standard; DNA, 360 BP.

XX AAF29076;

DT 03-APR-2001 (first entry)

DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 32.

KM Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;

XX envelope glycoprotein; gp120; diagnosis; ds.

OS Homo sapiens.

XX MO20010678-A1.

XX 04-JAN-2001.

PF 23-JUN-2000; 2000MO-US017327.

XX 30-JUN-1999; 99US-0141701P.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Watkins BA, Reitz MS;

DR WPI; 2001-112438/12.

XX P-PSDB; AAB62775.

PT Novel human monoclonal antibody immunoreactive with human

PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

PT in biological sample and providing passive immunotherapy to HIV-1

PS infected mammal.

XX Claim 4; Page 45; 81pp; English.

CC The present invention provides the protein and coding sequences for the

CC variable regions of human monoclonal antibodies which are immunoreactive

CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.

CC These can be used in diagnosis and therapy of HIV-1 infection

XX Sequence 360 BP; 73 A; 104 C; 107 G; 76 T; 0 U; 0 Other;

SO Query Match 80.8%; Score 276.4; DB 4; Length 360;

Best Local Similarity 90.1%; Pred. No. 2.9e-69;

Matches 308; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCGAGAGCTGTGTAAGCTGCACAGACCCCTGCTCAGCTGGCTCTCT 63

Db 19 GAGTCTGGCCCGAGAGCTGTGTAAGCTGCACAGACCCCTGCTCAGCTGGCTCTCT 78

QY 64 GGCCTGCTCCATCCCGAGTGTGTTACTACTGAGTTGGATCCGCCAACCCAGGGAAG 123

Db 79 GGTGGCTCCATCAGCAGTGTGTTACTACTGAGTGTGATCCGCCAACCCAGGGAAG 138

QY 124 GGCCTGAGTGAATTTGGGTACATCTATCAGAGTGGGAACACCTTCAACACCCGTCCTC 183

Db 139 GGCCTGAGTGAATTTGGGTACATCTATCAGAGTGGGAACACCTTCAACACCCGTCCTC 198

QY 184 AAGAGTGAATTTGCAATGCTGTGTAAGCAAGTCTGAGAAACAAGTCTCCCTAGGCTGAAC 243

Db 199 AAGAGTGAATTTGCAATGCTGTGTAAGCAAGTCTGAGAAACAAGTCTCCCTAGGCTGAAC 258

QY 244 TCTGTGACTGCGCGGACACCGCGGTGATTAATGTCGCA--GGTATGATGGCTACT 300

Db 259 TCTGTGACTGCGCGGACACCGCGGTGATTAATGTCGCA--GGTATGATGGCTACT 318

QY 301 TTGGACATCTGGGGCCAGGGAACCCCTGTGTCACCGTCTCTCA 342  
 Db 319 TTGGACATCTGGGGCCAGGGAACCCCTGTGTCACCGTCTCTCA 360

## RESULT 5

ADC99786 ID ADC99786 standard; DNA, 352 BP.

XX ADC99786;

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 15.

KM anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

XX cytosstatic; melanoma; oesophageal; pancreatic; colorectal tumour;

XX cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

XX lung cancer; human; ds; gene.

XX Homo sapiens.

XX MO2003057838-A2.

XX 17-JUL-2003.

PF 26-DEC-2002; 2002MO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

PA (ABGE-) ABGENIX INC.

PI Gudas J;

DR WPI; 2003-58713/55.

XX P-PSDB; ADC99784.

PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease

PT or condition associated with expression of MUC18 in a patient, e.g.

PT tumours, cancers, and other malignancies.

XX Claim 8; SEQ ID NO 15; 78pp; English.

CC The invention relates to a novel isolated monoclonal antibody comprising

CC a heavy or light chain amino acid or a heavy or light chain variable

CC domain where the antibody binds to MUC18. The monoclonal antibody of the

CC invention demonstrates cytosstatic activity and may be useful for treating

CC a disease or condition associated with the expression of MUC18 on the

CC cell surface such as tumours, specifically melanoma, oesophageal,

CC pancreatic or colorectal tumours, carcinomas, particularly cervical

CC carcinomas and cervical intraepithelial neoplasia and cancers including

CC colorectal, breast or lung cancer, as well as other malignancies. The

CC current sequence is that of the anti-human MUC18 monoclonal antibody

CC heavy chain variable domain DNA of the invention.

XX Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

SO Query Match 80.4%; Score 275; DB 10; Length 352;

Best Local Similarity 90.3%; Pred. No. 7.2e-69;

Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCGAGAGCTGTGTAAGCTGCACAGACCCCTGCTCAGCTGGCTCTCT 63

Db 16 GAGTCTGGCCCGAGAGCTGTGTAAGCTGCACAGACCCCTGCTCAGCTGGCTCTCT 75

QY 64 GGCCTGCTCCATCCCGAGTGTGTTACTACTGAGTTGGATCCGCCAACCCAGGGAAG 123

Db 76 GGTGGCTCCATCAGCAGTGTGTTACTACTGAGTGTGATCCGCCAACCCAGGGAAG 135

QY 124 GGCCTGAGTGAATTTGGGTACATCTATCAGAGTGGGAACACCTTCAACACCCGTCCTC 183

Db 136 GGCCTGAGTGAATTTGGGTACATCTATCTATCAGTGGGAACACCTTCAACACCCGTCCTC 195

Query Match	80.4%	Score 275;	DB 10;	Length 352;
Best Local Similarity	90.3%	Pred. No. 7.2e-69;		
Matches 306; Conservative	0;	Mismatches 30;	Indels 3;	Gaps 1;

CC carcinomas, cancer and other malignancies. The present DNA sequence  
CC encodes a heavy chain from an MUC18 tumour antigen-specific monoclonal  
CC antibody.

SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;  
Query Match 80.4%; Score 275; DB 10; Length 352;  
Best Local Similarity 90.3%; Pred. No. 7.2e-69;  
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;  
QY 4 GAGTCTGGCCAGAGACTGTGTAAAGCTTGACAGACCTGTCTCTGAGTGGCTGTCTT 63  
DB 16 GAGTCGGGCCAGAGACTGTGTAAAGCTTGACAGACCTGTCTCTGAGTGGCTGTCTT 75  
QY 64 GGGGGCTCCATCCGAGTGTGTACTACTAGTGGATTGGATCCGCCAAACCCAGGGAG 123  
DB 76 GGTGGCTCCATCCAGAGTGTGTACTACTAGTGGATTGGATCCGCCAGACCCAGGGAG 135  
QY 124 GGCCTGAGTGTGTGTGTATCATCTATCAAGTGGAAACCTTCAACAAACCCGTCTC 183  
DB 136 GGCCTGAGTGTGTGTGTATCATCTATCAAGTGGAAACCTTCAACAAACCCGTCTC 195  
QY 184 AAGAGTGAATTGCCATGTCCGTATGACACGCTGTGAACAAGTTCTCTGAGCTGAAC 243  
DB 196 AAGAGTGAATTGCATATCATATGACACGCTGTGAACAAGTTCTCTGAGCTGAAC 255  
QY 244 TCTGTGACTGCGGGACAGCGCGGTATTAAGTGGAGTTAGATGGCTACACTTTG 303  
DB 256 TCTGTGACTGCGGGACAGCGCGGTATTAAGTGGAGTTAGATGGCTACACTTTG 312  
QY 304 GACATCTGGGGCCAGGGAAACCTGTGTCAACCGTCTCTCA 342  
DB 313 GACTACTGGGGCCAGGGAAACCTGTGTCAACCGTCTCTCA 351  
RESULT 8  
ID ADS84403 standard; DNA; 354 BP.  
XX ADS84403;  
AC  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human anti-EPO-R antibody heavy chain variable region DNA SEQ ID NO:42.  
XX  
KW human; erythropoietin receptor; EPO receptor;  
KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
KW antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;  
KW wound healing; neural cell damage protection;  
KW neural tissue damage protection; brain injury; spinal cord injury;  
KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;  
KW ds.  
XX  
OS Homo sapiens.  
XX  
PN W02004035603-A2.  
XX  
PD 29-APR-2004.  
XX  
PF 14-OCT-2003; 2003WO-US032243.  
XX  
PR 14-OCT-2002; 2002US-00269711.  
PR 10-OCT-2003; 2003US-00684109.  
XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Devices PJ, Green LL, Ostrow DH, Reilly EB, Wielez J;  
XX  
DR WPI: 2004-348433/32.  
DR P-PSDB: ADS84404.  
XX  
PT New antibodies that bind to or activate an endogenous human  
PT erythropoietin receptor, useful for diagnosing, preventing or treating  
PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
PT anemia.  
XX  
PS Claim 47; SEQ ID NO 42; 192pp; English.

XX  
CC The present invention describes an antibody or its fragment that binds to  
CC or activates an endogenous activity of a human erythropoietin (EPO)  
CC receptor in a mammal, but does not interact with a peptide having a  
CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
CC methods of modulating or activating an endogenous activity of a human EPO  
CC receptor in a mammal, comprising administering to the mammal a  
CC therapeutic amount of the above antibody or its fragment to modulate or  
CC activate the receptor; (2) a method of treating a mammal suffering from  
CC aplasia, comprising administering to the mammal a therapeutic amount of  
CC the above antibody or its fragment to modulate or activate the receptor;  
CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
CC an isolated and purified polynucleotide sequence; and (5) an isolated and  
CC purified amino acid sequence, and their fragments. The EPO receptor  
CC binding antibody has antianaemic, neuroprotective and vulnerary  
CC activities, and can be used in gene therapy. The compositions and methods  
CC from the present invention can be used for modulating an endogenous  
CC activity of a human EPO receptor or for treating mammals suffering from  
CC aplasia or anaemia. They may also be used for identifying mammals having  
CC a dysfunctional EPO receptor. The composition may also be used in  
CC promoting wound healing or in protecting against neural cell and/or  
CC tissue damage resulting from brain/spinal cord injury, stroke and the  
CC like. The present sequence encodes a human anti-EPO-R antibody heavy  
CC chain variable region, which is given in the exemplification of the  
CC present invention.  
XX

SQ Sequence 354 BP; 76 A; 105 C; 97 G; 76 T; 0 U; 0 Other;

Query Match 78.5%; Score 268.6; DB 13; Length 354;  
Best Local Similarity 87.0%; Pred. No. 5e-67;  
Matches 295; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGACTGTGTAAAGCTTGACAGACCTGTCTCTGAGTGGCTGTCTT 63  
DB 16 GAGTCGGGCCAGAGACTGTGTAAAGCTTGACAGACCTGTCTCTGAGTGGCTGTCTT 75  
QY 64 GGCCTGCTCATCCGAGTGTGTGTACTACTGAGTTGATCCGCCAAACCCAGGGAG 123  
DB 76 GGTGGCTCCATCCAGAGTGTGTGTACTACTGAGTTGATCCGCCAGACCCAGGGAG 135  
QY 124 GGCCTGAGTGTGTGTGTATCATCTATCAAGTGGAAACCTTCAACAAACCCGTCTC 183  
DB 136 GGCCTGAGTGTGTGTGTATCATCTATCAAGTGGAAACCTTCAACAAACCCGTCTC 195  
QY 184 AAGAGTGAATTGCCATGTCCGTATGACACGCTGTGAACAAGTTCTCTGAGCTGAAC 243  
DB 196 AAGAGTGAATTGCCTATATGACACGCTGTGAACAAGTTCTCTGAGCTGAAC 255  
QY 244 TCTGTGACTGCGGGACAGCGCGGTATTAAGTGGAGTTAGATGGCTACACTTTG 303  
DB 256 TCTGTGACTGCGGGACAGCGCGGTATTAAGTGGAGTTAGATGGCTACACTTTG 315  
QY 304 GACATCTGGGGCCAGGGAAACCTGTGTCAACCGTCTCTCA 342  
DB 316 GACTACTGGGGCCAGGGAAACCTGTGTCAACCGTCTCTCA 354  
RESULT 9  
ID ADR68545 standard; DNA; 354 BP.  
XX ADR68545;  
AC  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Anti-EPO-R-antibody heavy chain variable region DNA seqid 42.  
DB  
XX  
KW antianaemic; respiratory; vulnerary; gene therapy; vaccine;  
KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
KW wound healing; neural cell damage; tissue damage; brain injury;



XX	spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;	
XX	variable region; ds	
OS	Homo sapiens.	
XX		
PN	US2004175379-A1.	
XX		
PD	09-SEP-2004.	
XX		
PF	10-OCT-2003; 2003US-00684109.	
XX		
PR	14-OCT-2002; 2002US-0418031P.	
XX		
PA	(DEVIR/) DEVIRIES P. J.	
PA	(OSTR/) OSTROW D. H.	
PA	(REIL/) REILLY E. B.	
PA	(GREE/) GREEN J. L.	
XX	(WIEL/) WIELER J.	
PI	Deviries PJ, Ostrow DH, Reilly EB, Green JL, Wieler J;	
DR	WPI: 2004-661369/64.	
DR	P-PSDB; ADR68546.	
XX		
PT	New antibody or its antibody fragment that activates an	
PT	activity or is capable of binding to a human erythropoietin receptor in a	
PT	mammal, useful for treating a mammal suffering aplasia or anemia.	
PS	Claim 47; SEQ ID NO 42; 156pp; English.	
XX		
XX	The invention describes an antibody or its fragment that activates an	
CC	endogenous activity or capable of binding to a human erythropoietin	
CC	receptor in a mammal, or that comprises at least one heavy or light chain	
CC	variable region having a sequence comprising 116 or 107 amino acids (SEQ	
CC	ID NO: 3 or 5) given in the specification or its fragment, but does not	
CC	interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also	
CC	given in the specification. Also described are: a method of activating or	
CC	modulating an endogenous activity of a human erythropoietin receptor in a	
CC	mammal; a pharmaceutical composition comprising a therapeutic amount of	
CC	an antibody or antibody fragment above and a pharmaceutical excipient; an	
CC	isolated and purified polynucleotide sequence selected from 28 sequences	
CC	comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in	
CC	the specification, and their fragments, complements, and degenerate codon	
CC	equivalents; and an isolated and purified amino acid sequence selected	
CC	from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between	
CC	SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or	
CC	their fragments. The antibody or its antibody fragment that activates or	
CC	modulates the activity of the receptor is useful in a method of treating for	
CC	a mammal suffering aplasia or anemia. The antibodies are also useful for	
CC	treating disorders characterised by decreased or subnormal levels of	
CC	oxygen in the blood or tissue such as hypoxemia or chronic tissue	
CC	hypoxia and/or diseases characterised by inadequate blood circulation or	
CC	reduced blood flow. They are also useful for promoting wound healing or	
CC	for protecting against neural cell and/or tissue damage, resulting from	
CC	brain/spinal cord injury, stroke and the like. The antibodies are also	
CC	useful for identifying or diagnosing mammals having dysfunctional	
CC	erythropoietin receptor. This sequence encodes an anti-EPO-R-antibody	
CC	heavy chain variable region.	
XX		
XX		
SO	Sequence 354 BP, 76 A, 105 C, 97 G, 76 T, 0 U, 0 Other;	
QY	Query Match 78.5%; Score 260.6; DB 13; Length 354;	
QY	Best Local Similarity 87.0%; Pred. No. 5e-67;	
QY	Matches 295; Conservative 0; Mismatches 44; Indels 0; Gaps 0	
Db		
4	GAGTCTGGCCGACGACTGGTTGAAGCCTGACAGACCCCTGCTCTAGCTGCGCTCTCT 63	
16	GAGTGGGGCCGACGACTGGTGAAGCCTTACAGACCCCTGCTCTCTACCTGCACTGCTCT 75	
64	GCGGCTCCATCCGACGAGTGTGTACTACTGAGTGTGATCGCCACACCCAGGGAAG 123	
76	GGTGGCTCATGACGAGTGTGTCTTACTACTGAGTGTGATCGCCACAGACCCAGGGAAG 135	

OY	124	GGCCGGAAGTGGATTGGGTATCATCTATACAGTGGAAACACCTAACAAACCCGTC	183
DB	136	GCCCTGAGTGGATTGGGTATCTATTAAGATGAGACTCTTACTACAAACCCGTC	195
OY	184	AAGAGTCAATTGGCCATGTCGGTAGACACGTCCTGGAACAAGTCTCCCTGAGCTGAAC	243
DB	196	AAGAGTCACTTACCTCATCTAGTAGACACGTTTAGAACAAGTCTCCCTGAACCTGATC	255
OY	244	TCTGTGACTGCGCGGACACGCGCCGTATTACTGTGCGAGGTTAGATGCTACACTTGG	303
DB	256	TCTGTGACTGCGCGGACACGCGCCGTATTAATTGTGCGAGAGATAAACTGGGAGTCGCG	315
OY	304	GACATCTGGGGCCAGGGAACCTGTGACCCGTCCTCTCA	342
DB	316	GACTACTGGGGCCAGGGAACCTGTGACCCGTCCTCTCA	354
RESULT 10			
AD	ADS84454/c		
ID	ADS84454 standard; DNA; 1996 BP.		
XX	AD	ADS84454;	
XX	AC		
XX	DT	18-NOV-2004 (first entry)	
DE	DE	Human anti-EPO-R antibody Ab412 heavy chain complementary DNA SEQ ID:93.	
XX	XX		
KW	KW	human; erythropoietin receptor; EPO receptor;	
KW	KW	erythropoietin receptor binding antibody; EPO receptor binding antibody;	
KW	KW	antianemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;	
KW	KW	wound healing; neural cell damage protection;	
KW	KW	neural tissue damage protection; brain injury; spinal cord injury;	
KW	KW	stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;	
XX	XX	ds.	
OS	OS	Homo sapiens.	
XX	XX		
XX	XX	WO2004035603-A2.	
XX	XX		
XX	XX	29-APR-2004.	
XX	XX		
PF	PF	14-OCT-2003; 2003WO-US032243.	
XX	XX		
PR	PR	14-OCT-2002; 2002US-00269711.	
XX	XX		
PR	PR	10-OCT-2003; 2003US-00684109.	
XX	XX		
PA	PA	(ABBO ) ABBOTT LAB.	
XX	XX		
PI	PI	Devries PJ, Green LL, Ostrow DH, Reilly EB, Wiewler J;	
XX	XX		
DR	DR	WPI; 2004-34843/32.	
XX	XX		
DR	DR	P-PSDB; ADS84455.	
XX	XX		
PT	PT	New antibodies that bind to or activate an endogenous human	
PT	PT	erythropoietin receptor, useful for diagnosing, preventing or treating	
PT	PT	disorders associated with dysfunctional erythropoietin receptor, e.g.	
PT	PT	anemia.	
XX	XX		
PS	PS	Disclosure: SEQ ID NO 93; 192pb; English.	
XX	XX		
CC	CC	The present invention describes an antibody or its fragment that binds to	
CC	CC	or activates an endogenous activity of a human erythropoietin (EPO)	
CC	CC	receptor in a mammal, but does not interact with a peptide having a	
CC	CC	sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)	
CC	CC	method of modulating or activating an endogenous activity of a human EPO	
CC	CC	receptor in a mammal, comprising administering to the mammal a	
CC	CC	therapeutic amount of the above antibody or its fragment to modulate or	
CC	CC	activate the receptor; (2) a method of treating a mammal suffering from	
CC	CC	aplasia, comprising administering to the mammal a therapeutic amount of	
CC	CC	the above antibody or its fragment to modulate or activate the receptor;	
CC	CC	(3) a pharmaceutical composition comprising a therapeutic amount of the	
CC	CC	above antibody or antibody fragment, and a pharmaceutical excipient; (4)	
CC	CC	an isolated and purified polynucleotide sequence, and their fragments,	

CC complements and degenerate codon equivalents; and (5) an isolated and  
CC purified amino acid sequence, and their fragments. The EPO receptor  
CC binding antibody has antineutropenic, neuroprotective and vulnary  
CC activities, and can be used in gene therapy. The compositions and methods  
CC from the present invention can be used for modulating an endogenous  
CC activity of a human EPO receptor or for treating mammals suffering from  
CC aplasia or anaemia. They may also be used for identifying mammals having  
CC a dysfunctional EPO receptor. The composition may also be used in  
CC promoting wound healing or in protecting against neural cell and/or  
CC tissue damage resulting from brain/spinal cord injury, stroke and the  
CC like. The present sequence represents a human anti-EPO-R antibody heavy  
CC chain complementary DNA sequence, which is given in the exemplification  
CC of the present invention.

XX  
XX Sequence 1996 BP; 351 A; 537 C; 686 G; 422 T; 0 U; 0 Other;

Query Match 78.5%; Score 268.6; DB 13; Length 1996;  
Best Local Similarity 87.0%; Pred. No. 8.1e-67;  
Matches 295; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 4 GAGCTCTGGCCAGAGCTGTGTAAGCCCTGACAGACCCCTGCTCAGCTGCTGCTCT 63  
Db 1924 GAGTCGGGGCCAGAGCTGTGTAAGCCCTGACAGACCCCTGCTCAGCTGCTGCTCT 1865

QY 64 GGGGGCTTCATCCGAGTGTGTTACTGAGTGGATCCGCCAACACCCAGGGAAG 123  
Db 1864 GGTGGCTTCATCCAGAGTGTGTTACTGAGTGGATCCGCCAACACCCAGGGAAG 1805

QY 124 GGGCTGAGAGTGGATGGTGCATCTATCAAGTGGGAACCTTCAACACCCCTGCTC 183  
Db 1804 GGGCTGAGAGTGGATGGTGCATCTATTAAGTGAAGACCTTCTCAACACCCCTGCTC 1745

QY 184 AAGAGTGAATTGGCATGTGCTGAGACACGTCGTGAGAACAGTCTCCCTGAGGCTGAC 243  
Db 1744 AAGAGTGAATTGGCATGTGCTGAGACACGTCGTGAGAACAGTCTCCCTGAGGCTGAC 1685

QY 244 TCTGTGACTGCGCGGACAGCGCCGTGTATTACTGTGCGAGGTAGATGCTACACTTTG 303  
Db 1684 TCTGTGACTGCGCGGACAGCGCCGTGTATTACTGTGCGAGGTAGATGCTGCGCG 1625

QY 304 GACATCTGGGGCCAGGGAACCTGTGTCACCGCTCTCCCTCA 342  
Db 1624 GACATCTGGGGCCAGGGAACCTGTGTCACCGCTCTCCCTCA 1586

RESULT 11  
ID ADS84453 standard; DNA; 1996 BP.  
AC ADS84453;  
XX 18-NOV-2004 (first entry)  
DT XX  
DE Human anti-EPO-R antibody Ab412 heavy chain DNA SEQ ID NO:92.  
XX  
XX human; erythropoietin receptor; EPO receptor;  
KM erythropoietin receptor binding antibody; EPO receptor binding antibody;  
KM antineutropenic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;  
KM wound healing; neural cell damage protection;  
KM neural tissue damage protection; brain injury; spinal cord injury;  
KM stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;  
KM ds.  
XX  
XX Homo sapiens.  
OS  
PN WO2004035603-A2.  
XX  
PD 29-APR-2004.  
XX  
PF 14-OCT-2003; 2003WO-US032243.  
XX  
PR 14-OCT-2002; 2002US-00269711.  
PR 10-OCT-2003; 2003US-00684109.

XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Deviles PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;  
XX WPI; 2004-348433/32.  
XX P-PSDB; ADS84455.  
XX  
PT New antibodies that bind to or activate an endogenous human  
PT erythropoietin receptor, useful for diagnosing, preventing or treating  
PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
PT anemia.  
XX  
XX Disclosure; SEQ ID NO 92; 192bp; English.

XX  
PS The present invention describes an antibody or its fragment that binds to  
CC or activates an endogenous activity of a human erythropoietin (EPO)  
CC receptor in a mammal, but does not interact with a peptide having a  
CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
CC methods of modulating or activating an endogenous activity of a human EPO  
CC receptor in a mammal, comprising administering to the mammal a  
CC therapeutic amount of the above antibody or its fragment to modulate or  
CC activate the receptor; (2) a method of treating a mammal suffering from  
CC aplasia, comprising administering to the mammal a therapeutic amount of  
CC the above antibody or its fragment to modulate or activate the receptor;  
CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
CC an isolated and purified polynucleotide sequence, and their fragments,  
CC complements and degenerate codon equivalents; and (5) an isolated and  
CC purified amino acid sequence, and their fragments. The EPO receptor  
CC binding antibody has antineutropenic, neuroprotective and vulnary  
CC activities, and can be used in gene therapy. The compositions and methods  
CC from the present invention can be used for modulating an endogenous  
CC activity of a human EPO receptor or for treating mammals suffering from  
CC aplasia or anaemia. They may also be used for identifying mammals having  
CC a dysfunctional EPO receptor. The composition may also be used in  
CC promoting wound healing or in protecting against neural cell and/or  
CC tissue damage resulting from brain/spinal cord injury, stroke and the  
CC like. The present sequence encodes a human anti-EPO-R antibody heavy  
CC chain, which is given in the exemplification of the present invention.

XX  
SQ Sequence 1996 BP; 422 A; 686 C; 537 G; 351 T; 0 U; 0 Other;

Query Match 78.5%; Score 268.6; DB 13; Length 1996;  
Best Local Similarity 87.0%; Pred. No. 8.1e-67;  
Matches 295; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 4 GAGCTCTGGCCAGAGCTGTGTAAGCCCTGACAGACCCCTGCTCAGCTGCTGCTCT 63  
Db 73 GAGTCGGGGCCAGAGCTGTGTAAGCCCTTCAAGACCCCTGCTCAGCTGCTCT 132

QY 64 GGGGGCTTCATCCGAGTGTGTTACTGAGTGGATCCGCCAACACCCAGGGAAG 123  
Db 133 GGTGGCTTCATCCAGAGTGTGTTACTGAGTGGATCCGCCAACACCCAGGGAAG 192

QY 124 GGGCTGAGAGTGGATGGTGCATCTATCAAGTGGGAACCTTCAACACCCCTGCTC 183  
Db 193 GGGCTGAGAGTGGATGGTGCATCTATTAAGTGAAGACCTTCTCAACACCCCTGCTC 252

QY 184 AAGAGTGAATTGGCATGTGCTGAGACACGTCGTGAGAACAGTCTCCCTGAGGCTGAC 243  
Db 253 AAGAGTGAATTGGCATGTGCTGAGACACGTCGTGAGAACAGTCTCCCTGAGGCTGAC 312

QY 244 TCTGTGACTGCGCGGACAGCGCCGTGTATTACTGTGCGAGGTAGATGCTACACTTTG 303  
Db 313 TCTGTGACTGCGCGGACAGCGCCGTGTATTATTGTGCGAGGTAGATGCTGCGCG 372

QY 304 GACATCTGGGGCCAGGGAACCTGTGTCACCGCTCTCCCTCA 342  
Db 373 GACATCTGGGGCCAGGGAACCTGTGTCACCGCTCTCCCTCA 411

RESULT 12



CC The invention describes an antibody or its fragment that activates an  
CC endogenous activity or capable of binding to a human erythropoietin  
CC receptor in a mammal, or that comprises at least one heavy or light chain  
CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
CC given in the specification. Also described are: a method of activating or  
CC modulating an endogenous activity of a human erythropoietin receptor in a  
CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
CC isolated and purified polynucleotide sequence selected from 28 sequences  
CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in  
CC the specification, and their fragments, complements, and degenerate codon  
CC equivalents; and an isolated and purified amino acid sequence selected  
CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between  
CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
CC their fragments. The antibody or its antibody fragment that activates or  
CC modulates the activity of the receptor is useful in a method of treating  
CC a mammal suffering aplasia or anaemia. The antibodies are also useful for  
CC treating disorders characterised by decreased or subnormal levels of  
CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
CC hypoxia and/or diseases characterised by inadequate blood circulation or  
CC reduced blood flow. They are also useful for promoting wound healing or  
CC for protecting against neural cell and/or tissue damage, resulting from  
CC brain/spinal cord injury, stroke and the like. The antibodies are also  
CC useful for identifying or diagnosing mammals having dysfunctional  
CC erythropoietin receptor. This sequence represents a human Ab412 antibody  
CC heavy chain polynucleotide.

XX Sequence 1996 BP; 351 A; 537 C; 686 G; 422 T; 0 U; 0 Other;

Query Match 78.5%; Score 268.6; DB 13; Length 1996;

Best Local Similarity 87.0%; Pred. No. 8.1e-67; Matches 295; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 4 GAGTCTGCCCCAGAGCTGTGGAAGCCGACAGACCCGTCCTCAGCTGCGTCTCT 63  
DB 1924 GAGTCGGGCCCAAGACTGTGTGAAGCCCTTCACAGACCCTGCTCCACCTGACATGCTCT 1865  
QY 64 GGGCGCTCCATCCGACAGTGTGTGTTACTACTGAGTGTGATCCGCCAACCCAGGAG 123  
DB 1864 GGTGGCTCCATCAGCACTGGTGTCTTACTACTGAGTGTGATCCGCCAACCCAGGAG 1805  
QY 124 GGCCTGAGTGTGATGGGTATCATCTATCAAGTGGGAACACTTAAACCCGTCCTC 183  
DB 1804 GGCCTGAGTGTGATGGGTATCATCTATCAAGTGGGAACACTTAAACCCGTCCTC 1745  
QY 184 AAGAGTGAATTGGCATGTGGTGTAGACAGCTGTGAACAAGTTCTCCGAGGCTGAC 243  
DB 1744 AAGAGTGAATTGGCATGTGGTGTAGACAGCTGTGAACAAGTTCTCCGAGGCTGAC 1685  
QY 244 TCTGTGACTGCGCGGAGACAGCGCGGTATATTACTGTGCGAGGTTAGATGCTACATTTTG 303  
DB 1684 TCTGTGACTGCGCGGAGACAGCGCGGTATATTACTGTGCGAGGTTAGATGCGG 1625  
QY 304 GACATCTGGGGCCAGGGAACCTGTGTCAACGCTCTCTCA 342  
DB 1624 GACATCTGGGGCCAGGGAACCTGTGTCAACGCTCTCTCA 1586

RESULT 14  
ADK52387  
ID ADK52387 standard; DNA, 560 BP.

XX ADK52387;

XX 20-MAY-2004 (first entry)

DE Human anti-MCP-1 variable region heavy chain DNA sequence #24.  
XX monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
KM Antineoplastic; Nephrotoxic; Antiarteriosclerotic; Antiproliferative;  
KM Vasotrophic; Immunosuppressive; Neuroprotective; Neoplastic;

KW inflammatory condition; cancer; arthritis; multiple sclerosis; de;  
KM anti-MCP-1; heavy chain; light chain.

XX Homo sapiens.

XX W02004016769-A2.

XX 26-FEB-2004.

PF 19-AUG-2003; 2003WO-US026232.

XX 19-AUG-2002; 2002US-0404802P.

PA (ABGE-) ABGENIX INC.

PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K,

DR WPI; 2004-203794/19.

XX P-P-SDB; ADK52388.

PT New human monoclonal antibody that binds to monocyte chemo-attractant  
PT protein-1 and is immobilized on an insoluble matrix, useful for  
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
PT rheumatoid arthritis or psoriasis.

PS Disclosure; SEQ ID NO 93; 154pp; English.

XX The present invention relates to a human monoclonal antibody that binds  
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
CC for the preparation of a medicament useful for treating neoplastic or  
CC inflammatory conditions. The neoplastic disease is selected from breast  
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer or prostate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for the determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region heavy chain DNA sequence.

XX Sequence 560 BP; 106 A; 191 C; 151 G; 112 T; 0 U; 0 Other;

Query Match 78.3%; Score 267.8; DB 12; Length 560;

Best Local Similarity 88.0%; Pred. No. 9.6e-67; Matches 307; Conservative 0; Mismatches 32; Indels 10; Gaps 1;

QY 4 GAGTCTGCCCCAGAGCTGTGGAAGCCGTCACAGACCCGTCCTCAGCTGCGTCTCT 63  
DB 16 GAGTCGGGCCCAAGACTGTGTGAAGCCGTCACAGACCCGTCCTCAGCTGCTCTCT 75  
QY 64 GGGCGCTCCATCCGACAGTGTGTGTTACTACTGAGTGTGATCCGCCAACCCAGGAG 123  
DB 76 GGTGGCTCCATCAGCACTGGTGTCTTACTACTGAGTGTGATCCGCCAACCCAGGAG 135  
QY 124 GGCCTGAGTGTGATGGGTATCATCTATCAAGTGGGAACACTTAAACCCGTCCTC 183  
DB 136 GGCCTGAGTGTGATGGGTATCATCTATCAAGTGGGAACACTTAAACCCGTCCTC 195  
QY 184 AAGAGTGAATTGGCATGTGGTGTAGACAGCTGTGAACAAGTTCTCCGAGGCTGAC 243  
DB 196 AAGAGTGAATTGGCATGTGGTGTAGACAGCTGTGAACAAGTTCTCCGAGGCTGAC 255  
QY 244 TCTGTGACTGCGCGGAGACAGCGCGGTATATTACTGTGCGAGGTTAGATGCTACATTTTG 293  
DB 256 TCTGTGACTGCGCGGAGACAGCGCGGTATATTACTGTGCGAGGTTAGATGCTGCTCC 315  
QY 294 CTAACATTTGAGATCTGGGGCCAGGGAACCTGTGTCAACGCTCTCTCA 342  
DB 316 CTAACATTTGAGATCTGGGGCCAGGGAACCTGTGTCAACGCTCTCTCA 364

Search completed: July 27, 2005, 05:59:43  
Job time : 325.618 secs

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RESULT 15
AAF29046
ID AAF29046 standard; DNA; 369 BP.
XX
XX AAF29046;
AC
XX
XX 03-APR-2001 (first entry)
DT
XX
DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 2.
XX
XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW envelope glycoprotein; gp120; diagnosis; ds.
XX
OS Homo sapiens.
XX
XX WO20010678-A1.
XX
XX 04-JAN-2001.
XX
XX 23-JUN-2000; 2000MO-US017327.
XX
XX 30-JUN-1999; 99US-0141701P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Watkins BA, Reitz MS;
XX
XX WPI; 2001-112438/12.
XX
XX P-PSDB; AAB62745.
XX
XX
XX Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal.
XX
XX
XX Claim 4; Page 34-35; 81pp; English.
XX
XX
XX The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection
XX
XX
XX Sequence 369 BP; 75 A; 104 C; 107 G; 83 T; 0 U; 0 Other;
SQ
Query Match 77.7%; Score 265.8; DB 4; Length 369;
Best Local Similarity 87.5%; Pred. No. 3.2e-66;
Matches 307; Conservative 0; Mismatches 32; Indels 12; Gaps 1;
QY 4 GAGCTGGCCGAGAGCTGTGTAAGCCCTGACAGACCCCTGCTCAGCTGGCTGCTCT 63
Db 19 GAGTCGAGCCGAGAGCTGTGTAAGCCCTGACAGACCCCTGCTCAGCTGGCTGCTCT 78
QY 64 GGCAGCTCCATCCGAGTGTGTTACTACTGAGTTGATCCGCCAACACCCAGGGAAG 123
Db 79 GGTGGCTCCATCAGAGTGTGTTACTACTGAGTGTGATCCGCCAACACCCAGGGAAG 138
QY 124 GGCCTGAGTGTGATTTGGTACATCTATCAGAGTGGGAACACCTTACAAACCCGTCCTC 183
Db 139 GGCCTGAGTGTGATTTGGTACATCTATCAGAGTGGGAACACCTTACAAACCCGTCCTC 198
QY 184 AAGAGTGAATTGGCATGTGCTAGACACGCTGAGAACCAAGTCTCCCTGAGGCTGAAC 243
Db 199 AAGAGTGAATTGATTCATATCAATAGACACGCTAAGAACCAAGTCTCCCTGAGGCTGAGC 258
QY 244 TCTGTGACTGCGCGGAGACACGCGGTATTTACTGTGCGAGG-----TTAGAT 291
Db 259 TCTGTGACTGCGCGGAGACACGCGGTATTTACTGTGCGAGGCGCGGTATTTGTGTGTGT 318
QY 292 GGCCTACACTTTGGCATTTGGGGCAGGGAACCCCTGTCAACCGTCTCTCA 342
Db 319 GATTGCTCTCTTGTACTACTGAGGCGCAAGGAACCCCTGTCAACCGTCTCTCA 369

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Qy 1 CTCGAGTCTGGCCAGGACTGGTAAGCCCTGCACAGCCCTGTCCCTCACTGGCGCTGC 60

Db 1 CTCGAGTCTGGCCAGGACTGGTAAGCCCTGCACAGCCCTGTCCCTCACTGGCGCTGC 60

Qy 61 TCTGGCGGCTCATCCGACGTGGTGGTTACTCTGAGTTGGATCCGCCAACACCCAGGG 120

Db 61 TCTGCGGCTCCATCCGAGTGTGTTACTGAGATTGGATCCGCCAACACCCAGGG 120  
Qy 121 AAGGCGCTGGAGTGGATTGGGTACATCATACAGTGGGACACCTCAACAACCCGTC 180  
Db 121 AAGGCGCTGGAGTGGATTGGGTACATCATACAGTGGGACACCTCAACAACCCGTC 180  
Qy 181 CTCAAGAGTGGAAATTCATGCTGCTGAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240  
Db 181 CTCAAGAGTGGAAATTCATGCTGCTGAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240  
Qy 241 AACTCTGTGACTGCGCGGAGACAGCGCGGTGATTACTGTGCGAGGTTAGATGCTTACACT 300  
Db 241 AACTCTGTGACTGCGCGGAGACAGCGCGGTGATTACTGTGCGAGGTTAGATGCTTACACT 300  
Qy 301 TTGGACATCTGGGGCGAGGGAACCTGTGTCACCGTCTCCCTCA 342  
Db 301 TTGGACATCTGGGGCGAGGGAACCTGTGTCACCGTCTCCCTCA 342

## RESULT 2

US-10-027-725A-3  
; Sequence 3, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 342  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-027-725A-3

Query Match 90.6%; Score 310; DB 14; Length 342;

Best Local Similarity 94.2%; Pred. No. 1e-90; Mismatches 20; Indels 0; Gaps 0;

Matches 322; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CTCGAGTCTGGCCCGAGAGTGTGTAAGCTCAGACAGACCTGTCCCTCAGCTGCGCTGTC 60  
Db 1 CTCGAGTCTGGCCCGAGAGTGTGTAAGCTCAGACAGACCTGTCCCTCAGCTGCGCTGTC 60  
Qy 61 TCTGCGGCTTCATCCGAGTGTGTTACTACTGAGATTGAGTCCGCCAACACCCAGGG 120  
Db 61 TCTGCGGCTTCATCCGAGTGTGTTACTACTGAGATTGAGTCCGCCAACACCCAGGG 120  
Qy 121 AAGGCGCTGGAGTGGATTGGGTACATCATACAGTGGGAAACACTTAACAACCCGTC 180  
Db 121 AAGGCGCTGGAGTGGATTGGGTACATCATACAGTGGGAAACACTTAACAACCCGTC 180  
Qy 181 CTCAAGAGTGGAAATTCATGCTGCTGAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240  
Db 181 CTCAAGAGTGGAAATTCATGCTGCTGAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240  
Qy 241 AACTCTGTGACTGCGCGGAGACAGCGCGGTGATTACTGTGCGAGGTTAGATGCTTACACT 300  
Db 241 AACTCTGTGACTGCGCGGAGACAGCGCGGTGATTACTGTGCGAGGTTAGATGCTTACACT 300  
Qy 301 TTGGACATCTGGGGCGAGGGAACCTGTGTCACCGTCTCCCTCA 342  
Db 301 TTGGACATCTGGGGCGAGGGAACCTGTGTCACCGTCTCCCTCA 342

## RESULT 3

US-10-027-725A-2  
; Sequence 2, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:

; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 342  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-027-725A-2

Query Match 87.4%; Score 298.8; DB 14; Length 342;

Best Local Similarity 92.1%; Pred. No. 4.6e-87; Mismatches 27; Indels 0; Gaps 0;

Matches 315; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 CTCGAGTCTGGCCCGAGAGTGTGTAAGCTCAGACAGACCTGTCCCTCAGCTGCGCTGTC 60  
Db 1 CTCGAGTCTGGCCCGAGAGTGTGTAAGCTCAGACAGACCTGTCCCTCAGCTGCGCTGTC 60  
Qy 61 TCTGCGGCTTCATCCGAGTGTGTTACTACTGAGATTGAGTCCGCCAACACCCAGGG 120  
Db 61 TCTGCGGCTTCATCCGAGTGTGTTACTACTGAGATTGAGTCCGCCAACACCCAGGG 120  
Qy 121 AAGGCGCTGGAGTGGATTGGGTACATCATACAGTGGGAAACACTTAACAACCCGTC 180  
Db 121 AAGGCGCTGGAGTGGATTGGGTACATCATACAGTGGGAAACACTTAACAACCCGTC 180  
Qy 181 CTCAAGAGTGGAAATTCATGCTGCTGAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240  
Db 181 CTCAAGAGTGGAAATTCATGCTGCTGAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240  
Qy 241 AACTCTGTGACTGCGCGGAGACAGCGCGGTGATTACTGTGCGAGGTTAGATGCTTACACT 300  
Db 241 AACTCTGTGACTGCGCGGAGACAGCGCGGTGATTACTGTGCGAGGTTAGATGCTTACACT 300  
Qy 301 TTGGACATCTGGGGCGAGGGAACCTGTGTCACCGTCTCCCTCA 342  
Db 301 TTGGACATCTGGGGCGAGGGAACCTGTGTCACCGTCTCCCTCA 342

## RESULT 4

US-10-330-613-15  
; Sequence 15, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudes, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ARGENTIX 022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 352  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-10-330-613-15

Query Match 80.4%; Score 275; DB 15; Length 352;

Best Local Similarity 90.3%; Pred. No. 2.6e-79; Mismatches 30; Indels 3; Gaps 1;

Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

Qy 4 GAGTCTGAGCCAGGAGTGTGTAAGCTCAGACAGACCTGTCCCTCAGCTGCGCTGTC 63  
Db 16 GAGTCTGAGCCAGGAGTGTGTAAGCTTTCACAGACCTGTCCCTCAGCTGCGCTGTC 75  
Qy 64 GCGGCTTCATCCGAGTGTGTTACTACTGAGATTGATCCGCCAACCCAGGAGG 123



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Db 76 GGTGCTCCATCAGACAGTGGTGTACTACTGAGCTTGGATCCCGCCAGACCCAGGAG 135
Qy 124 GGCCTGAGTGGATTTGGGTATCTATCAAGTGGGAACCTTACAAACCCGCTCCCTC 183
Db 136 GGCCTGAGTGGATTTGGGTATCTATCAAGTGGGAACCTTACAAACCCGCTCCCTC 195
Qy 184 AAGAGTGAATGGCATGTGGGTAGACAGCTGTAGAACAAAGTTCTCCCTGAGGCTGAC 243
Db 196 AAGAGTGAATGGCATGTGGGTAGACAGCTGTAGAACAAAGTTCTCCCTGAGGCTGAC 255
Qy 244 TCTGTGACTGCGCGGACAGCGCGGTATTAATCTGTGCGAGAGTTAGATGCTACATTTG 303
Db 256 TCTGTGACTGCGCGGACAGCGCGGTATTAATCTGTGCGAGAGTTAGATGCTACATTTG 312
Qy 304 GACATCTGGGGCCAGGGAACCTGTGTACACCGTCTCTCA 342
Db 313 GACTACTGGGGCCAGGGAACCTGTGTACACCGTCTCTCA 351
```

RESULT 5  
US-10-330-530-15  
; Sequence 15, Application US/10330530  
; Publication No. US20030152514A1  
; GENERAL INFORMATION:

APPLICANT: Gude, Jean  
TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES  
FILE REFERENCE: AGENIX.031A  
CURRENT APPLICATION NUMBER: US/10/330.530  
CURRENT FILING DATE: 2002-12-26  
PRIOR APPLICATION NUMBER: US 60/346414  
PRIOR FILING DATE: 2001-12-18  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 352  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-10-330-530-15

Query Match 80.4%; Score 275; DB 16; Length 352;  
Best Local Similarity 90.3%; Pred. No. 2.6e-79;

Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

```
Qy 4 GAGTCTGCCCCAGAGCTGTGTGAAGCTGTGACAGACCCCTGTCTCTGAGTGTCTCT 63
Db 16 GAGTCTGCCCCAGAGCTGTGTGAAGCTGTGACAGACCCCTGTCTCTGAGTGTCTCT 75
Qy 64 GCGGCTCCATCCGACAGTGTGTACTACTGAGTTGGATCCGCCAACCAGGGAG 123
Db 76 GGTGCTCCATCAGACAGTGGTGTACTACTGAGTTGGATCCGCCAACCAGGGAG 135
Qy 124 GGCCTGAGTGGATTTGGGTATCTATCAAGTGGGAACCTTACAAACCCGCTCCCTC 183
Db 136 GGCCTGAGTGGATTTGGGTATCTATCAAGTGGGAACCTTACAAACCCGCTCCCTC 195
Qy 184 AAGAGTGAATGGCATGTGGGTAGACAGCTGTAGAACAAAGTTCTCCCTGAGGCTGAC 243
Db 196 AAGAGTGAATGGCATGTGGGTAGACAGCTGTAGAACAAAGTTCTCCCTGAGGCTGAC 255
Qy 244 TCTGTGACTGCGCGGACAGCGCGGTATTAATCTGTGCGAGAGTTAGATGCTACATTTG 303
Db 256 TCTGTGACTGCGCGGACAGCGCGGTATTAATCTGTGCGAGAGTTAGATGCTACATTTG 312
Qy 304 GACATCTGGGGCCAGGGAACCTGTGTACACCGTCTCTCA 342
Db 313 GACTACTGGGGCCAGGGAACCTGTGTACACCGTCTCTCA 351
```

RESULT 6  
US-10-660-357-15  
; Sequence 15, Application US/10660357  
; Publication No. US20040115205A1

GENERAL INFORMATION:  
APPLICANT: Bar-Eli, Menashe  
APPLICANT: Green, Larry L.  
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18  
FILE REFERENCE: AGENIX.030C1  
CURRENT APPLICATION NUMBER: US/10/660.357  
CURRENT FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 10/350,580  
PRIOR FILING DATE: 2002-12-26  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 352  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-10-660-357-15

Query Match 80.4%; Score 275; DB 19; Length 352;  
Best Local Similarity 90.3%; Pred. No. 2.6e-79;

Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

```
Qy 4 GAGTCTGCCCCAGAGCTGTGTGAAGCTGTGACAGACCCCTGTCTCTGAGTGTCTCT 63
Db 16 GAGTCTGCCCCAGAGCTGTGTGAAGCTGTGACAGACCCCTGTCTCTGAGTGTCTCT 75
Qy 64 GCGGCTCCATCCGACAGTGTGTACTACTGAGTTGGATCCGCCAACCAGGGAG 123
Db 76 GGTGCTCCATCAGACAGTGGTGTACTACTGAGTTGGATCCGCCAACCAGGGAG 135
Qy 124 GGCCTGAGTGGATTTGGGTATCTATCAAGTGGGAACCTTACAAACCCGCTCCCTC 183
Db 136 GGTGCTCCATCAGACAGTGGTGTACTACTGAGTTGGATCCGCCAACCAGGGAG 195
Qy 184 AAGAGTGAATGGCATGTGGGTAGACAGCTGTAGAACAAAGTTCTCCCTGAGGCTGAC 243
Db 196 AAGAGTGAATGGCATGTGGGTAGACAGCTGTAGAACAAAGTTCTCCCTGAGGCTGAC 255
Qy 244 TCTGTGACTGCGCGGACAGCGCGGTATTAATCTGTGCGAGAGTTAGATGCTACATTTG 303
Db 256 TCTGTGACTGCGCGGACAGCGCGGTATTAATCTGTGCGAGAGTTAGATGCTACATTTG 312
Qy 304 GACATCTGGGGCCAGGGAACCTGTGTACACCGTCTCTCA 342
Db 313 GACTACTGGGGCCAGGGAACCTGTGTACACCGTCTCTCA 351
```

RESULT 7  
US-10-684-109-42

; Sequence 42, Application US/10684109  
; Publication No. US20040175379A1

GENERAL INFORMATION:

APPLICANT: DeVries, Peter J.  
APPLICANT: Green, Larry L.  
APPLICANT: Oestrow, David H.  
APPLICANT: Reilly, Edward B.

TITLE OF INVENTION: Erythropoietin Receptor Binding  
FILE REFERENCE: 6989 US.02

CURRENT APPLICATION NUMBER: US/10/684.109

PRIOR FILING DATE: 2003-10-10

PRIOR APPLICATION NUMBER: 10/269,711

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 42

LENGTH: 354

TYPE: DNA

ORGANISM: Homo sapiens

US-10-684-109-42

Query Match 78.5%; Score 268.6; DB 19; Length 354;

[illegible]

```

RESULT 8
US-10-684-109-92
; Sequence 92, Application US/10684109
; Publication No. US2004017539A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Weller, James
; TITLE OF INVENTION: Antihypotetic Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989, US, 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-684-109-92

```

Query Match	78.5%	Score 268.6;	DB 19;	Length 1996;
Best Local Similarity	87.0%	Pred. No. 4.7e-77;		
Matches 295; Conservative	0;	Mismatches 44;	Indels 0;	Gaps 0;

OY	4	GAGTGTGCCCCAGACCTGGTGAAGGCTGGACAGACCCTTCCTCAGCTGGCGTGTCT	63
Db	73	GAGTGGGGCCAGAGACTGTGAAGCCTTACAGACCCTTCCCTCACTGCACGTCTT	132
OY	64	GGCGGCTCCATCCGACGTGGTGTACTA CTGAGTTGGATCCGCCAACCCAGGGAAG	123
Db	133	GGTGCTCATCAGCAGTGGTGTCTTA CTAGAGTTGGATCCGCCAGCACCCAGGAAG	192
OY	124	GGCTCGAGTGGATTGGGTACATCTATCA CAGTGGGACACTCAACAACCCGTCCTC	183
Db	193	GGCTCGAGTGGATTGGGTACATCTATAAGATGAGACCTCTACTACAAACCCGTCCTC	252
OY	184	AAGAGTGAATTGGCATGTCCGATAGCACTGTGAGAAACAAGTCTCCCTGAGCGTGAAC	243
Db	253	AAGATGCACTTACCCCTTATCAGTATGACAGCTCTAAGAACACAGTCTCTCCCTGAACCTGAAC	312

Oy	244	TCGTGACACCGCGGACACAGCGCCGCTGATTAATCTAGTGGAGAGTTAGACGCTACATTTTG	303
Oy	244	TCGTGACACCGCGGACACAGCGCCGCTGATTAATCTAGTGGAGAGTTAGACGCTACATTTTG	303
Db	313	TCGTGACACCGCGGACACAGCGCCGCTGATTAATCTAGTGGAGAGATTAATCGGGATCGCG	372
Oy	304	GACATGTGGGCGAGAGAACTCTGTCAACCGTCTCCCA	342
Db	373	GACTTACTGGGGCCAGGAAACCTGTGTCAACCGTCTCTCCA	411

```

RESULT 9
US-10-684-109-93/c
; Sequence 93. Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Rellily, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989 US. 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Fasteq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-93

```

Query Match	78.5%;	Score 268.6;	DB 19;	Length 1996;
-------------	--------	--------------	--------	--------------

Matches	295	Conservative	0	Mismatches	44	Indels	0	Gaps	0
QY	4	GAGTCTGGCCAGGACGTGTGAAAGCCCTGCACAGACCCGTGTCCCTCAAGTGGCGTGTCTCT							63
Db	1924	GAGTCTGGGCGCCAGGACGTGTGAAAGCCCTTTCACAGACCCGTGTCCCTCAAGTGGCGTGTCTCT							1865
QY	64	GGCGGCTCCATCCGCGAGTGGTGTACTACTCGAGTGGATCCGCGCAACCCAGGGGAAG							123
Db	1864	GGTCCCTCCATCAGACAGAGTGGTGTACTACTCGAGTGGATCCCGCAGACCCAGGGGAAG							1805
QY	124	GGCCTGAGAGTGGATTTGGGTACATCTATCAACAGTGGAAACCTTCAACAAACCCGTCCTC							183
Db	1804	GGCCTGAGAGTGGATTTGGGTACATCTTAAAGAGTGAACCTCTACATCAACCCGTCCTC							1745
QY	184	AAGAGTCGAATTGTCATATGTCGTAGACACGTCTTGAGAAACATTTCTCCCTGAGGCTGAAC							243
Db	1744	AAGAGTCGACTTACCTCATCTACGTAGACACGCTTAAAGAACAGTTCTCCCTGAACCTGATC							1685
QY	244	TCTGTGACTGCGCGGGACACGGCCGTGTATTACTGTGTCCGAGGTAAAGATGGTAAACATTGG							303
Db	1684	TCTGTGACTGCGCGGGACACGGCCGTGTATTATTGTGTCCGAGATTAACCTGGGATCGCG							1625
QY	304	GACATCTGGGGCCAGGGAAACCGTGGTACACGGTCCCTCA							342
Db	1624	GACTACTGGGGCCAGGGAAACCTGTGTACACGGTCTCTCA							1586

RESULT 10  
US-10-644-277-93

Sequence 93, Application US/106442Z1  
Publication No. US20050058639A1  
GENERAL INFORMATION:  
APPLICANT: Gudaas, Dean M.  
APPLICANT: Haak-Frandscho, Mary  
APPLICANT: Foord, Orin  
APPLICANT: Liang, Meina L.  
APPLICANT: Ahluwalia, Kiran

5

```

; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; TITLE OF INVENTION: CHEMO-ANTITUMOR PROTEIN-1 (MCP-1) AND USES THEREOF
; FILE REFERENCE: AGENIX.091A
; CURRENT APPLICATION NUMBER: US/10/644,277
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-644-277-93

```

Query Match 78.3%; Score 267.8; DB 21; Length 560;  
 Best Local Similarity 88.0%; Pred. No. 6.5e-77;  
 Matches 307; Conservative 0; Mismatches 32; Indels 10; Gaps 1;

```

QY 4 GAGTCTGCGCCAGAGCTGTGTAAGCCCTGACAGACCCCTGCTCAGCTGCTCTCT 63
DB 16 GAGTCGGGCCCCAGAGCTGTGTAAGCCCTGACAGACCCCTGCTCAGCTGCTCTCT 75
QY 64 GCGGCTCCATCCGAGGTGTGTTACTACTGAGCTGTGATCCGACACCCAGGAG 123
DB 76 GGTGGCTCCATCCAGAGGTGTGTTACTACTGAGCTGTGATCCGACACCCAGGAG 135
QY 124 GCGCTGAGTGTGATGGGTATCATCTATCATAGTGGGAGACACCTCAACACCCGCTC 183
DB 136 GCGCTGAGTGTGATGGGTATCATCTATCATAGTGGGAGACACCTCAACACCCGCTC 195
QY 184 AAGAGTGAATTCATGTCGTGTGACACCGTGTGAACAAGTTCTCCCTGAGCTGAC 243
DB 196 AAGAGTGAATTCATGTCGTGTGACACCGTGTGAACAAGTTCTCCCTGAGCTGAC 255
QY 244 TCTGTGACTGCGCGGACACGCGGTGTATCTGTGAGAGTTAGATG----- 293
DB 256 TCTGTGACTGCGCGGACACGCGGTGTATCTGTGAGAGTTAGATG----- 315
QY 294 CTACATCTTGGACATCTGTGGGCGCAGGAAACCTGTGTCACGCTCTCTCA 342
DB 316 CCATCTGTTGACACCCCTGTGGGCGCAGGAAACCTGTGTCACGCTCTCTCA 364

```

```

RESULT 11
US-10-330-613-7
; Sequence 7, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-7

```

Query Match 77.6%; Score 265.4; DB 15; Length 352;  
 Best Local Similarity 88.5%; Pred. No. 3.6e-76;  
 Matches 300; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

```

QY 4 GAGTCTGCGCCAGAGCTGTGTAAGCCCTGACAGACCCCTGCTCAGCTGCTCTCT 63
DB 16 GAGTCGGGCCCCAGAGCTGTGTAAGCCCTGACAGACCCCTGCTCAGCTGCTCTCT 75

```

```

QY 64 GCGGCTCCATCCGAGGTGTGTTACTACTGAGCTGTGATCCGACACCCAGGAG 123
DB 76 GGTGGCTCCATCCAGAGGTGTGTTACTACTGAGCTGTGATCCGACACCCAGGAG 135
QY 124 GCGCTGAGTGTGATGGGTATCATCTATCATAGTGGGAGACACCTCAACACCCGCTC 183
DB 136 GCGCTGAGTGTGATGGGTATCATCTATCATAGTGGGAGACACCTCAACACCCGCTC 195
QY 184 AAGAGTGAATTCATGTCGTGTGACACCGTGTGAACAAGTTCTCCCTGAGCTGAC 243
DB 196 AAGAGTGAATTCATGTCGTGTGACACCGTGTGAACAAGTTCTCCCTGAGCTGAC 255
QY 244 TCTGTGACTGCGCGGACACGCGGTGTATCTGTGAGAGTTAGATG----- 303
DB 256 TCTGTGACTGCGCGGACACGCGGTGTATCTGTGAGAGTTAGATG----- 312
QY 304 GACATCTGGGGCGCAGGAGACCCCTGTGTCACCGTCTCTCA 342
DB 313 AAGTACTGGGGCGCAGGAGACCCCTGTGTCACCGTCTCTCA 351

```

```

RESULT 12
US-10-530-7
; Sequence 7, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: AGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-530-530-7

```

Query Match 77.6%; Score 265.4; DB 16; Length 352;  
 Best Local Similarity 88.5%; Pred. No. 3.6e-76;  
 Matches 300; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

```

QY 4 GAGTCTGCGCCAGAGCTGTGTAAGCCCTGACAGACCCCTGCTCAGCTGCTCTCT 63
DB 16 GAGTCGGGCCCCAGAGCTGTGTAAGCCCTTACAGACCCCTGCTCAGCTGCTCTCT 75
QY 64 GCGGCTCCATCCGAGGTGTGTTACTACTGAGCTGTGATCCGACACCCAGGAG 123
DB 76 GGTGGCTCCATCCAGAGGTGTGTTACTACTGAGCTGTGATCCGACACCCAGGAG 135
QY 124 GCGCTGAGTGTGATGGGTATCATCTATCATAGTGGGAGACACCTCAACACCCGCTC 183
DB 136 GCGCTGAGTGTGATGGGTATCATCTATCATAGTGGGAGACACCTCAACACCCGCTC 195
QY 184 AAGAGTGAATTCATGTCGTGTGACACCGTGTGAACAAGTTCTCCCTGAGCTGAC 243
DB 196 AAGAGTGAATTCATGTCGTGTGACACCGTGTGAACAAGTTCTCCCTGAGCTGAC 255
QY 244 TCTGTGACTGCGCGGACACGCGGTGTATCTGTGAGAGTTAGATG----- 303
DB 256 TCTGTGACTGCGCGGACACGCGGTGTATCTGTGAGAGTTAGATG----- 312
QY 304 GACATCTGGGGCGCAGGAGACCCCTGTGTCACCGTCTCTCA 342
DB 313 AAGTACTGGGGCGCAGGAGACCCCTGTGTCACCGTCTCTCA 351

```

```

RESULT 13
US-10-660-357-7
; Sequence 7, Application US/10660357

```

```
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030CI
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-7
```

```
Query Match 77.6%; Score 265.4; DB 19; Length 352;
Best Local Similarity 88.5%; Pred. No. 3.6e-76;
Matches 300; Conservative 0; Mismatches 36; Indels 3; Gaps 1;
```

```
OY 4 GAGTCTGGCCCGCAGAGCTGTGAAGCCTTGACAGACCCCTGCTCAGCTGGCTGTCTCT 63
DB 16 GAGTCGGGCCCGCAGAGCTGTGAAGCCTTGACAGACCCCTGCTCAGCTGTCTCT 75
OY 64 GCGGCTCCATCCGAGTGTGTACTACTGAGTTGATCCGCCAACCAGGGAG 123
DB 76 GGTGGCTCCATCCAGTGTGTACTACTGAGTTGATCCGCCAACCAGGGAG 135
OY 124 GCGCTGAGTGTGTGTGTGTATCATATCAAGTGGAAACACCTTCAACACCCGTCTC 183
DB 136 GCGCTGAGTGTGTGTGTGTATCATATCAAGTGGAAACACCTTCAACACCCGTCTC 195
OY 184 AAGAGTGAATTTGCATGTGGTGTAGACACGCTGAGAACAGTCTCTCCAGGCTGAG 243
DB 196 AAGAGTGAATTTGCATGTGGTGTAGACACGCTGAGAACAGTCTCTCCAGGCTGAG 255
OY 244 TCTGTGACTGCGCGGACACGCGGTGATTAATCTGTGCGAGGTTAGAGCTTAC 303
DB 256 TCTGTGACTGCGCGGACACGCGGTGATTAATCTGTGCGAGGTTAGAGCTTAC 312
OY 304 GACATCTGGGGCCAGAGAACCTTGTCACCGTCTCTCA 342
DB 313 AAGTACTGGGGCCAGAGAACCTTGTCACCGTCTCTCA 351
```

```
RESULT 14
US-10-330-613-27
; Sequence 27, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-27
```

```
Query Match 77.5%; Score 265.2; DB 15; Length 358;
Best Local Similarity 88.0%; Pred. No. 4.1e-76;
Matches 301; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
```

```
OY 4 GAGTCTGGCCCGCAGAGCTGTGAAGCCTTGACAGACCCCTGCTCAGCTGGCTGTCTCT 63
```

```
DB 16 GAGTCGGGCCCGCAGAGCTGTGAAGCCTTGACAGACCCCTGCTCAGCTGTCTCT 75
OY 64 GCGGCTCCATCCGAGTGTGTACTACTGAGTTGATCCGCCAACCAGGGAG 123
DB 76 GGTGGCTCCATCCAGTGTGTACTACTGAGTTGATCCGCCAACCAGGGAG 135
OY 124 GCGCTGAGTGTGTGTGTGTATCATATCAAGTGGAAACACCTTCAACACCCGTCTC 183
DB 136 GCGCTGAGTGTGTGTGTGTATCATATCAAGTGGAAACACCTTCAACACCCGTCTC 195
OY 184 AAGAGTGAATTTGCATGTGGTGTAGACACGCTGAGAACAGTCTCTCCAGGCTGAG 243
DB 196 AAGAGTGAATTTGCATGTGGTGTAGACACGCTGAGAACAGTCTCTCCAGGCTGAG 255
OY 244 TCTGTGACTGCGCGGACACGCGGTGATTAATCTGTGCGAGGTTAGAGCTTAC 300
DB 256 TCTGTGACTGCGCGGACACGCGGTGATTAATCTGTGCGAGGTTAGAGCTTAC 315
OY 301 TTGACATCTGGGGCCAGAGAACCTTGTCACCGTCTCTCA 342
DB 316 TTGACTACTGGGGCCAGAGAACCTTGTCACCGTCTCTCA 357
```

```
RESULT 15
US-10-530-27
; Sequence 27, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-530-27
```

```
Query Match 77.5%; Score 265.2; DB 16; Length 358;
Best Local Similarity 88.0%; Pred. No. 4.1e-76;
Matches 301; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
```

```
OY 4 GAGTCTGGCCCGCAGAGCTGTGAAGCCTTGACAGACCCCTGCTCAGCTGGCTGTCTCT 63
DB 16 GAGTCGGGCCCGCAGAGCTGTGAAGCCTTGACAGACCCCTGCTCAGCTGTCTCT 75
OY 64 GCGGCTCCATCCGAGTGTGTACTACTGAGTTGATCCGCCAACCAGGGAG 123
DB 76 GGTGGCTCCATCCAGTGTGTACTACTGAGTTGATCCGCCAACCAGGGAG 135
OY 124 GCGCTGAGTGTGTGTGTGTATCATATCAAGTGGAAACACCTTCAACACCCGTCTC 183
DB 136 GCGCTGAGTGTGTGTGTGTATCATATCAAGTGGAAACACCTTCAACACCCGTCTC 195
OY 184 AAGAGTGAATTTGCATGTGGTGTAGACACGCTGAGAACAGTCTCTCCAGGCTGAG 243
DB 196 AAGAGTGAATTTGCATGTGGTGTAGACACGCTGAGAACAGTCTCTCCAGGCTGAG 255
OY 244 TCTGTGACTGCGCGGACACGCGGTGATTAATCTGTGCGAGGTTAGAGCTTAC 300
DB 256 TCTGTGACTGCGCGGACACGCGGTGATTAATCTGTGCGAGGTTAGAGCTTAC 315
OY 301 TTGACATCTGGGGCCAGAGAACCTTGTCACCGTCTCTCA 342
DB 316 TTGACTACTGGGGCCAGAGAACCTTGTCACCGTCTCTCA 357
```

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Job time : 513.827 secs

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